

- Alignment No. 8372
- gi No. 1666232
- % Identity 93.4
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8373
- gi No. 1666234
- % Identity 89.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8374
- gi No. 1669387
- % Identity 92.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8375
- gi No. 1669389
- % Identity 92.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8376
- gi No. 167589
- % Identity 88
- Alignment Length 83
- Location of Alignment in SEQ ID NO 923: from 25 to 107

- Alignment No. 8377
- gi No. 167600
- % Identity 90.2
- Alignment Length 61
- Location of Alignment in SEQ ID NO 923: from 47 to 107

- Alignment No. 8378
- gi No. 167605
- % Identity 87.7
- Alignment Length 65
- Location of Alignment in SEQ ID NO 923: from 43 to 107

- Alignment No. 8379
- gi No. 167612
- % Identity 88.5
- Alignment Length 87
- Location of Alignment in SEQ ID NO 923: from 21 to 107

- Alignment No. 8380
- gi No. 167642
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 923: from 20 to 107

- Alignment No. 8381
- gi No. 167652
- % Identity 90.7
- Alignment Length 54
- Location of Alignment in SEQ ID NO 923: from 54 to 107

- Alignment No. 8382

- gi No. 168404
- % Identity 84.8
- Alignment Length 138
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8383
- gi No. 1703100
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8384
- gi No. 1703101
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8385
- gi No. 1703102
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8386
- gi No. 1703103
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8387
- gi No. 1703106
- % Identity 87.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8388
- gi No. 1703107
- % Identity 88.3
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8389
- gi No. 1703108
- % Identity 98.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8390
- gi No. 1703109
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8391
- gi No. 1703110
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8392
- gi No. 1703111

- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8393
- gi No. 1703112
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8394
- gi No. 1703114
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8395
- gi No. 1703115
- % Identity 92.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8396
- gi No. 1703116
- % Identity 85.3
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8397
- gi No. 1703117
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8398
- gi No. 1703118
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8399
- gi No. 1703119
- % Identity 92
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8400
- gi No. 1703120
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8401
- gi No. 1703121
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8402
- gi No. 1703122
- % Identity 86.1

- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8403
- gi No. 1703123
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8404
- gi No. 1703124
- % Identity 83.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8405
- gi No. 1703125
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8406
- gi No. 1703127
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8407
- gi No. 1703128
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8408
- gi No. 1703129
- % Identity 93.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8409
- gi No. 1703130
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8410
- gi No. 1703131
- % Identity 92
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8411
- gi No. 1703132
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8412
- gi No. 1703133
- % Identity 86.1
- Alignment Length 137

- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8413
- gi No. 1703134
- % Identity 83.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8414
- gi No. 1703135
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8415
- gi No. 1703136
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8416
- gi No. 1703137
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8417
- gi No. 1703138
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8418
- gi No. 1703139
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8419
- gi No. 1703140
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8420
- gi No. 1703141
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8421
- gi No. 1703142
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8422
- gi No. 1703147
- % Identity 78.7
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8423
 - gi No. 1703148
 - % Identity 77.4
 - Alignment Length 137
 - Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8424
 - gi No. 1703149
 - % Identity 82.5
 - Alignment Length 137
 - Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8425
 - gi No. 1703151
 - % Identity 89.7
 - Alignment Length 136
 - Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8426
 - gi No. 1703152
 - % Identity 74.3
 - Alignment Length 136
 - Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8427
 - gi No. 1703153
 - % Identity 81.6
 - Alignment Length 136
 - Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8428
 - gi No. 1703154
 - % Identity 83
 - Alignment Length 141
 - Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8429
 - gi No. 1703156
 - % Identity 83.9
 - Alignment Length 137
 - Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8430
 - gi No. 1703157
 - % Identity 83
 - Alignment Length 141
 - Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8431
 - gi No. 1703158
 - % Identity 86.1
 - Alignment Length 137
 - Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8432
 - gi No. 1703160
 - % Identity 78.1
 - Alignment Length 137
 - Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8433
- gi No. 1703161
- % Identity 70.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8434
- gi No. 178067
- % Identity 82.2
- Alignment Length 90
- Location of Alignment in SEQ ID NO 923: from 1 to 60

- Alignment No. 8435
- gi No. 1813478
- % Identity 72.3
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8436
- gi No. 1871174
- % Identity 86.8
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8437
- gi No. 1882997
- % Identity 79.6
- Alignment Length 108
- Location of Alignment in SEQ ID NO 923: from 1 to 87

- Alignment No. 8438
- gi No. 1883024
- % Identity 83.3
- Alignment Length 108
- Location of Alignment in SEQ ID NO 923: from 1 to 87

- Alignment No. 8439
- gi No. 1883032
- % Identity 78.7
- Alignment Length 108
- Location of Alignment in SEQ ID NO 923: from 1 to 87

- Alignment No. 8440
- gi No. 1906607
- % Identity 89.7
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8441
- gi No. 20322
- % Identity 91.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8442
- gi No. 2072156
- % Identity 81.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8443

- gi No. 2119321
- % Identity 83.7
- Alignment Length 43
- Location of Alignment in SEQ ID NO 923: from 1 to 13

- Alignment No. 8444
- gi No. 2119323
- % Identity 80.3
- Alignment Length 71
- Location of Alignment in SEQ ID NO 923: from 1 to 64

- Alignment No. 8445
- gi No. 2119324
- % Identity 89.6
- Alignment Length 67
- Location of Alignment in SEQ ID NO 923: from 41 to 107

- Alignment No. 8446
- gi No. 2119325
- % Identity 88.9
- Alignment Length 54
- Location of Alignment in SEQ ID NO 923: from 34 to 87

- Alignment No. 8447
- gi No. 2119327
- % Identity 84
- Alignment Length 25
- Location of Alignment in SEQ ID NO 923: from 1 to 12

- Alignment No. 8448
- gi No. 2119330
- % Identity 91.5
- Alignment Length 47
- Location of Alignment in SEQ ID NO 923: from 61 to 107

- Alignment No. 8449
- gi No. 2129524
- % Identity 92
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8450
- gi No. 2129529
- % Identity 92
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8451
- gi No. 2136927
- % Identity 84.1
- Alignment Length 44
- Location of Alignment in SEQ ID NO 923: from 1 to 14

- Alignment No. 8452
- gi No. 2136927
- % Identity 84.7
- Alignment Length 72
- Location of Alignment in SEQ ID NO 923: from 36 to 107

- Alignment No. 8453
- gi No. 223071

- % Identity 87.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8454
- gi No. 2231555
- % Identity 73.9
- Alignment Length 92
- Location of Alignment in SEQ ID NO 923: from 1 to 63

- Alignment No. 8455
- gi No. 2231557
- % Identity 76.1
- Alignment Length 92
- Location of Alignment in SEQ ID NO 923: from 1 to 63

- Alignment No. 8456
- gi No. 2231561
- % Identity 72.8
- Alignment Length 92
- Location of Alignment in SEQ ID NO 923: from 1 to 63

- Alignment No. 8457
- gi No. 223597
- % Identity 73
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8458
- gi No. 223855
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8459
- gi No. 224304
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8460
- gi No. 224305
- % Identity 87.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8461
- gi No. 224306
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8462
- gi No. 2244734
- % Identity 96.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8463
- gi No. 225100
- % Identity 78.8

- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8464
- gi No. 2253214
- % Identity 94.8
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86

- Alignment No. 8465
- gi No. 2253217
- % Identity 84.5
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86

- Alignment No. 8466
- gi No. 2253219
- % Identity 95.7
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86

- Alignment No. 8467
- gi No. 2253221
- % Identity 84.3
- Alignment Length 115
- Location of Alignment in SEQ ID NO 923: from 1 to 86

- Alignment No. 8468
- gi No. 2253223
- % Identity 76.7
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86

- Alignment No. 8469
- gi No. 2289966
- % Identity 84.5
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86

- Alignment No. 8470
- gi No. 2289971
- % Identity 81.9
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86

- Alignment No. 8471
- gi No. 2289975
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8472
- gi No. 229690
- % Identity 84.3
- Alignment Length 134
- Location of Alignment in SEQ ID NO 923: from 1 to 104

- Alignment No. 8473
- gi No. 2304965
- % Identity 85.4
- Alignment Length 137

- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8474
- gi No. 2304969
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8475
- gi No. 231494
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8476
- gi No. 231495
- % Identity 94.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8477
- gi No. 231496
- % Identity 94.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8478
- gi No. 231498
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8479
- gi No. 231499
- % Identity 94.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8480
- gi No. 231501
- % Identity 94.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8481
- gi No. 231503
- % Identity 94.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8482
- gi No. 231504
- % Identity 94.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8483
- gi No. 231505
- % Identity 94.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8484
- gi No. 231506
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8485
- gi No. 2315847
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8486
- gi No. 2315849
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8487
- gi No. 2318133
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8488
- gi No. 2318135
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8489
- gi No. 2492664
- % Identity 84.7
- Alignment Length 118
- Location of Alignment in SEQ ID NO 923: from 1 to 88

- Alignment No. 8490
- gi No. 2492666
- % Identity 82
- Alignment Length 111
- Location of Alignment in SEQ ID NO 923: from 1 to 81

- Alignment No. 8491
- gi No. 2492667
- % Identity 96.9
- Alignment Length 32
- Location of Alignment in SEQ ID NO 923: from 76 to 107

- Alignment No. 8492
- gi No. 2492668
- % Identity 83
- Alignment Length 141
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8493
- gi No. 2492669
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8494
- gi No. 2492670
- % Identity 82.2
- Alignment Length 129
- Location of Alignment in SEQ ID NO 923: from 1 to 99

- Alignment No. 8495
- gi No. 2492671
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8496
- gi No. 2492672
- % Identity 82.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8497
- gi No. 2492674
- % Identity 76.8
- Alignment Length 139
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8498
- gi No. 2588914
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8499
- gi No. 2624850
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8500
- gi No. 2641233
- % Identity 74.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 923: from 1 to 82

- Alignment No. 8501
- gi No. 2641235
- % Identity 73.2
- Alignment Length 112
- Location of Alignment in SEQ ID NO 923: from 1 to 82

- Alignment No. 8502
- gi No. 2665740
- % Identity 77.2
- Alignment Length 123
- Location of Alignment in SEQ ID NO 923: from 1 to 93

- Alignment No. 8503
- gi No. 2673902
- % Identity 86.8
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8504

- gi No. 2706871
- % Identity 91.1
- Alignment Length 56
- Location of Alignment in SEQ ID NO 923: from 52 to 107

- Alignment No. 8505
- gi No. 2724046
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8506
- gi No. 2738264
- % Identity 80
- Alignment Length 30
- Location of Alignment in SEQ ID NO 923: from 1 to 26

- Alignment No. 8507
- gi No. 2829750
- % Identity 83.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8508
- gi No. 2829754
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8509
- gi No. 2829755
- % Identity 83.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8510
- gi No. 2833326
- % Identity 87.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8511
- gi No. 2944389
- % Identity 92
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8512
- gi No. 294850
- % Identity 88
- Alignment Length 100
- Location of Alignment in SEQ ID NO 923: from 8 to 107

- Alignment No. 8513
- gi No. 294852
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8514
- gi No. 2967678

- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8515
- gi No. 2982279
- % Identity 96.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 923: from 55 to 107

- Alignment No. 8516
- gi No. 2996154
- % Identity 91.3
- Alignment Length 23
- Location of Alignment in SEQ ID NO 923: from 85 to 107

- Alignment No. 8517
- gi No. 3036959
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8518
- gi No. 3044210
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8519
- gi No. 3046986
- % Identity 77.2
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8520
- gi No. 309090
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8521
- gi No. 3107919
- % Identity 89.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8522
- gi No. 311755
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8523
- gi No. 3121741
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8524
- gi No. 3121742
- % Identity 85.4

- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8525
- gi No. 3123181
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8526
- gi No. 3127131
- % Identity 87.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8527
- gi No. 3127133
- % Identity 92.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8528
- gi No. 3127135
- % Identity 89.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8529
- gi No. 3127137
- % Identity 83.8
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 106

- Alignment No. 8530
- gi No. 3182886
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8531
- gi No. 3182891
- % Identity 83.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8532
- gi No. 3182892
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8533
- gi No. 3182893
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8534
- gi No. 3182894
- % Identity 86.1
- Alignment Length 137

- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8535
- gi No. 3182895
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8536
- gi No. 3182896
- % Identity 77.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8537
- gi No. 3182897
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8538
- gi No. 3182898
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8539
- gi No. 3182899
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8540
- gi No. 3182902
- % Identity 87.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8541
- gi No. 3182903
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8542
- gi No. 3182904
- % Identity 77.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8543
- gi No. 3182905
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8544
- gi No. 3182906
- % Identity 78.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8545
- gi No. 321010
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 923: from 22 to 35

- Alignment No. 8546
- gi No. 3219758
- % Identity 94.8
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86

- Alignment No. 8547
- gi No. 3219759
- % Identity 94
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86

- Alignment No. 8548
- gi No. 3219760
- % Identity 94.8
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86

- Alignment No. 8549
- gi No. 3219761
- % Identity 94
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86

- Alignment No. 8550
- gi No. 3219762
- % Identity 94
- Alignment Length 117
- Location of Alignment in SEQ ID NO 923: from 1 to 87

- Alignment No. 8551
- gi No. 3219763
- % Identity 91.4
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86

- Alignment No. 8552
- gi No. 3219764
- % Identity 94.8
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86

- Alignment No. 8553
- gi No. 3219765
- % Identity 96.6
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86

- Alignment No. 8554
- gi No. 3219766
- % Identity 94
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86

- Alignment No. 8555
- gi No. 3219767
- % Identity 95.6
- Alignment Length 114
- Location of Alignment in SEQ ID NO 923: from 1 to 85
- Alignment No. 8556
- gi No. 3219768
- % Identity 95.7
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
- Alignment No. 8557
- gi No. 3219769
- % Identity 94.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 923: from 1 to 86
- Alignment No. 8558
- gi No. 3219770
- % Identity 89.7
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
- Alignment No. 8559
- gi No. 3219771
- % Identity 93.1
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
- Alignment No. 8560
- gi No. 3219772
- % Identity 95.7
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
- Alignment No. 8561
- gi No. 3219773
- % Identity 94
- Alignment Length 116
- Location of Alignment in SEQ ID NO 923: from 1 to 86
- Alignment No. 8562
- gi No. 3249717
- % Identity 79.6
- Alignment Length 98
- Location of Alignment in SEQ ID NO 923: from 1 to 68
- Alignment No. 8563
- gi No. 3287956
- % Identity 92
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8564
- gi No. 3319951
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8565

- gi No. 3328
- % Identity 80.3
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8566
- gi No. 3336984
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8567
- gi No. 3348131
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8568
- gi No. 3386376
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8569
- gi No. 3386380
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8570
- gi No. 3386382
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8571
- gi No. 3396073
- % Identity 83.5
- Alignment Length 115
- Location of Alignment in SEQ ID NO 923: from 1 to 85

- Alignment No. 8572
- gi No. 3420239
- % Identity 94.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8573
- gi No. 3421457
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8574
- gi No. 3550350
- % Identity 82.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8575
- gi No. 3642631

- % Identity 80.7
- Alignment Length 88
- Location of Alignment in SEQ ID NO 923: from 1 to 59

- Alignment No. 8576
- gi No. 3746936
- % Identity 89.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8577
- gi No. 3746938
- % Identity 94.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8578
- gi No. 3746940
- % Identity 91.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8579
- gi No. 3746942
- % Identity 94.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8580
- gi No. 3860317
- % Identity 96.1
- Alignment Length 103
- Location of Alignment in SEQ ID NO 923: from 5 to 107

- Alignment No. 8581
- gi No. 3860544
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8582
- gi No. 387082
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8583
- gi No. 3879474
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8584
- gi No. 3880219
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8585
- gi No. 3907620
- % Identity 81

- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8586
- gi No. 3907622
- % Identity 76.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8587
- gi No. 3912969
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8588
- gi No. 3924630
- % Identity 87.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8589
- gi No. 399003
- % Identity 82.3
- Alignment Length 141
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8590
- gi No. 4009328
- % Identity 83.7
- Alignment Length 49
- Location of Alignment in SEQ ID NO 923: from 1 to 19

- Alignment No. 8591
- gi No. 409694
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8592
- gi No. 4105262
- % Identity 91.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8593
- gi No. 4139264
- % Identity 97.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8594
- gi No. 4204812
- % Identity 82.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8595
- gi No. 4220623
- % Identity 85.8
- Alignment Length 120

- Location of Alignment in SEQ ID NO 923: from 1 to 90
- Alignment No. 8596
- gi No. 4235277
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8597
- gi No. 4249564
- % Identity 82.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8598
- gi No. 4376057
- % Identity 83.8
- Alignment Length 105
- Location of Alignment in SEQ ID NO 923: from 1 to 75
- Alignment No. 8599
- gi No. 4490385
- % Identity 82.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8600
- gi No. 4501881
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8601
- gi No. 4501883
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8602
- gi No. 4501885
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8603
- gi No. 4501887
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8604
- gi No. 4501889
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8605
- gi No. 4574288
- % Identity 86.3
- Alignment Length 131
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8606
- gi No. 4587217
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8607
- gi No. 461465
- % Identity 94.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8608
- gi No. 467215
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8609
- gi No. 4691448
- % Identity 93.6
- Alignment Length 94
- Location of Alignment in SEQ ID NO 923: from 1 to 71

- Alignment No. 8610
- gi No. 476332
- % Identity 84.9
- Alignment Length 119
- Location of Alignment in SEQ ID NO 923: from 1 to 89

- Alignment No. 8611
- gi No. 476768
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8612
- gi No. 477248
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8613
- gi No. 481515
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8614
- gi No. 482262
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 923: from 48 to 65

- Alignment No. 8615
- gi No. 482696
- % Identity 81.3
- Alignment Length 113
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8616
- gi No. 4837604
- % Identity 75.2
- Alignment Length 129
- Location of Alignment in SEQ ID NO 923: from 1 to 99

- Alignment No. 8617
- gi No. 4837606
- % Identity 77.5
- Alignment Length 129
- Location of Alignment in SEQ ID NO 923: from 1 to 99

- Alignment No. 8618
- gi No. 4837610
- % Identity 72.1
- Alignment Length 129
- Location of Alignment in SEQ ID NO 923: from 1 to 99

- Alignment No. 8619
- gi No. 4850238
- % Identity 75.2
- Alignment Length 129
- Location of Alignment in SEQ ID NO 923: from 1 to 99

- Alignment No. 8620
- gi No. 4850240
- % Identity 77.5
- Alignment Length 129
- Location of Alignment in SEQ ID NO 923: from 1 to 99

- Alignment No. 8621
- gi No. 4885049
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8622
- gi No. 4887630
- % Identity 81
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8623
- gi No. 4902905
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8624
- gi No. 49864
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8625
- gi No. 49868
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8626

- gi No. 5031514
- % Identity 80
- Alignment Length 135
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8627
- gi No. 5031524
- % Identity 73.5
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 106
- Alignment No. 8628
- gi No. 5053109
- % Identity 79.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8629
- gi No. 5114428
- % Identity 87.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8630
- gi No. 5230839
- % Identity 78.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8631
- gi No. 5230841
- % Identity 97.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8632
- gi No. 543484
- % Identity 77.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8633
- gi No. 543766
- % Identity 82.4
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8634
- gi No. 543767
- % Identity 77.1
- Alignment Length 144
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8635
- gi No. 543768
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8636
- gi No. 544861

- % Identity 95.6
- Alignment Length 114
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8637
- gi No. 55675
- % Identity 88
- Alignment Length 25
- Location of Alignment in SEQ ID NO 923: from 83 to 107
- Alignment No. 8638
- gi No. 5578749
- % Identity 71.7
- Alignment Length 46
- Location of Alignment in SEQ ID NO 923: from 1 to 16
- Alignment No. 8639
- gi No. 5597005
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8640
- gi No. 567192
- % Identity 84.9
- Alignment Length 119
- Location of Alignment in SEQ ID NO 923: from 1 to 89
- Alignment No. 8641
- gi No. 5702223
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8642
- gi No. 5702225
- % Identity 83.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8643
- gi No. 5702227
- % Identity 83.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8644
- gi No. 5702229
- % Identity 86.5
- Alignment Length 89
- Location of Alignment in SEQ ID NO 923: from 19 to 107
- Alignment No. 8645
- gi No. 5714394
- % Identity 86.5
- Alignment Length 37
- Location of Alignment in SEQ ID NO 923: from 71 to 107
- Alignment No. 8646
- gi No. 5726016
- % Identity 94.1

- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8647
- gi No. 5726018
- % Identity 94.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8648
- gi No. 5726020
- % Identity 87.5
- Alignment Length 136
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8649
- gi No. 5751
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8650
- gi No. 576368
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8651
- gi No. 602958
- % Identity 92
- Alignment Length 50
- Location of Alignment in SEQ ID NO 923: from 1 to 20

- Alignment No. 8652
- gi No. 627304
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8653
- gi No. 627834
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8654
- gi No. 63018
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8655
- gi No. 630802
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8656
- gi No. 631529
- % Identity 76.3
- Alignment Length 97

- Location of Alignment in SEQ ID NO 923: from 9 to 105
- Alignment No. 8657
- gi No. 64509
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8658
- gi No. 6628
- % Identity 83.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8659
- gi No. 693709
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8660
- gi No. 71611
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8661
- gi No. 71614
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8662
- gi No. 71616
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8663
- gi No. 71620
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8664
- gi No. 71621
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8665
- gi No. 71622
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8666
- gi No. 71625
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8667
- gi No. 71627
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8668
- gi No. 71629
- % Identity 87.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8669
- gi No. 71634
- % Identity 90.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8670
- gi No. 71638
- % Identity 91.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8671
- gi No. 71639
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8672
- gi No. 728791
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8673
- gi No. 728792
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8674
- gi No. 728793
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8675
- gi No. 728796
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8676
- gi No. 728798
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8677
- gi No. 797290
- % Identity 83.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8678
- gi No. 809561
- % Identity 86.1
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8679
- gi No. 818016
- % Identity 87.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 923: from 15 to 107
- Alignment No. 8680
- gi No. 825616
- % Identity 86.2
- Alignment Length 123
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8681
- gi No. 83999
- % Identity 71.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8682
- gi No. 84000
- % Identity 71.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8683
- gi No. 84082
- % Identity 87.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8684
- gi No. 84344
- % Identity 78.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8685
- gi No. 84751
- % Identity 86.9
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8686
- gi No. 84879
- % Identity 88.3
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107
- Alignment No. 8687

- gi No. 84880
- % Identity 92.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 923: from 55 to 107

- Alignment No. 8688
- gi No. 85358
- % Identity 83.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8689
- gi No. 85495
- % Identity 81.1
- Alignment Length 90
- Location of Alignment in SEQ ID NO 923: from 1 to 60

- Alignment No. 8690
- gi No. 86169
- % Identity 80.6
- Alignment Length 129
- Location of Alignment in SEQ ID NO 923: from 1 to 99

- Alignment No. 8691
- gi No. 86742
- % Identity 84.7
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8692
- gi No. 871546
- % Identity 83.2
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8693
- gi No. 90263
- % Identity 85.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 923: from 1 to 107

- Alignment No. 8694
- gi No. 91918
- % Identity 95.2
- Alignment Length 42
- Location of Alignment in SEQ ID NO 923: from 66 to 107

- Alignment No. 8695
- gi No. 950002
- % Identity 81.6
- Alignment Length 87
- Location of Alignment in SEQ ID NO 923: from 1 to 57

Maximum Length Sequence corresponding to clone ID 159438

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 924
- Ceres seq_id 1499214

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 925
- Ceres seq_id 1499215
- Location of start within SEQ ID NO 924: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8696
- EF hand
- Location within SEQ ID NO 925: from 40 to 68 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 926
- Ceres seq_id 1499216
- Location of start within SEQ ID NO 924: at 437 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8697
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 926: from 15 to 66 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8698
- gi No. 2129684
- % Identity 79.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 926: from 15 to 48
- Alignment No. 8699
- gi No. 2827715
- % Identity 82.6
- Alignment Length 163
- Location of Alignment in SEQ ID NO 926: from 15 to 175

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 927
- Ceres seq_id 1499217
- Location of start within SEQ ID NO 924: at 446 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8700
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 927: from 12 to 63 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8701
- gi No. 2129684
- % Identity 79.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 927: from 12 to 45
- Alignment No. 8702
- gi No. 2827715
- % Identity 82.6
- Alignment Length 163
- Location of Alignment in SEQ ID NO 927: from 12 to 172

Maximum Length Sequence corresponding to clone ID 159568

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 928
- Ceres seq_id 1499218

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 929
- Ceres seq_id 1499219
- Location of start within SEQ ID NO 928: at 305 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8703
- Tetrapyrrole (Corrin/Porphyrin) Methylases.
- Location within SEQ ID NO 929: from 116 to 329 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8704
- gi No. 1146165
- % Identity 100
- Alignment Length 369
- Location of Alignment in SEQ ID NO 929: from 1 to 369

- Alignment No. 8705
- gi No. 1490606
- % Identity 99.2
- Alignment Length 369
- Location of Alignment in SEQ ID NO 929: from 1 to 369

- Alignment No. 8706
- gi No. 1531541
- % Identity 73.1
- Alignment Length 334
- Location of Alignment in SEQ ID NO 929: from 35 to 368

Maximum Length Sequence corresponding to clone ID 159614

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 930
- Ceres seq_id 1499220

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 931
- Ceres seq_id 1499221
- Location of start within SEQ ID NO 930: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8707
- SRP54-type protein
- Location within SEQ ID NO 931: from 146 to 427 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8708
- gi No. 2911886
- % Identity 70.7
- Alignment Length 133
- Location of Alignment in SEQ ID NO 931: from 296 to 427

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 932
- Ceres seq_id 1499222
- Location of start within SEQ ID NO 930: at 270 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8709
- SRP54-type protein

- Location within SEQ ID NO 932: from 57 to 338 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8710
- gi No. 2911886
- % Identity 70.7
- Alignment Length 133
- Location of Alignment in SEQ ID NO 932: from 207 to 338

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 933
- Ceres seq_id 1499223
- Location of start within SEQ ID NO 930: at 273 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8711
- SRP54-type protein
- Location within SEQ ID NO 933: from 56 to 337 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8712
- gi No. 2911886
- % Identity 70.7
- Alignment Length 133
- Location of Alignment in SEQ ID NO 933: from 206 to 337

Maximum Length Sequence corresponding to clone ID 205489

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 934
- Ceres seq_id 1499224

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 935
- Ceres seq_id 1499225
- Location of start within SEQ ID NO 934: at 146 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8713
- Zinc-binding dehydrogenases
- Location within SEQ ID NO 935: from 18 to 124 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8714
- gi No. 2498731
- % Identity 84.3
- Alignment Length 127
- Location of Alignment in SEQ ID NO 935: from 1 to 124

- Alignment No. 8715
- gi No. 2498732
- % Identity 97.6
- Alignment Length 125
- Location of Alignment in SEQ ID NO 935: from 1 to 124

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 936
- Ceres seq_id 1499226
- Location of start within SEQ ID NO 934: at 302 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8716
- Zinc-binding dehydrogenases
- Location within SEQ ID NO 936: from 1 to 72 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8717
- gi No. 2498731
- % Identity 84.3
- Alignment Length 127
- Location of Alignment in SEQ ID NO 936: from 1 to 72
- Alignment No. 8718
- gi No. 2498732
- % Identity 97.6
- Alignment Length 125
- Location of Alignment in SEQ ID NO 936: from 1 to 72

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 937
- Ceres seq_id 1499227
- Location of start within SEQ ID NO 934: at 314 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8719
- Zinc-binding dehydrogenases
- Location within SEQ ID NO 937: from 1 to 68 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8720
- gi No. 2498731
- % Identity 84.3
- Alignment Length 127
- Location of Alignment in SEQ ID NO 937: from 1 to 68
- Alignment No. 8721
- gi No. 2498732
- % Identity 97.6
- Alignment Length 125
- Location of Alignment in SEQ ID NO 937: from 1 to 68

Maximum Length Sequence corresponding to clone ID 205976

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 938
- Ceres seq_id 1499228

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 939
- Ceres seq_id 1499229
- Location of start within SEQ ID NO 938: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8722
- gi No. 4836868
- % Identity 98.8
- Alignment Length 509
- Location of Alignment in SEQ ID NO 939: from 20 to 528

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 940
 - Ceres seq_id 1499230
 - Location of start within SEQ ID NO 938: at 59 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 8723
 - gi No. 4836868
 - % Identity 98.8
 - Alignment Length 509
 - Location of Alignment in SEQ ID NO 940: from 1 to 509

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 941
 - Ceres seq_id 1499231
 - Location of start within SEQ ID NO 938: at 374 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 8724
 - gi No. 4836868
 - % Identity 98.8
 - Alignment Length 509
 - Location of Alignment in SEQ ID NO 941: from 1 to 404

Maximum Length Sequence corresponding to clone ID 206045

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 942
 - Ceres seq_id 1499232
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 943
 - Ceres seq_id 1499233
 - Location of start within SEQ ID NO 942: at 115 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8725
- Mucin-like glycoprotein
- Location within SEQ ID NO 943: from 8 to 89 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 206237

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 944
 - Ceres seq_id 1499242
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 945
 - Ceres seq_id 1499243
 - Location of start within SEQ ID NO 944: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8726
- Pectinesterase
- Location within SEQ ID NO 945: from 70 to 123 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 946
- Ceres seq_id 1499244
- Location of start within SEQ ID NO 944: at 872 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 947
- Ceres seq_id 1499245
- Location of start within SEQ ID NO 944: at 995 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 206518

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 948
- Ceres seq_id 1499250

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 949
- Ceres seq_id 1499251
- Location of start within SEQ ID NO 948: at 125 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8727
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 949: from 102 to 404 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8728
- gi No. 2911716
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 949: from 377 to 387

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 950
- Ceres seq_id 1499252
- Location of start within SEQ ID NO 948: at 287 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8729
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 950: from 48 to 350 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8730
- gi No. 2911716
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 950: from 323 to 333

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 951

- Ceres seq_id 1499253
- Location of start within SEQ ID NO 948: at 356 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8731
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 951: from 25 to 327 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8732
- gi No. 2911716
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 951: from 300 to 310

Maximum Length Sequence corresponding to clone ID 207043

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 952
- Ceres seq_id 1499254

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 953
- Ceres seq_id 1499255
- Location of start within SEQ ID NO 952: at 23 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8733
- gi No. 1946364
- % Identity 100
- Alignment Length 447
- Location of Alignment in SEQ ID NO 953: from 83 to 529

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 954
- Ceres seq_id 1499256
- Location of start within SEQ ID NO 952: at 269 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8734
- gi No. 1946364
- % Identity 100
- Alignment Length 447
- Location of Alignment in SEQ ID NO 954: from 1 to 447

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 955
- Ceres seq_id 1499257
- Location of start within SEQ ID NO 952: at 374 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8735
- gi No. 1946364
- % Identity 100
- Alignment Length 447
- Location of Alignment in SEQ ID NO 955: from 1 to 412

Maximum Length Sequence corresponding to clone ID 207137

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 956
- Ceres seq_id 1499258

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 957
- Ceres seq_id 1499259
- Location of start within SEQ ID NO 956: at 65 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8736
- L1P family of ribosomal proteins
- Location within SEQ ID NO 957: from 124 to 329 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8737
- gi No. 1350625
- % Identity 79.5
- Alignment Length 176
- Location of Alignment in SEQ ID NO 957: from 89 to 264

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 958
- Ceres seq_id 1499260
- Location of start within SEQ ID NO 956: at 95 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8738
- L1P family of ribosomal proteins
- Location within SEQ ID NO 958: from 114 to 319 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8739
- gi No. 1350625
- % Identity 79.5
- Alignment Length 176
- Location of Alignment in SEQ ID NO 958: from 79 to 254

Maximum Length Sequence corresponding to clone ID 207419

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 959
- Ceres seq_id 1499261

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 960
- Ceres seq_id 1499262
- Location of start within SEQ ID NO 959: at 74 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8740
- Zinc finger C-x8-C-x5-C-x3-H type (and similar).
- Location within SEQ ID NO 960: from 235 to 262 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 961
- Ceres seq_id 1499263

- Location of start within SEQ ID NO 959: at 395 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8741
- Zinc finger C-x8-C-x5-C-x3-H type (and similar).
- Location within SEQ ID NO 961: from 128 to 155 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 207558

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 962
- Ceres seq_id 1499264

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 963
- Ceres seq_id 1499265
- Location of start within SEQ ID NO 962: at 96 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8742
- Adhesion lipoprotein
- Location within SEQ ID NO 963: from 182 to 232 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8743
- gi No. 1001307
- % Identity 70.4
- Alignment Length 28
- Location of Alignment in SEQ ID NO 963: from 184 to 210
- Alignment No. 8744
- gi No. 2983552
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 963: from 210 to 220
- Alignment No. 8745
- gi No. 3510254
- % Identity 100
- Alignment Length 398
- Location of Alignment in SEQ ID NO 963: from 1 to 398
- Alignment No. 8746
- gi No. 3560024
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 963: from 181 to 198
- Alignment No. 8747
- gi No. 4206640
- % Identity 98
- Alignment Length 398
- Location of Alignment in SEQ ID NO 963: from 1 to 398
- Alignment No. 8748
- gi No. 4584498
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 963: from 181 to 195

- Alignment No. 8749
- gi No. 539415
- % Identity 81.3
- Alignment Length 16
- Location of Alignment in SEQ ID NO 963: from 181 to 196

- Alignment No. 8750
- gi No. 539415
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 963: from 182 to 198

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 964
- Ceres_seq_id 1499266
- Location of start within SEQ ID NO 962: at 258 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8751
- Adhesion lipoprotein
- Location within SEQ ID NO 964: from 128 to 178 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8752
- gi No. 1001307
- % Identity 70.4
- Alignment Length 28
- Location of Alignment in SEQ ID NO 964: from 130 to 156

- Alignment No. 8753
- gi No. 2983552
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 964: from 156 to 166

- Alignment No. 8754
- gi No. 3510254
- % Identity 100
- Alignment Length 398
- Location of Alignment in SEQ ID NO 964: from 1 to 344

- Alignment No. 8755
- gi No. 3560024
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 964: from 127 to 144

- Alignment No. 8756
- gi No. 4206640
- % Identity 98
- Alignment Length 398
- Location of Alignment in SEQ ID NO 964: from 1 to 344

- Alignment No. 8757
- gi No. 4584498
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 964: from 127 to 141

- Alignment No. 8758
- gi No. 539415
- % Identity 81.3
- Alignment Length 16
- Location of Alignment in SEQ ID NO 964: from 127 to 142
- Alignment No. 8759
- gi No. 539415
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 964: from 128 to 144

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 965
- Ceres seq_id 1499267
- Location of start within SEQ ID NO 962: at 300 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8760
- Adhesion lipoprotein
- Location within SEQ ID NO 965: from 114 to 164 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8761
- gi No. 1001307
- % Identity 70.4
- Alignment Length 28
- Location of Alignment in SEQ ID NO 965: from 116 to 142
- Alignment No. 8762
- gi No. 2983552
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 965: from 142 to 152
- Alignment No. 8763
- gi No. 3510254
- % Identity 100
- Alignment Length 398
- Location of Alignment in SEQ ID NO 965: from 1 to 330
- Alignment No. 8764
- gi No. 3560024
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 965: from 113 to 130
- Alignment No. 8765
- gi No. 4206640
- % Identity 98
- Alignment Length 398
- Location of Alignment in SEQ ID NO 965: from 1 to 330
- Alignment No. 8766
- gi No. 4584498
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 965: from 113 to 127
- Alignment No. 8767

- gi No. 539415
- % Identity 81.3
- Alignment Length 16
- Location of Alignment in SEQ ID NO 965: from 113 to 128
- Alignment No. 8768
- gi No. 539415
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 965: from 114 to 130

Maximum Length Sequence corresponding to clone ID 218944

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 966
- Ceres seq_id 1499310

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 967
- Ceres seq_id 1499311
- Location of start within SEQ ID NO 966: at 202 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8769
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 967: from 40 to 109 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 968
- Ceres seq_id 1499312
- Location of start within SEQ ID NO 966: at 232 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8770
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 968: from 30 to 99 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 969
- Ceres seq_id 1499313
- Location of start within SEQ ID NO 966: at 256 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8771
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 969: from 22 to 91 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 219286

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 970
- Ceres seq_id 1499314

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 971
- Ceres seq_id 1499315

- Location of start within SEQ ID NO 970: at 155 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8772
- 60s Acidic ribosomal protein
- Location within SEQ ID NO 971: from 73 to 129 aa.
- Alignment No. 8773
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 971: from 64 to 167 aa.
- Alignment No. 8774
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 971: from 75 to 171 aa.
- Alignment No. 8775
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 971: from 99 to 171 aa.
- Alignment No. 8776
- Syndecan domain
- Location within SEQ ID NO 971: from 1 to 142 aa.
- Alignment No. 8777
- 11-S plant seed storage protein
- Location within SEQ ID NO 971: from 76 to 170 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8778
- gi No. 482700
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 971: from 151 to 161

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 972
- Ceres seq_id 1499316
- Location of start within SEQ ID NO 970: at 266 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8779
- 60s Acidic ribosomal protein
- Location within SEQ ID NO 972: from 36 to 92 aa.
- Alignment No. 8780
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 972: from 27 to 130 aa.
- Alignment No. 8781
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 972: from 38 to 134 aa.
- Alignment No. 8782
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 972: from 62 to 134 aa.
- Alignment No. 8783
- Syndecan domain
- Location within SEQ ID NO 972: from 1 to 105 aa.

- Alignment No. 8784
- 11-S plant seed storage protein
- Location within SEQ ID NO 972: from 39 to 133 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8785
- gi No. 482700
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 972: from 114 to 124

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 973
- Ceres seq_id 1499317
- Location of start within SEQ ID NO 970: at 285 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 219894

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 974
- Ceres seq_id 1499344

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 975
- Ceres seq_id 1499345
- Location of start within SEQ ID NO 974: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 976
- Ceres seq_id 1499346
- Location of start within SEQ ID NO 974: at 90 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8786
- gi No. 3108209
- % Identity 78.8
- Alignment Length 179
- Location of Alignment in SEQ ID NO 976: from 35 to 213

Maximum Length Sequence corresponding to clone ID 220920

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 977
- Ceres seq_id 1499353

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 978
- Ceres seq_id 1499354
- Location of start within SEQ ID NO 977: at 106 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8787

- gi No. 129805
- % Identity 72.4
- Alignment Length 29
- Location of Alignment in SEQ ID NO 978: from 28 to 56
-
- Alignment No. 8788
- gi No. 1491776
- % Identity 75.9
- Alignment Length 29
- Location of Alignment in SEQ ID NO 978: from 28 to 56
-
- Alignment No. 8789
- gi No. 1633130
- % Identity 73.1
- Alignment Length 26
- Location of Alignment in SEQ ID NO 978: from 31 to 56
-
- Alignment No. 8790
- gi No. 520570
- % Identity 71.9
- Alignment Length 32
- Location of Alignment in SEQ ID NO 978: from 24 to 55

Maximum Length Sequence corresponding to clone ID 221164

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 979
- Ceres seq_id 1499362

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 980
- Ceres seq_id 1499363
- Location of start within SEQ ID NO 979: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 981
- Ceres seq_id 1499364
- Location of start within SEQ ID NO 979: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8791
- EF hand
- Location within SEQ ID NO 981: from 45 to 73 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8792
- gi No. 115480
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 981: from 47 to 80
-
- Alignment No. 8793
- gi No. 115500
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 981: from 47 to 80
-
- Alignment No. 8794

- gi No. 115534
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 981: from 47 to 80

- Alignment No. 8795
- gi No. 16225
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 981: from 47 to 80

- Alignment No. 8796
- gi No. 167676
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 981: from 47 to 80

- Alignment No. 8797
- gi No. 189020
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 981: from 70 to 80

- Alignment No. 8798
- gi No. 189022
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 981: from 70 to 80

- Alignment No. 8799
- gi No. 2119353
- % Identity 70.5
- Alignment Length 44
- Location of Alignment in SEQ ID NO 981: from 37 to 80

- Alignment No. 8800
- gi No. 2129557
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 981: from 38 to 61

- Alignment No. 8801
- gi No. 2267084
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 981: from 47 to 80

- Alignment No. 8802
- gi No. 228408
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 981: from 46 to 80

- Alignment No. 8803
- gi No. 4379369
- % Identity 70.5
- Alignment Length 44
- Location of Alignment in SEQ ID NO 981: from 37 to 80

- Alignment No. 8804
- gi No. 71673

- % Identity 70.5
- Alignment Length 44
- Location of Alignment in SEQ ID NO 981: from 37 to 80

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 982
- Ceres seq_id 1499365
- Location of start within SEQ ID NO 979: at 98 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8805
- EF hand
- Location within SEQ ID NO 982: from 13 to 41 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8806
- gi No. 115480
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 982: from 15 to 48
- Alignment No. 8807
- gi No. 115500
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 982: from 15 to 48
- Alignment No. 8808
- gi No. 115534
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 982: from 15 to 48
- Alignment No. 8809
- gi No. 16225
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 982: from 15 to 48
- Alignment No. 8810
- gi No. 167676
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 982: from 15 to 48
- Alignment No. 8811
- gi No. 189020
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 982: from 38 to 48
- Alignment No. 8812
- gi No. 189022
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 982: from 38 to 48
- Alignment No. 8813
- gi No. 2119353
- % Identity 70.5

- Alignment Length 44
- Location of Alignment in SEQ ID NO 982: from 5 to 48
- Alignment No. 8814
- gi No. 2129557
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 982: from 6 to 29
- Alignment No. 8815
- gi No. 2267084
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 982: from 15 to 48
- Alignment No. 8816
- gi No. 228408
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 982: from 14 to 48
- Alignment No. 8817
- gi No. 4379369
- % Identity 70.5
- Alignment Length 44
- Location of Alignment in SEQ ID NO 982: from 5 to 48
- Alignment No. 8818
- gi No. 71673
- % Identity 70.5
- Alignment Length 44
- Location of Alignment in SEQ ID NO 982: from 5 to 48

Maximum Length Sequence corresponding to clone ID 221169

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 983
- Ceres seq_id 1499370

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 984
- Ceres seq_id 1499371
- Location of start within SEQ ID NO 983: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8819
- gi No. 1070652
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 984: from 68 to 81
- Alignment No. 8820
- gi No. 131007
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 984: from 68 to 81
- Alignment No. 8821
- gi No. 350218
- % Identity 71.4
- Alignment Length 14

- Location of Alignment in SEQ ID NO 984: from 68 to 81

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 985
- Ceres seq_id 1499372
- Location of start within SEQ ID NO 983: at 455 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 986
- Ceres seq_id 1499373
- Location of start within SEQ ID NO 983: at 473 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 221212

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 987
- Ceres seq_id 1499380

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 988
- Ceres seq_id 1499381
- Location of start within SEQ ID NO 987: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8822
- ADP-ribosylation factor family
- Location within SEQ ID NO 988: from 54 to 230 aa.
- Alignment No. 8823
- Ras family
- Location within SEQ ID NO 988: from 70 to 219 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 989
- Ceres seq_id 1499382
- Location of start within SEQ ID NO 987: at 150 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8824
- ADP-ribosylation factor family
- Location within SEQ ID NO 989: from 5 to 181 aa.
- Alignment No. 8825
- Ras family
- Location within SEQ ID NO 989: from 21 to 170 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 990
- Ceres seq_id 1499383

- Location of start within SEQ ID NO 987: at 207 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8826
- ADP-ribosylation factor family
- Location within SEQ ID NO 990: from 1 to 162 aa.
- Alignment No. 8827
- Ras family
- Location within SEQ ID NO 990: from 2 to 151 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 221234

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 991
- Ceres seq_id 1499384

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 992
- Ceres seq_id 1499385
- Location of start within SEQ ID NO 991: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8828
- Papain family cysteine protease
- Location within SEQ ID NO 992: from 123 to 158 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8829
- gi No. 108585
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 992: from 122 to 141
- Alignment No. 8830
- gi No. 1093503
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 992: from 125 to 162
- Alignment No. 8831
- gi No. 115738
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 992: from 125 to 162
- Alignment No. 8832
- gi No. 1340178
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 992: from 125 to 162
- Alignment No. 8833
- gi No. 1498185
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 992: from 125 to 162
- Alignment No. 8834

- gi No. 162042
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 992: from 141 to 159

- Alignment No. 8835
- gi No. 162044
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 992: from 141 to 161

- Alignment No. 8836
- gi No. 1705639
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 992: from 125 to 162

- Alignment No. 8837
- gi No. 1911708
- % Identity 89.5
- Alignment Length 19
- Location of Alignment in SEQ ID NO 992: from 141 to 159

- Alignment No. 8838
- gi No. 2144502
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 992: from 125 to 162

- Alignment No. 8839
- gi No. 2146900
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 992: from 125 to 162

- Alignment No. 8840
- gi No. 2665820
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 992: from 141 to 158

- Alignment No. 8841
- gi No. 2706547
- % Identity 73.7
- Alignment Length 38
- Location of Alignment in SEQ ID NO 992: from 125 to 162

- Alignment No. 8842
- gi No. 2914174
- % Identity 75
- Alignment Length 36
- Location of Alignment in SEQ ID NO 992: from 127 to 162

- Alignment No. 8843
- gi No. 3929737
- % Identity 78.6
- Alignment Length 28
- Location of Alignment in SEQ ID NO 992: from 135 to 162

- Alignment No. 8844
- gi No. 3929819

- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 992: from 144 to 157

- Alignment No. 8845
- gi No. 419920
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 992: from 141 to 159

- Alignment No. 8846
- gi No. 452254
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 992: from 141 to 162

- Alignment No. 8847
- gi No. 541900
- % Identity 70
- Alignment Length 30
- Location of Alignment in SEQ ID NO 992: from 128 to 157

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 993
- Ceres seq_id 1499386
- Location of start within SEQ ID NO 991: at 26 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8848
- Papain family cysteine protease
- Location within SEQ ID NO 993: from 115 to 150 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8849
- gi No. 108585
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 993: from 114 to 133

- Alignment No. 8850
- gi No. 1093503
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 993: from 117 to 154

- Alignment No. 8851
- gi No. 115738
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 993: from 117 to 154

- Alignment No. 8852
- gi No. 1340178
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 993: from 117 to 154

- Alignment No. 8853
- gi No. 1498185
- % Identity 71.1

- Alignment Length 38
- Location of Alignment in SEQ ID NO 993: from 117 to 154
- Alignment No. 8854
- gi No. 162042
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 993: from 133 to 151
- Alignment No. 8855
- gi No. 162044
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 993: from 133 to 153
- Alignment No. 8856
- gi No. 1705639
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 993: from 117 to 154
- Alignment No. 8857
- gi No. 1911708
- % Identity 89.5
- Alignment Length 19
- Location of Alignment in SEQ ID NO 993: from 133 to 151
- Alignment No. 8858
- gi No. 2144502
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 993: from 117 to 154
- Alignment No. 8859
- gi No. 2146900
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 993: from 117 to 154
- Alignment No. 8860
- gi No. 2665820
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 993: from 133 to 150
- Alignment No. 8861
- gi No. 2706547
- % Identity 73.7
- Alignment Length 38
- Location of Alignment in SEQ ID NO 993: from 117 to 154
- Alignment No. 8862
- gi No. 2914174
- % Identity 75
- Alignment Length 36
- Location of Alignment in SEQ ID NO 993: from 119 to 154
- Alignment No. 8863
- gi No. 3929737
- % Identity 78.6
- Alignment Length 28

- Location of Alignment in SEQ ID NO 993: from 127 to 154
- Alignment No. 8864
- gi No. 3929819
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 993: from 136 to 149
- Alignment No. 8865
- gi No. 419920
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 993: from 133 to 151
- Alignment No. 8866
- gi No. 452254
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 993: from 133 to 154
- Alignment No. 8867
- gi No. 541900
- % Identity 70
- Alignment Length 30
- Location of Alignment in SEQ ID NO 993: from 120 to 149

Maximum Length Sequence corresponding to clone ID 222003

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 994
- Ceres seq_id 1499389

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 995
- Ceres seq_id 1499390
- Location of start within SEQ ID NO 994: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8868
- Lipase/Acylhydrolase with GDSL-like motif
- Location within SEQ ID NO 995: from 86 to 145 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 996
- Ceres seq_id 1499391
- Location of start within SEQ ID NO 994: at 157 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8869
- Lipase/Acylhydrolase with GDSL-like motif
- Location within SEQ ID NO 996: from 34 to 93 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 222544

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 997
- Ceres seq_id 1499402

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 998
- Ceres seq_id 1499403
- Location of start within SEQ ID NO 997: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 8870
 - gi No. 400249
 - % Identity 94.4
 - Alignment Length 36
 - Location of Alignment in SEQ ID NO 998: from 17 to 52

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 999
- Ceres seq_id 1499404
- Location of start within SEQ ID NO 997: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1000
- Ceres seq_id 1499405
- Location of start within SEQ ID NO 997: at 49 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8871
- gi No. 400249
- % Identity 94.4
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1000: from 1 to 36

Maximum Length Sequence corresponding to clone ID 222547

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1001
- Ceres seq_id 1499406

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1002
- Ceres seq_id 1499407
- Location of start within SEQ ID NO 1001: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8872
- gi No. 4204294
- % Identity 75.1
- Alignment Length 198
- Location of Alignment in SEQ ID NO 1002: from 54 to 247

Maximum Length Sequence corresponding to clone ID 223028

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1003
- Ceres seq_id 1499408

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1004
- Ceres seq_id 1499409

- Location of start within SEQ ID NO 1003: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1005
- Ceres seq_id 1499410
- Location of start within SEQ ID NO 1003: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8873
- gi No. 5042457
- % Identity 95.5
- Alignment Length 66
- Location of Alignment in SEQ ID NO 1005: from 15 to 80

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1006
- Ceres seq_id 1499411
- Location of start within SEQ ID NO 1003: at 45 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8874
- gi No. 5042457
- % Identity 95.5
- Alignment Length 66
- Location of Alignment in SEQ ID NO 1006: from 1 to 66

Maximum Length Sequence corresponding to clone ID 225428

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1007
- Ceres seq_id 1499412

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1008
- Ceres seq_id 1499413
- Location of start within SEQ ID NO 1007: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1009
- Ceres seq_id 1499414
- Location of start within SEQ ID NO 1007: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8875
- gi No. 113003
- % Identity 95.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1009: from 18 to 41

- Alignment No. 8876
- gi No. 168397
- % Identity 95.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1009: from 18 to 41
- Alignment No. 8877
- gi No. 168422
- % Identity 100
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1009: from 18 to 41

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1010
- Ceres seq_id 1499415
- Location of start within SEQ ID NO 1007: at 54 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8878
- gi No. 113003
- % Identity 95.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1010: from 1 to 24
- Alignment No. 8879
- gi No. 168397
- % Identity 95.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1010: from 1 to 24
- Alignment No. 8880
- gi No. 168422
- % Identity 100
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1010: from 1 to 24

Maximum Length Sequence corresponding to clone ID 225429

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1011
- Ceres seq_id 1499416

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1012
- Ceres seq_id 1499417
- Location of start within SEQ ID NO 1011: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1013
- Ceres seq_id 1499418
- Location of start within SEQ ID NO 1011: at 105 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8881
- S-adenosylmethionine synthetase
- Location within SEQ ID NO 1013: from 5 to 95 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8882
- gi No. 1076485
- % Identity 92.7
- Alignment Length 82
- Location of Alignment in SEQ ID NO 1013: from 3 to 84

- Alignment No. 8883
- gi No. 1170936
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95

- Alignment No. 8884
- gi No. 1170937
- % Identity 89.7
- Alignment Length 97
- Location of Alignment in SEQ ID NO 1013: from 1 to 95

- Alignment No. 8885
- gi No. 1170938
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95

- Alignment No. 8886
- gi No. 1170939
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95

- Alignment No. 8887
- gi No. 127041
- % Identity 92.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95

- Alignment No. 8888
- gi No. 127045
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95

- Alignment No. 8889
- gi No. 127046
- % Identity 87.6
- Alignment Length 97
- Location of Alignment in SEQ ID NO 1013: from 1 to 95

- Alignment No. 8890
- gi No. 1346520
- % Identity 92.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95

- Alignment No. 8891
- gi No. 1346523
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95

- Alignment No. 8892
- gi No. 1346524
- % Identity 93.6
- Alignment Length 94
- Location of Alignment in SEQ ID NO 1013: from 3 to 95

- Alignment No. 8893
- gi No. 1346525
- % Identity 70.2
- Alignment Length 94
- Location of Alignment in SEQ ID NO 1013: from 3 to 95

- Alignment No. 8894
- gi No. 1346526
- % Identity 90.6
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1013: from 1 to 95

- Alignment No. 8895
- gi No. 147855
- % Identity 71.7
- Alignment Length 46
- Location of Alignment in SEQ ID NO 1013: from 7 to 52

- Alignment No. 8896
- gi No. 1708995
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95

- Alignment No. 8897
- gi No. 1709000
- % Identity 94.8
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1013: from 1 to 95

- Alignment No. 8898
- gi No. 1709001
- % Identity 85.1
- Alignment Length 67
- Location of Alignment in SEQ ID NO 1013: from 30 to 95

- Alignment No. 8899
- gi No. 1709002
- % Identity 92.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95

- Alignment No. 8900
- gi No. 1709004
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95

- Alignment No. 8901
- gi No. 1709006
- % Identity 90.2
- Alignment Length 61
- Location of Alignment in SEQ ID NO 1013: from 36 to 95

- Alignment No. 8902
- gi No. 172534
- % Identity 70.2
- Alignment Length 94
- Location of Alignment in SEQ ID NO 1013: from 3 to 95
- Alignment No. 8903
- gi No. 2129889
- % Identity 90.6
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1013: from 1 to 95
- Alignment No. 8904
- gi No. 2315140
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95
- Alignment No. 8905
- gi No. 2665652
- % Identity 72.9
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1013: from 1 to 95
- Alignment No. 8906
- gi No. 3024121
- % Identity 88.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95
- Alignment No. 8907
- gi No. 3024122
- % Identity 95.8
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1013: from 1 to 95
- Alignment No. 8908
- gi No. 3024126
- % Identity 92.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95
- Alignment No. 8909
- gi No. 3024127
- % Identity 92.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95
- Alignment No. 8910
- gi No. 3024148
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95
- Alignment No. 8911
- gi No. 3914019
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95
- Alignment No. 8912

- gi No. 4883604
- % Identity 87.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95
- Alignment No. 8913
- gi No. 4894592
- % Identity 72.9
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1013: from 1 to 95
- Alignment No. 8914
- gi No. 4927188
- % Identity 71.9
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1013: from 1 to 95
- Alignment No. 8915
- gi No. 5726594
- % Identity 90.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1013: from 4 to 95
- Alignment No. 8916
- gi No. 609557
- % Identity 85.1
- Alignment Length 67
- Location of Alignment in SEQ ID NO 1013: from 30 to 95

Maximum Length Sequence corresponding to clone ID 225478

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1014
- Ceres seq_id 1499422

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1015
- Ceres seq_id 1499423
- Location of start within SEQ ID NO 1014: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1016
- Ceres seq_id 1499424
- Location of start within SEQ ID NO 1014: at 73 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8917
- 3' exoribonuclease family
- Location within SEQ ID NO 1016: from 40 to 134 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1017
- Ceres seq_id 1499425
- Location of start within SEQ ID NO 1014: at 121 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8918
- 3' exoribonuclease family
- Location within SEQ ID NO 1017: from 24 to 118 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 230791

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1018
- Ceres seq_id 1499446

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1019
- Ceres seq_id 1499447
- Location of start within SEQ ID NO 1018: at 111 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8919
- Mur ligase family
- Location within SEQ ID NO 1019: from 60 to 127 aa.

- Alignment No. 8920
- Mur ligase family
- Location within SEQ ID NO 1019: from 121 to 305 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8921
- gi No. 1706885
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1019: from 452 to 468

- Alignment No. 8922
- gi No. 2137297
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1019: from 452 to 468

- Alignment No. 8923
- gi No. 2137812
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1019: from 452 to 468

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1020
- Ceres seq_id 1499448
- Location of start within SEQ ID NO 1018: at 282 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8924
- Mur ligase family
- Location within SEQ ID NO 1020: from 3 to 70 aa.

- Alignment No. 8925
- Mur ligase family
- Location within SEQ ID NO 1020: from 64 to 248 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8926
- gi No. 1706885
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1020: from 395 to 411

- Alignment No. 8927
- gi No. 2137297
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1020: from 395 to 411

- Alignment No. 8928
- gi No. 2137812
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1020: from 395 to 411

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1021
- Ceres seq_id 1499449
- Location of start within SEQ ID NO 1018: at 612 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8929
- Mur ligase family
- Location within SEQ ID NO 1021: from 1 to 138 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8930
- gi No. 1706885
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1021: from 285 to 301

- Alignment No. 8931
- gi No. 2137297
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1021: from 285 to 301

- Alignment No. 8932
- gi No. 2137812
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1021: from 285 to 301

Maximum Length Sequence corresponding to clone ID 230831

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1022
- Ceres seq_id 1499450

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1023
- Ceres seq_id 1499451
- Location of start within SEQ ID NO 1022: at 501 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8933
- gi No. 4204290
- % Identity 82.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1023: from 282 to 356
- Alignment No. 8934
- gi No. 4204290
- % Identity 80.6
- Alignment Length 248
- Location of Alignment in SEQ ID NO 1023: from 3 to 250
- Alignment No. 8935
- gi No. 4322421
- % Identity 98.6
- Alignment Length 355
- Location of Alignment in SEQ ID NO 1023: from 3 to 357
- Alignment No. 8936
- gi No. 4768281
- % Identity 99.2
- Alignment Length 355
- Location of Alignment in SEQ ID NO 1023: from 3 to 357
- Alignment No. 8937
- gi No. 5305736
- % Identity 99.2
- Alignment Length 355
- Location of Alignment in SEQ ID NO 1023: from 3 to 357

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1024
- Ceres seq_id 1499452
- Location of start within SEQ ID NO 1022: at 552 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8938
- gi No. 4204290
- % Identity 82.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1024: from 265 to 339
- Alignment No. 8939
- gi No. 4204290
- % Identity 80.6
- Alignment Length 248
- Location of Alignment in SEQ ID NO 1024: from 1 to 233
- Alignment No. 8940
- gi No. 4322421
- % Identity 98.6
- Alignment Length 355
- Location of Alignment in SEQ ID NO 1024: from 1 to 340
- Alignment No. 8941
- gi No. 4768281
- % Identity 99.2
- Alignment Length 355
- Location of Alignment in SEQ ID NO 1024: from 1 to 340

- Alignment No. 8942
- gi No. 5305736
- % Identity 99.2
- Alignment Length 355
- Location of Alignment in SEQ ID NO 1024: from 1 to 340

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1025
- Ceres seq_id 1499453
- Location of start within SEQ ID NO 1022: at 639 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8943
 - gi No. 4204290
 - % Identity 82.7
 - Alignment Length 75
 - Location of Alignment in SEQ ID NO 1025: from 236 to 310
-
- Alignment No. 8944
 - gi No. 4204290
 - % Identity 80.6
 - Alignment Length 248
 - Location of Alignment in SEQ ID NO 1025: from 1 to 204
-
- Alignment No. 8945
 - gi No. 4322421
 - % Identity 98.6
 - Alignment Length 355
 - Location of Alignment in SEQ ID NO 1025: from 1 to 311
-
- Alignment No. 8946
 - gi No. 4768281
 - % Identity 99.2
 - Alignment Length 355
 - Location of Alignment in SEQ ID NO 1025: from 1 to 311
-
- Alignment No. 8947
 - gi No. 5305736
 - % Identity 99.2
 - Alignment Length 355
 - Location of Alignment in SEQ ID NO 1025: from 1 to 311

Maximum Length Sequence corresponding to clone ID 230894

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1026
- Ceres seq_id 1499458

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1027
- Ceres seq_id 1499459
- Location of start within SEQ ID NO 1026: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8948
- gi No. 2191127
- % Identity 99.4
- Alignment Length 177

- Location of Alignment in SEQ ID NO 1027: from 227 to 403
- Alignment No. 8949
- gi No. 3193306
- % Identity 97
- Alignment Length 201
- Location of Alignment in SEQ ID NO 1027: from 1 to 201

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1028
- Ceres seq_id 1499460
- Location of start within SEQ ID NO 1026: at 55 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8950
- gi No. 2191127
- % Identity 99.4
- Alignment Length 177
- Location of Alignment in SEQ ID NO 1028: from 209 to 385
- Alignment No. 8951
- gi No. 3193306
- % Identity 97
- Alignment Length 201
- Location of Alignment in SEQ ID NO 1028: from 1 to 183

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1029
- Ceres seq_id 1499461
- Location of start within SEQ ID NO 1026: at 85 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8952
- gi No. 2191127
- % Identity 99.4
- Alignment Length 177
- Location of Alignment in SEQ ID NO 1029: from 199 to 375
- Alignment No. 8953
- gi No. 3193306
- % Identity 97
- Alignment Length 201
- Location of Alignment in SEQ ID NO 1029: from 1 to 173

Maximum Length Sequence corresponding to clone ID 230897

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1030
- Ceres seq_id 1499462

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1031
- Ceres seq_id 1499463
- Location of start within SEQ ID NO 1030: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1032
 - Ceres seq_id 1499464
 - Location of start within SEQ ID NO 1030: at 84 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 8954
 - gi No. 2651297
 - % Identity 92.3
 - Alignment Length 39
 - Location of Alignment in SEQ ID NO 1032: from 1 to 39

Maximum Length Sequence corresponding to clone ID 230925

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1033
 - Ceres seq_id 1499465

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1034
 - Ceres seq_id 1499466
 - Location of start within SEQ ID NO 1033: at 105 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 8955
 - gi No. 3834313
 - % Identity 99
 - Alignment Length 195
 - Location of Alignment in SEQ ID NO 1034: from 1 to 195

Maximum Length Sequence corresponding to clone ID 231096

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1035
 - Ceres seq_id 1499467

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1036
 - Ceres seq_id 1499468
 - Location of start within SEQ ID NO 1035: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1037
 - Ceres seq_id 1499469
 - Location of start within SEQ ID NO 1035: at 591 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 8956
 - gi No. 4835243
 - % Identity 77.7
 - Alignment Length 175
 - Location of Alignment in SEQ ID NO 1037: from 1 to 119

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1038

- Ceres seq_id 1499470
- Location of start within SEQ ID NO 1035: at 651 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8957
- gi No. 4835243
- % Identity 77.7
- Alignment Length 175
- Location of Alignment in SEQ ID NO 1038: from 1 to 99

Maximum Length Sequence corresponding to clone ID 231239

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1039
- Ceres seq_id 1499474

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1040
- Ceres seq_id 1499475
- Location of start within SEQ ID NO 1039: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1041
- Ceres seq_id 1499476
- Location of start within SEQ ID NO 1039: at 573 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8958
- Syntaxin
- Location within SEQ ID NO 1041: from 1 to 140 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1042
- Ceres seq_id 1499477
- Location of start within SEQ ID NO 1039: at 756 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8959
- Syntaxin
- Location within SEQ ID NO 1042: from 1 to 79 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 231303

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1043
- Ceres seq_id 1499486

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1044
- Ceres seq_id 1499487
- Location of start within SEQ ID NO 1043: at 84 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8960
- gi No. 2129778
- % Identity 70.3
- Alignment Length 64
- Location of Alignment in SEQ ID NO 1044: from 22 to 85

- Alignment No. 8961
- gi No. 3236241
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1044: from 13 to 25

- Alignment No. 8962
- gi No. 4581965
- % Identity 70.3
- Alignment Length 64
- Location of Alignment in SEQ ID NO 1044: from 22 to 85

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1045
- Ceres seq_id 1499488
- Location of start within SEQ ID NO 1043: at 99 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8963
- gi No. 2129778
- % Identity 70.3
- Alignment Length 64
- Location of Alignment in SEQ ID NO 1045: from 17 to 80

- Alignment No. 8964
- gi No. 3236241
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1045: from 8 to 20

- Alignment No. 8965
- gi No. 4581965
- % Identity 70.3
- Alignment Length 64
- Location of Alignment in SEQ ID NO 1045: from 17 to 80

Maximum Length Sequence corresponding to clone ID 231598

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1046
- Ceres seq_id 1499501

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1047
- Ceres seq_id 1499502
- Location of start within SEQ ID NO 1046: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 8966
- Para family ATPase
- Location within SEQ ID NO 1047: from 278 to 364 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1048
- Ceres seq_id 1499503
- Location of start within SEQ ID NO 1046: at 49 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8967
- ParA family ATPase
- Location within SEQ ID NO 1048: from 262 to 348 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1049
- Ceres seq_id 1499504
- Location of start within SEQ ID NO 1046: at 445 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8968
- ParA family ATPase
- Location within SEQ ID NO 1049: from 130 to 216 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 231731

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1050
- Ceres seq_id 1499509

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1051
- Ceres seq_id 1499510
- Location of start within SEQ ID NO 1050: at 52 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8969
- alpha/beta hydrolase fold
- Location within SEQ ID NO 1051: from 92 to 159 aa.
- Alignment No. 8970
- alpha/beta hydrolase fold
- Location within SEQ ID NO 1051: from 259 to 322 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1052
- Ceres seq_id 1499511
- Location of start within SEQ ID NO 1050: at 55 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8971
- alpha/beta hydrolase fold
- Location within SEQ ID NO 1052: from 91 to 158 aa.

- Alignment No. 8972
- alpha/beta hydrolase fold
- Location within SEQ ID NO 1052: from 258 to 321 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1053
- Ceres seq_id 1499512
- Location of start within SEQ ID NO 1050: at 535 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8973
- alpha/beta hydrolase fold
- Location within SEQ ID NO 1053: from 98 to 161 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 231750

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1054
- Ceres seq_id 1499513

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1055
- Ceres seq_id 1499514
- Location of start within SEQ ID NO 1054: at 318 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8974
- Helix-loop-helix DNA-binding domain
- Location within SEQ ID NO 1055: from 134 to 182 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8975
- gi No. 2244797
- % Identity 97.8
- Alignment Length 274
- Location of Alignment in SEQ ID NO 1055: from 12 to 283

Maximum Length Sequence corresponding to clone ID 231906

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1056
- Ceres seq_id 1499519

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1057
- Ceres seq_id 1499520
- Location of start within SEQ ID NO 1056: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8976
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 1057: from 99 to 169 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1058
- Ceres seq_id 1499521

- Location of start within SEQ ID NO 1056: at 70 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8977
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 1058: from 76 to 146 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1059
- Ceres seq_id 1499522
- Location of start within SEQ ID NO 1056: at 136 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8978
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 1059: from 54 to 124 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 231948

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1060
- Ceres seq_id 1499523

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1061
- Ceres seq_id 1499524
- Location of start within SEQ ID NO 1060: at 187 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8979
- Zinc finger, CCHC class
- Location within SEQ ID NO 1061: from 196 to 213 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8980
- gi No. 2760333
- % Identity 99.7
- Alignment Length 287
- Location of Alignment in SEQ ID NO 1061: from 116 to 402

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1062
- Ceres seq_id 1499525
- Location of start within SEQ ID NO 1060: at 244 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8981
- Zinc finger, CCHC class
- Location within SEQ ID NO 1062: from 177 to 194 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8982
- gi No. 2760333
- % Identity 99.7
- Alignment Length 287

- Location of Alignment in SEQ ID NO 1062: from 97 to 383

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1063
- Ceres seq_id 1499526
- Location of start within SEQ ID NO 1060: at 256 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 8983
- Zinc finger, CCHC class
- Location within SEQ ID NO 1063: from 173 to 190 aa.

(D) Related Amino Acid Sequences

- Alignment No. 8984
- gi NO. 2760333
- % Identity 99.7
- Alignment Length 287
- Location of Alignment in SEQ ID NO 1063: from 93 to 379

Maximum Length Sequence corresponding to clone ID 231976

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1064
- Ceres seq_id 1499527

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1065
- Ceres seq_id 1499528
- Location of start within SEQ ID NO 1064: at 107 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8985
- gi NO. 4586255
- % Identity 90.5
- Alignment Length 95
- Location of Alignment in SEQ ID NO 1065: from 1 to 95
- Alignment No. 8986
- gi NO. 4586255
- % Identity 79.3
- Alignment Length 213
- Location of Alignment in SEQ ID NO 1065: from 59 to 271

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1066
- Ceres seq_id 1499529
- Location of start within SEQ ID NO 1064: at 203 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8987
- gi NO. 4586255
- % Identity 90.5
- Alignment Length 95
- Location of Alignment in SEQ ID NO 1066: from 1 to 63
- Alignment No. 8988
- gi NO. 4586255
- % Identity 79.3

- Alignment Length 213
- Location of Alignment in SEQ ID NO 1066: from 27 to 239

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1067
- Ceres seq_id 1499530
- Location of start within SEQ ID NO 1064: at 257 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8989
- gi No. 4586255
- % Identity 90.5
- Alignment Length 95
- Location of Alignment in SEQ ID NO 1067: from 1 to 45
- Alignment No. 8990
- gi No. 4586255
- % Identity 79.3
- Alignment Length 213
- Location of Alignment in SEQ ID NO 1067: from 9 to 221

Maximum Length Sequence corresponding to clone ID 232208

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1068
- Ceres seq_id 1499538

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1069
- Ceres seq_id 1499539
- Location of start within SEQ ID NO 1068: at 172 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8991
- gi No. 1168470
- % Identity 72.5
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1069: from 1 to 90
- Alignment No. 8992
- gi No. 3461835
- % Identity 92.3
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1069: from 1 to 90

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1070
- Ceres seq_id 1499540
- Location of start within SEQ ID NO 1068: at 241 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8993
- gi No. 1168470
- % Identity 72.5
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1070: from 1 to 67

- Alignment No. 8994
- gi No. 3461835
- % Identity 92.3
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1070: from 1 to 67

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1071
- Ceres seq_id 1499541
- Location of start within SEQ ID NO 1068: at 257 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 232227

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1072
- Ceres seq_id 1499542

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1073
- Ceres seq_id 1499543
- Location of start within SEQ ID NO 1072: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8995
- gi No. 3776560
- % Identity 72.8
- Alignment Length 245
- Location of Alignment in SEQ ID NO 1073: from 190 to 432
- Alignment No. 8996
- gi No. 4587563
- % Identity 99.8
- Alignment Length 420
- Location of Alignment in SEQ ID NO 1073: from 14 to 433

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1074
- Ceres seq_id 1499544
- Location of start within SEQ ID NO 1072: at 40 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8997
- gi No. 3776560
- % Identity 72.8
- Alignment Length 245
- Location of Alignment in SEQ ID NO 1074: from 177 to 419
- Alignment No. 8998
- gi No. 4587563
- % Identity 99.8
- Alignment Length 420
- Location of Alignment in SEQ ID NO 1074: from 1 to 420

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1075

- Ceres seq_id 1499545
- Location of start within SEQ ID NO 1072: at 397 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 8999
- gi No. 3776560
- % Identity 72.8
- Alignment Length 245
- Location of Alignment in SEQ ID NO 1075: from 58 to 300

- Alignment No. 9000
- gi No. 4587563
- % Identity 99.8
- Alignment Length 420
- Location of Alignment in SEQ ID NO 1075: from 1 to 301

Maximum Length Sequence corresponding to clone ID 232986

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1076
- Ceres seq_id 1499547

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1077
- Ceres seq_id 1499548
- Location of start within SEQ ID NO 1076: at 220 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9001
- gi No. 1076641
- % Identity 72.8
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1077: from 1 to 101

- Alignment No. 9002
- gi No. 1170711
- % Identity 71.6
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1077: from 1 to 101

- Alignment No. 9003
- gi No. 1431622
- % Identity 88.6
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1077: from 68 to 101

- Alignment No. 9004
- gi No. 1480078
- % Identity 71.8
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1077: from 32 to 101

- Alignment No. 9005
- gi No. 1709129
- % Identity 75
- Alignment Length 104
- Location of Alignment in SEQ ID NO 1077: from 1 to 101

- Alignment No. 9006

- gi No. 2129738
- % Identity 74.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1077: from 33 to 101

- Alignment No. 9007
- gi No. 2129739
- % Identity 76.5
- Alignment Length 68
- Location of Alignment in SEQ ID NO 1077: from 35 to 101

- Alignment No. 9008
- gi No. 2182029
- % Identity 75.4
- Alignment Length 61
- Location of Alignment in SEQ ID NO 1077: from 42 to 101

- Alignment No. 9009
- gi No. 2398519
- % Identity 71.6
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1077: from 1 to 101

- Alignment No. 9010
- gi No. 3201623
- % Identity 74.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1077: from 33 to 101

- Alignment No. 9011
- gi No. 4539390
- % Identity 76.5
- Alignment Length 68
- Location of Alignment in SEQ ID NO 1077: from 35 to 101

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1078
- Ceres seq_id 1499549
- Location of start within SEQ ID NO 1076: at 301 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9012
- gi No. 1076641
- % Identity 72.8
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1078: from 1 to 74

- Alignment No. 9013
- gi No. 1170711
- % Identity 71.6
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1078: from 1 to 74

- Alignment No. 9014
- gi No. 1431622
- % Identity 88.6
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1078: from 41 to 74

- Alignment No. 9015
- gi No. 1480078
- % Identity 71.8
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1078: from 5 to 74

- Alignment No. 9016
- gi No. 1709129
- % Identity 75
- Alignment Length 104
- Location of Alignment in SEQ ID NO 1078: from 1 to 74

- Alignment No. 9017
- gi No. 2129738
- % Identity 74.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1078: from 6 to 74

- Alignment No. 9018
- gi No. 2129739
- % Identity 76.5
- Alignment Length 68
- Location of Alignment in SEQ ID NO 1078: from 8 to 74

- Alignment No. 9019
- gi No. 2182029
- % Identity 75.4
- Alignment Length 61
- Location of Alignment in SEQ ID NO 1078: from 15 to 74

- Alignment No. 9020
- gi No. 2398519
- % Identity 71.6
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1078: from 1 to 74

- Alignment No. 9021
- gi No. 3201623
- % Identity 74.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1078: from 6 to 74

- Alignment No. 9022
- gi No. 4539390
- % Identity 76.5
- Alignment Length 68
- Location of Alignment in SEQ ID NO 1078: from 8 to 74

Maximum Length Sequence corresponding to clone ID 246205

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1079
- Ceres seq_id 1499558

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1080
- Ceres seq_id 1499559
- Location of start within SEQ ID NO 1079: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 9023

- gi No. 1172663
- % Identity 73.9
- Alignment Length 23
- Location of Alignment in SEQ ID NO 1080: from 100 to 122

- Alignment No. 9024
- gi No. 131185
- % Identity 89.5
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1080: from 101 to 119

- Alignment No. 9025
- gi No. 131186
- % Identity 88.9
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1080: from 101 to 118

- Alignment No. 9026
- gi No. 3885892
- % Identity 73.9
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1080: from 27 to 131

- Alignment No. 9027
- gi No. 478522
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1080: from 100 to 123

- Alignment No. 9028
- gi No. 548604
- % Identity 73.6
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1080: from 27 to 131

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1081
- Ceres seq_id 1499560
- Location of start within SEQ ID NO 1079: at 81 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9029
- gi No. 1172663
- % Identity 73.9
- Alignment Length 23
- Location of Alignment in SEQ ID NO 1081: from 74 to 96

- Alignment No. 9030
- gi No. 131185
- % Identity 89.5
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1081: from 75 to 93

- Alignment No. 9031
- gi No. 131186
- % Identity 88.9
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1081: from 75 to 92

- Alignment No. 9032
- gi No. 3885892
- % Identity 73.9
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1081: from 1 to 105
- Alignment No. 9033
- gi No. 478522
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1081: from 74 to 97
- Alignment No. 9034
- gi No. 548604
- % Identity 73.6
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1081: from 1 to 105

Maximum Length Sequence corresponding to clone ID 246509

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1082
- Ceres seq_id 1499567

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1083
- Ceres seq_id 1499568
- Location of start within SEQ ID NO 1082: at 111 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9035
- Iron/Ascorbate oxidoreductase family
- Location within SEQ ID NO 1083: from 11 to 78 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9036
- gi No. 3386565
- % Identity 95
- Alignment Length 80
- Location of Alignment in SEQ ID NO 1083: from 1 to 78

Maximum Length Sequence corresponding to clone ID 246543

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1084
- Ceres seq_id 1499576

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1085
- Ceres seq_id 1499577
- Location of start within SEQ ID NO 1084: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9037
- gi No. 100448
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52
- Alignment No. 9038
- gi No. 100449
- % Identity 76.9

- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52

- Alignment No. 9039
- gi No. 1076665
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52

- Alignment No. 9040
- gi No. 1086103
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52

- Alignment No. 9041
- gi No. 129640
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52

- Alignment No. 9042
- gi No. 129641
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52

- Alignment No. 9043
- gi No. 129642
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52

- Alignment No. 9044
- gi No. 129643
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52

- Alignment No. 9045
- gi No. 129644
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52

- Alignment No. 9046
- gi No. 169497
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1085: from 27 to 46

- Alignment No. 9047
- gi No. 169520
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52

- Alignment No. 9048
- gi No. 21415
- % Identity 76.9
- Alignment Length 26

- Location of Alignment in SEQ ID NO 1085: from 27 to 52
- Alignment No. 9049
- gi No. 261222
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52
- Alignment No. 9050
- gi No. 320598
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52
- Alignment No. 9051
- gi No. 695756
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52
- Alignment No. 9052
- gi No. 82272
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1085: from 27 to 52

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1086
- Ceres seq_id 1499578
- Location of start within SEQ ID NO 1084: at 22 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9053
- gi No. 100448
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45
- Alignment No. 9054
- gi No. 100449
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45
- Alignment No. 9055
- gi No. 1076665
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45
- Alignment No. 9056
- gi No. 1086103
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45
- Alignment No. 9057
- gi No. 129640
- % Identity 76.9

- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45

- Alignment No. 9058
- gi No. 129641
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45

- Alignment No. 9059
- gi No. 129642
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45

- Alignment No. 9060
- gi No. 129643
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45

- Alignment No. 9061
- gi No. 129644
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45

- Alignment No. 9062
- gi No. 169497
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1086: from 20 to 39

- Alignment No. 9063
- gi No. 169520
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45

- Alignment No. 9064
- gi No. 21415
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45

- Alignment No. 9065
- gi No. 261222
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45

- Alignment No. 9066
- gi No. 320598
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45

- Alignment No. 9067
- gi No. 695756
- % Identity 76.9
- Alignment Length 26

- Location of Alignment in SEQ ID NO 1086: from 20 to 45
- Alignment No. 9068
- gi No. 82272
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1086: from 20 to 45

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1087
- Ceres seq_id 1499579
- Location of start within SEQ ID NO 1084: at 104 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 246728

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1088
- Ceres seq_id 1499591

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1089
- Ceres seq_id 1499592
- Location of start within SEQ ID NO 1088: at 94 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9069
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 1089: from 43 to 127 aa.

- Alignment No. 9070
- Adhesion lipoprotein
- Location within SEQ ID NO 1089: from 24 to 113 aa.

- Alignment No. 9071
- Adhesion lipoprotein
- Location within SEQ ID NO 1089: from 74 to 125 aa.

- Alignment No. 9072
- Osteopontin
- Location within SEQ ID NO 1089: from 6 to 124 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9073
- gi No. 2209095
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1089: from 106 to 123

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1090
- Ceres seq_id 1499593
- Location of start within SEQ ID NO 1088: at 187 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9074
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 1090: from 12 to 96 aa.

- Alignment No. 9075
- Adhesion lipoprotein
- Location within SEQ ID NO 1090: from 1 to 82 aa.

- Alignment No. 9076
- Adhesion lipoprotein
- Location within SEQ ID NO 1090: from 43 to 94 aa.

- Alignment No. 9077
- Osteopontin
- Location within SEQ ID NO 1090: from 1 to 93 aa.

- (D) Related Amino Acid Sequences
- Alignment No. 9078
 - gi No. 2209095
 - % Identity 72.2
 - Alignment Length 18
 - Location of Alignment in SEQ ID NO 1090: from 75 to 92

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 1091
 - Ceres seq_id 1499594
 - Location of start within SEQ ID NO 1088: at 214 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9079
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 1091: from 3 to 87 aa.

- Alignment No. 9080
- Adhesion lipoprotein
- Location within SEQ ID NO 1091: from 1 to 73 aa.

- Alignment No. 9081
- Adhesion lipoprotein
- Location within SEQ ID NO 1091: from 34 to 85 aa.

- Alignment No. 9082
- Osteopontin
- Location within SEQ ID NO 1091: from 1 to 84 aa.

- (D) Related Amino Acid Sequences
- Alignment No. 9083
 - gi No. 2209095
 - % Identity 72.2
 - Alignment Length 18
 - Location of Alignment in SEQ ID NO 1091: from 66 to 83

Maximum Length Sequence corresponding to clone ID 246776

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1092
- Ceres seq_id 1499605

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1093
- Ceres seq_id 1499606
- Location of start within SEQ ID NO 1092: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9084
- gi No. 1172977
- % Identity 88.5
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1093: from 23 to 48

- Alignment No. 9085
- gi No. 2501187
- % Identity 97.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1093: from 48 to 84

- Alignment No. 9086
- gi No. 2501188
- % Identity 91.9
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1093: from 48 to 84

- Alignment No. 9087
- gi No. 2501189
- % Identity 97.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1093: from 48 to 84

- Alignment No. 9088
- gi No. 2529670
- % Identity 84
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1093: from 24 to 48

- Alignment No. 9089
- gi No. 2582665
- % Identity 92.3
- Alignment Length 39
- Location of Alignment in SEQ ID NO 1093: from 48 to 86

- Alignment No. 9090
- gi No. 3021348
- % Identity 78.3
- Alignment Length 23
- Location of Alignment in SEQ ID NO 1093: from 26 to 48

- Alignment No. 9091
- gi No. 3650384
- % Identity 71.9
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1093: from 50 to 81

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1094
- Ceres seq_id 1499607
- Location of start within SEQ ID NO 1092: at 68 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9092
- gi No. 1172977
- % Identity 88.5
- Alignment Length 26

- Location of Alignment in SEQ ID NO 1094: from 1 to 26
- Alignment No. 9093
- gi No. 2501187
- % Identity 97.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1094: from 26 to 62
- Alignment No. 9094
- gi No. 2501188
- % Identity 91.9
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1094: from 26 to 62
- Alignment No. 9095
- gi No. 2501189
- % Identity 97.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1094: from 26 to 62
- Alignment No. 9096
- gi No. 2529670
- % Identity 84
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1094: from 2 to 26
- Alignment No. 9097
- gi No. 2582665
- % Identity 92.3
- Alignment Length 39
- Location of Alignment in SEQ ID NO 1094: from 26 to 64
- Alignment No. 9098
- gi No. 3021348
- % Identity 78.3
- Alignment Length 23
- Location of Alignment in SEQ ID NO 1094: from 4 to 26
- Alignment No. 9099
- gi No. 3650384
- % Identity 71.9
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1094: from 28 to 59

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1095
- Ceres seq_id 1499608
- Location of start within SEQ ID NO 1092: at 152 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9100
- gi No. 2501187
- % Identity 97.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1095: from 1 to 34
- Alignment No. 9101
- gi No. 2501188
- % Identity 91.9

- Alignment Length 37
- Location of Alignment in SEQ ID NO 1095: from 1 to 34
- Alignment No. 9102
- gi No. 2501189
- % Identity 97.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1095: from 1 to 34
- Alignment No. 9103
- gi No. 2582665
- % Identity 92.3
- Alignment Length 39
- Location of Alignment in SEQ ID NO 1095: from 1 to 36
- Alignment No. 9104
- gi No. 3650384
- % Identity 71.9
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1095: from 1 to 31

Maximum Length Sequence corresponding to clone ID 246878

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1096
- Ceres seq_id 1499627

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1097
- Ceres seq_id 1499628
- Location of start within SEQ ID NO 1096: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9105
- gi No. 4006881
- % Identity 78.9
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1097: from 8 to 45

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1098
- Ceres seq_id 1499629
- Location of start within SEQ ID NO 1096: at 331 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1099
- Ceres seq_id 1499630
- Location of start within SEQ ID NO 1096: at 337 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 247172

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1100
- Ceres seq_id 1499649

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1101
 - Ceres seq_id 1499650
 - Location of start within SEQ ID NO 1100: at 3 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 9106
 - 11-S plant seed storage protein
 - Location within SEQ ID NO 1101: from 18 to 105 aa.

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1102
 - Ceres seq_id 1499651
 - Location of start within SEQ ID NO 1100: at 58 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1103
 - Ceres seq_id 1499652
 - Location of start within SEQ ID NO 1100: at 94 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 247194

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1104
 - Ceres seq_id 1499655
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1105
 - Ceres seq_id 1499656
 - Location of start within SEQ ID NO 1104: at 3 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 9107
 - gi No. 1071974
 - % Identity 72.5
 - Alignment Length 40
 - Location of Alignment in SEQ ID NO 1105: from 26 to 65
 - Alignment No. 9108
 - gi No. 1173217
 - % Identity 72.5
 - Alignment Length 40
 - Location of Alignment in SEQ ID NO 1105: from 26 to 65
 - Alignment No. 9109
 - gi No. 1173218
 - % Identity 95
 - Alignment Length 40
 - Location of Alignment in SEQ ID NO 1105: from 26 to 65

- Alignment No. 9110
- gi No. 1173219
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65

- Alignment No. 9111
- gi No. 1173220
- % Identity 77.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65

- Alignment No. 9112
- gi No. 133793
- % Identity 92.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65

- Alignment No. 9113
- gi No. 133884
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65

- Alignment No. 9114
- gi No. 1350954
- % Identity 77.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65

- Alignment No. 9115
- gi No. 2130985
- % Identity 90
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65

- Alignment No. 9116
- gi No. 2281972
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65

- Alignment No. 9117
- gi No. 2429452
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65

- Alignment No. 9118
- gi No. 3355488
- % Identity 88.6
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1105: from 22 to 65

- Alignment No. 9119
- gi No. 3758866
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1105: from 26 to 63

- Alignment No. 9120

- gi No. 417715
- % Identity 70
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65

- Alignment No. 9121
- gi No. 4506689
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65

- Alignment No. 9122
- gi No. 464711
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65

- Alignment No. 9123
- gi No. 5679124
- % Identity 77.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1105: from 26 to 65

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1106
- Ceres seq_id 1499657
- Location of start within SEQ ID NO 1104: at 78 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9124
- gi No. 1071974
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40

- Alignment No. 9125
- gi No. 1173217
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40

- Alignment No. 9126
- gi No. 1173218
- % Identity 95
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40

- Alignment No. 9127
- gi No. 1173219
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40

- Alignment No. 9128
- gi No. 1173220
- % Identity 77.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40

- Alignment No. 9129
- gi No. 133793
- % Identity 92.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40

- Alignment No. 9130
- gi No. 133884
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40

- Alignment No. 9131
- gi No. 1350954
- % Identity 77.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40

- Alignment No. 9132
- gi No. 2130985
- % Identity 90
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40

- Alignment No. 9133
- gi No. 2281972
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40

- Alignment No. 9134
- gi No. 2429452
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40

- Alignment No. 9135
- gi No. 3355488
- % Identity 88.6
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1106: from 1 to 40

- Alignment No. 9136
- gi No. 3758866
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1106: from 1 to 38

- Alignment No. 9137
- gi No. 417715
- % Identity 70
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40

- Alignment No. 9138
- gi No. 4506689
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40

- Alignment No. 9139

- gi No. 464711
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40

- Alignment No. 9140
- gi No. 5679124
- % Identity 77.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1106: from 1 to 40

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1107
- Ceres seq_id 1499658
- Location of start within SEQ ID NO 1104: at 117 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9141
- gi No. 1071974
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27

- Alignment No. 9142
- gi No. 1173217
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27

- Alignment No. 9143
- gi No. 1173218
- % Identity 95
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27

- Alignment No. 9144
- gi No. 1173219
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27

- Alignment No. 9145
- gi No. 1173220
- % Identity 77.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27

- Alignment No. 9146
- gi No. 133793
- % Identity 92.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27

- Alignment No. 9147
- gi No. 133884
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27

- Alignment No. 9148
- gi No. 1350954
- % Identity 77.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27

- Alignment No. 9149
- gi No. 2130985
- % Identity 90
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27

- Alignment No. 9150
- gi No. 2281972
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27

- Alignment No. 9151
- gi No. 2429452
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27

- Alignment No. 9152
- gi No. 3355488
- % Identity 88.6
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1107: from 1 to 27

- Alignment No. 9153
- gi No. 3758866
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1107: from 1 to 25

- Alignment No. 9154
- gi No. 417715
- % Identity 70
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27

- Alignment No. 9155
- gi No. 4506689
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27

- Alignment No. 9156
- gi No. 464711
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27

- Alignment No. 9157
- gi No. 5679124
- % Identity 77.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1107: from 1 to 27

Maximum Length Sequence corresponding to clone ID 247264

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 1108
- Ceres seq_id 1499667
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 1109
- Ceres seq_id 1499668
- Location of start within SEQ ID NO 1108: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
- (D) Related Amino Acid Sequences
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 1110
- Ceres seq_id 1499669
- Location of start within SEQ ID NO 1108: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
- Alignment No. 9158
- Uncharacterized protein family
- Location within SEQ ID NO 1110: from 81 to 166 aa.
- (D) Related Amino Acid Sequences
- Alignment No. 9159
- gi No. 4886288
- % Identity 86.1
- Alignment Length 79
- Location of Alignment in SEQ ID NO 1110: from 82 to 160
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 1111
- Ceres seq_id 1499670
- Location of start within SEQ ID NO 1108: at 21 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
- Alignment No. 9160
- Uncharacterized protein family
- Location within SEQ ID NO 1111: from 75 to 160 aa.
- (D) Related Amino Acid Sequences
- Alignment No. 9161
- gi No. 4886288
- % Identity 86.1
- Alignment Length 79
- Location of Alignment in SEQ ID NO 1111: from 76 to 154
- Maximum Length Sequence corresponding to clone ID 247265
- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 1112
- Ceres seq_id 1499671
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 1113
- Ceres seq_id 1499672
- Location of start within SEQ ID NO 1112: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
- (D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1114
 - Ceres seq_id 1499673
 - Location Of start within SEQ ID NO 1112: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 9162
 - gi No. 1523800
 - % Identity 71.4
 - Alignment Length 15
 - Location of Alignment in SEQ ID NO 1114: from 16 to 29
 - Alignment No. 9163
 - gi No. 3219273
 - % Identity 71.4
 - Alignment Length 15
 - Location of Alignment in SEQ ID NO 1114: from 16 to 29

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1115
 - Ceres seq_id 1499674
 - Location of start within SEQ ID NO 1112: at 193 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9164
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1115: from 21 to 115 aa.

- (D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 247273

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1116
- Ceres seq_id 1499675

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1117
- Ceres seq_id 1499676
- Location of start within SEQ ID NO 1116: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 9165
 - gi No. 123704
 - % Identity 70
 - Alignment Length 20
 - Location of Alignment in SEQ ID NO 1117: from 52 to 70

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1118
 - Ceres seq_id 1499677
 - Location of start within SEQ ID NO 1116: at 92 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences

- (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1119
- Ceres seq_id 1499678
- Location of start within SEQ ID NO 1116: at 115 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 247522

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1120
- Ceres seq_id 1499686

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1121
- Ceres seq_id 1499687
- Location of start within SEQ ID NO 1120: at 61 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9166
- Sugar (and other) transporter
- Location within SEQ ID NO 1121: from 24 to 142 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1122
- Ceres seq_id 1499688
- Location of start within SEQ ID NO 1120: at 148 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9167
- Sugar (and other) transporter
- Location within SEQ ID NO 1122: from 1 to 113 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1123
- Ceres seq_id 1499689
- Location of start within SEQ ID NO 1120: at 184 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9168
- Sugar (and other) transporter
- Location within SEQ ID NO 1123: from 1 to 101 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 247534

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1124
- Ceres seq_id 1499690

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1125
- Ceres seq_id 1499691
- Location of start within SEQ ID NO 1124: at 75 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9169
- 4 transmembrane segments integral membrane proteins
- Location within SEQ ID NO 1125: from 78 to 131 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1126
- Ceres seq_id 1499692
- Location of start within SEQ ID NO 1124: at 150 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9170
- 4 transmembrane segments integral membrane proteins
- Location within SEQ ID NO 1126: from 53 to 106 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1127
- Ceres seq_id 1499693
- Location of start within SEQ ID NO 1124: at 186 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9171
- 4 transmembrane segments integral membrane proteins
- Location within SEQ ID NO 1127: from 41 to 94 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 247548

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1128
- Ceres seq_id 1499694

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1129
- Ceres seq_id 1499695
- Location of start within SEQ ID NO 1128: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9172
- gi No. 1418990
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1129: from 70 to 93

- Alignment No. 9173
- gi No. 2443890
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1129: from 71 to 92

- Alignment No. 9174
- gi No. 2459430
- % Identity 73.1

- Alignment Length 26
- Location of Alignment in SEQ ID NO 1129: from 70 to 95

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1130
- Ceres seq_id 1499696
- Location of start within SEQ ID NO 1128: at 183 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9175
- gi No. 1418990
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1130: from 10 to 33

- Alignment No. 9176
- gi No. 2443890
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1130: from 11 to 32

- Alignment No. 9177
- gi No. 2459430
- % Identity 73.1
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1130: from 10 to 35

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1131
- Ceres seq_id 1499697
- Location of start within SEQ ID NO 1128: at 198 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9178
- gi No. 1418990
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1131: from 5 to 28

- Alignment No. 9179
- gi No. 2443890
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1131: from 6 to 27

- Alignment No. 9180
- gi No. 2459430
- % Identity 73.1
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1131: from 5 to 30

Maximum Length Sequence corresponding to clone ID 247645

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1132
- Ceres seq_id 1499720

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1133

- Ceres seq_id 1499721
- Location of start within SEQ ID NO 1132: at 118 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 9181
 - gi No. 4883616
 - % Identity 73.3
 - Alignment Length 60
 - Location of Alignment in SEQ ID NO 1133: from 57 to 116

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 1134
 - Ceres seq_id 1499722
 - Location of start within SEQ ID NO 1132: at 172 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 9182
 - gi No. 4883616
 - % Identity 73.3
 - Alignment Length 60
 - Location of Alignment in SEQ ID NO 1134: from 39 to 98

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 1135
 - Ceres seq_id 1499723
 - Location of start within SEQ ID NO 1132: at 214 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 9183
 - gi No. 4883616
 - % Identity 73.3
 - Alignment Length 60
 - Location of Alignment in SEQ ID NO 1135: from 25 to 84

Maximum Length Sequence corresponding to clone ID 247783

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 1136
 - Ceres seq_id 1499728

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 1137
 - Ceres seq_id 1499729
 - Location of start within SEQ ID NO 1136: at 146 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 9184
- tRNA pseudouridine synthase
- Location within SEQ ID NO 1137: from 46 to 146 aa.
- Alignment No. 9185
- tRNA pseudouridine synthase
- Location within SEQ ID NO 1137: from 256 to 355 aa.

- (D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1138
- Ceres seq_id 1499730
- Location of start within SEQ ID NO 1136: at 257 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9186
- tRNA pseudouridine synthase
- Location within SEQ ID NO 1138: from 9 to 109 aa.
- Alignment No. 9187
- tRNA pseudouridine synthase
- Location within SEQ ID NO 1138: from 219 to 318 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1139
- Ceres seq_id 1499731
- Location of start within SEQ ID NO 1136: at 617 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9188
- tRNA pseudouridine synthase
- Location within SEQ ID NO 1139: from 99 to 198 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 247881

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1140
- Ceres seq_id 1499732

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1141
- Ceres seq_id 1499733
- Location of start within SEQ ID NO 1140: at 80 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9189
- Helix-loop-helix DNA-binding domain
- Location within SEQ ID NO 1141: from 134 to 181 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1142
- Ceres seq_id 1499734
- Location of start within SEQ ID NO 1140: at 89 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9190
- Helix-loop-helix DNA-binding domain
- Location within SEQ ID NO 1142: from 131 to 178 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1143
- Ceres seq_id 1499735
- Location of start within SEQ ID NO 1140: at 332 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9191
- Helix-loop-helix DNA-binding domain
- Location within SEQ ID NO 1143: from 50 to 97 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 248288

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1144
- Ceres seq_id 1499740

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1145
- Ceres seq_id 1499741
- Location of start within SEQ ID NO 1144: at 116 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1146
- Ceres seq_id 1499742
- Location of start within SEQ ID NO 1144: at 185 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1147
- Ceres seq_id 1499743
- Location of start within SEQ ID NO 1144: at 744 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9192
- Integral membrane protein
- Location within SEQ ID NO 1147: from 1 to 122 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 248560

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1148
- Ceres seq_id 1499748

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1149
- Ceres seq_id 1499749
- Location of start within SEQ ID NO 1148: at 89 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9193
- gi No. 3004561

- % Identity 100
- Alignment Length 125
- Location of Alignment in SEQ ID NO 1149: from 1 to 125

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1150
- Ceres seq_id 1499750
- Location of start within SEQ ID NO 1148: at 188 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9194
- gi No. 3004561
- % Identity 100
- Alignment Length 125
- Location of Alignment in SEQ ID NO 1150: from 1 to 92

Maximum Length Sequence corresponding to clone ID 248721

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1151
- Ceres seq_id 1499751

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1152
- Ceres seq_id 1499752
- Location of start within SEQ ID NO 1151: at 31 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9195
- gi No. 5262162
- % Identity 97.5
- Alignment Length 197
- Location of Alignment in SEQ ID NO 1152: from 1 to 197

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1153
- Ceres seq_id 1499753
- Location of start within SEQ ID NO 1151: at 112 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9196
- gi No. 5262162
- % Identity 97.5
- Alignment Length 197
- Location of Alignment in SEQ ID NO 1153: from 1 to 170

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1154
- Ceres seq_id 1499754
- Location of start within SEQ ID NO 1151: at 139 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9197
- gi No. 5262162
- % Identity 97.5

- Alignment Length 197
- Location of Alignment in SEQ ID NO 1154: from 1 to 161

Maximum Length Sequence corresponding to clone ID 248969

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1155
- Ceres seq_id 1499755

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1156
- Ceres seq_id 1499756
- Location of start within SEQ ID NO 1155: at 184 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1157
- Ceres seq_id 1499757
- Location of start within SEQ ID NO 1155: at 320 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 9198
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1157: from 63 to 115 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 248974

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1158
- Ceres seq_id 1499758

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1159
- Ceres seq_id 1499759
- Location of start within SEQ ID NO 1158: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 9199
- Ribosomal L10
- Location within SEQ ID NO 1159: from 19 to 70 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9200
- gi No. 1172806
- % Identity 92.3
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1159: from 19 to 70

- Alignment No. 9201
- gi No. 1172807
- % Identity 78.7
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1159: from 19 to 65

- Alignment No. 9202
- gi No. 1172808
- % Identity 75.6
- Alignment Length 41

- Location of Alignment in SEQ ID NO 1159: from 25 to 65
- Alignment No. 9203
 - gi No. 1172809
 - % Identity 88.5
 - Alignment Length 52
 - Location of Alignment in SEQ ID NO 1159: from 19 to 70
- Alignment No. 9204
 - gi No. 1172810
 - % Identity 76.6
 - Alignment Length 47
 - Location of Alignment in SEQ ID NO 1159: from 19 to 65
- Alignment No. 9205
 - gi No. 1172811
 - % Identity 88.5
 - Alignment Length 52
 - Location of Alignment in SEQ ID NO 1159: from 19 to 70
- Alignment No. 9206
 - gi No. 1172812
 - % Identity 74.5
 - Alignment Length 47
 - Location of Alignment in SEQ ID NO 1159: from 19 to 65
- Alignment No. 9207
 - gi No. 1172813
 - % Identity 93.5
 - Alignment Length 46
 - Location of Alignment in SEQ ID NO 1159: from 19 to 64
- Alignment No. 9208
 - gi No. 2317762
 - % Identity 80.8
 - Alignment Length 52
 - Location of Alignment in SEQ ID NO 1159: from 19 to 70
- Alignment No. 9209
 - gi No. 2500351
 - % Identity 76.6
 - Alignment Length 47
 - Location of Alignment in SEQ ID NO 1159: from 19 to 65
- Alignment No. 9210
 - gi No. 2500352
 - % Identity 70.2
 - Alignment Length 47
 - Location of Alignment in SEQ ID NO 1159: from 19 to 65
- Alignment No. 9211
 - gi No. 2500353
 - % Identity 95.7
 - Alignment Length 46
 - Location of Alignment in SEQ ID NO 1159: from 19 to 64
- Alignment No. 9212
 - gi No. 2500354
 - % Identity 88.5
 - Alignment Length 52
 - Location of Alignment in SEQ ID NO 1159: from 19 to 70

- Alignment No. 9213
- gi No. 2500356
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1159: from 19 to 65

- Alignment No. 9214
- gi No. 3123840
- % Identity 74.5
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1159: from 19 to 65

- Alignment No. 9215
- gi No. 4063389
- % Identity 78.7
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1159: from 19 to 65

- Alignment No. 9216
- gi No. 4107323
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1159: from 19 to 65

- Alignment No. 9217
- gi No. 4262180
- % Identity 92.3
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1159: from 19 to 70

- Alignment No. 9218
- gi No. 4493745
- % Identity 72.3
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1159: from 19 to 65

- Alignment No. 9219
- gi No. 4929242
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1159: from 19 to 65

- Alignment No. 9220
- gi No. 5174431
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1159: from 19 to 65

- Alignment No. 9221
- gi No. 88079
- % Identity 77.1
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1159: from 18 to 65

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1160
- Ceres seq_id 1499760
- Location of start within SEQ ID NO 1158: at 56 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9222
- Ribosomal L10
- Location within SEQ ID NO 1160: from 1 to 52 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9223
- gi No. 1172806
- % Identity 92.3
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1160: from 1 to 52

- Alignment No. 9224
- gi No. 1172807
- % Identity 78.7
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1160: from 1 to 47

- Alignment No. 9225
- gi No. 1172808
- % Identity 75.6
- Alignment Length 41
- Location of Alignment in SEQ ID NO 1160: from 7 to 47

- Alignment No. 9226
- gi No. 1172809
- % Identity 88.5
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1160: from 1 to 52

- Alignment No. 9227
- gi No. 1172810
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1160: from 1 to 47

- Alignment No. 9228
- gi No. 1172811
- % Identity 88.5
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1160: from 1 to 52

- Alignment No. 9229
- gi No. 1172812
- % Identity 74.5
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1160: from 1 to 47

- Alignment No. 9230
- gi No. 1172813
- % Identity 93.5
- Alignment Length 46
- Location of Alignment in SEQ ID NO 1160: from 1 to 46

- Alignment No. 9231
- gi No. 2317762
- % Identity 80.8
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1160: from 1 to 52

- Alignment No. 9232
- gi No. 2500351
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1160: from 1 to 47
- Alignment No. 9233
- gi No. 2500352
- % Identity 70.2
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1160: from 1 to 47
- Alignment No. 9234
- gi No. 2500353
- % Identity 95.7
- Alignment Length 46
- Location of Alignment in SEQ ID NO 1160: from 1 to 46
- Alignment No. 9235
- gi No. 2500354
- % Identity 88.5
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1160: from 1 to 52
- Alignment No. 9236
- gi No. 2500356
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1160: from 1 to 47
- Alignment No. 9237
- gi No. 3123840
- % Identity 74.5
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1160: from 1 to 47
- Alignment No. 9238
- gi No. 4063389
- % Identity 78.7
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1160: from 1 to 47
- Alignment No. 9239
- gi No. 4107323
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1160: from 1 to 47
- Alignment No. 9240
- gi No. 4262180
- % Identity 92.3
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1160: from 1 to 52
- Alignment No. 9241
- gi No. 4493745
- % Identity 72.3
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1160: from 1 to 47
- Alignment No. 9242

- gi No. 4929242
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1160: from 1 to 47

- Alignment No. 9243
- gi No. 5174431
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1160: from 1 to 47

- Alignment No. 9244
- gi No. 88079
- % Identity 77.1
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1160: from 1 to 47

Maximum Length Sequence corresponding to clone ID 249321

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1161
- Ceres seq_id 1499765

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1162
- Ceres seq_id 1499766
- Location of start within SEQ ID NO 1161: at 608 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9245
- gi No. 123530
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1162: from 29 to 39

- Alignment No. 9246
- gi No. 3875708
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1162: from 4 to 14

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1163
- Ceres seq_id 1499767
- Location of start within SEQ ID NO 1161: at 773 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1164
- Ceres seq_id 1499768
- Location of start within SEQ ID NO 1161: at 777 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 249331

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1165
- Ceres seq_id 1499769
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1166
 - Ceres seq_id 1499770
 - Location of start within SEQ ID NO 1165: at 68 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 9247
 - gi No. 4972053
 - % Identity 90.4
 - Alignment Length 115
 - Location of Alignment in SEQ ID NO 1166: from 1 to 102

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1167
 - Ceres seq_id 1499771
 - Location of start within SEQ ID NO 1165: at 131 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 9248
 - gi No. 4972053
 - % Identity 90.4
 - Alignment Length 115
 - Location of Alignment in SEQ ID NO 1167: from 1 to 81

Maximum Length Sequence corresponding to clone ID 249334

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1168
 - Ceres seq_id 1499772
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1169
 - Ceres seq_id 1499773
 - Location of start within SEQ ID NO 1168: at 159 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9249
- alpha/beta hydrolase fold
- Location within SEQ ID NO 1169: from 180 to 249 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 249340

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1170
 - Ceres seq_id 1499777
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1171
 - Ceres seq_id 1499778
 - Location of start within SEQ ID NO 1170: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 9250
 - gi No. 1531760

- % Identity 99.3
- Alignment Length 273
- Location of Alignment in SEQ ID NO 1171: from 40 to 312
- Alignment No. 9251
- gi No. 1778015
- % Identity 98.5
- Alignment Length 273
- Location of Alignment in SEQ ID NO 1171: from 40 to 312
- Alignment No. 9252
- gi No. 1817544
- % Identity 99.6
- Alignment Length 273
- Location of Alignment in SEQ ID NO 1171: from 40 to 312
- Alignment No. 9253
- gi No. 4164139
- % Identity 100
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1171: from 40 to 58

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1172
- Ceres seq_id 1499779
- Location of start within SEQ ID NO 1170: at 120 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9254
- gi No. 1531760
- % Identity 99.3
- Alignment Length 273
- Location of Alignment in SEQ ID NO 1172: from 1 to 273
- Alignment No. 9255
- gi No. 1778015
- % Identity 98.5
- Alignment Length 273
- Location of Alignment in SEQ ID NO 1172: from 1 to 273
- Alignment No. 9256
- gi No. 1817544
- % Identity 99.6
- Alignment Length 273
- Location of Alignment in SEQ ID NO 1172: from 1 to 273
- Alignment No. 9257
- gi No. 4164139
- % Identity 100
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1172: from 1 to 19

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1173
- Ceres seq_id 1499780
- Location of start within SEQ ID NO 1170: at 402 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 9258
 - gi No. 1531760
 - % Identity 99.3
 - Alignment Length 273
 - Location of Alignment in SEQ ID NO 1173: from 1 to 179
- Alignment No. 9259
- gi No. 1778015
- % Identity 98.5
- Alignment Length 273
- Location of Alignment in SEQ ID NO 1173: from 1 to 179
- Alignment No. 9260
- gi No. 1817544
- % Identity 99.6
- Alignment Length 273
- Location of Alignment in SEQ ID NO 1173: from 1 to 179

Maximum Length Sequence corresponding to clone ID 249370

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1174
 - Ceres seq_id 1499785
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1175
 - Ceres seq_id 1499786
 - Location of start within SEQ ID NO 1174: at 50 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 9261
 - Zinc-binding dehydrogenases
 - Location within SEQ ID NO 1175: from 73 to 167 aa.
- (D) Related Amino Acid Sequences
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1176
 - Ceres seq_id 1499787
 - Location of start within SEQ ID NO 1174: at 62 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 9262
 - Zinc-binding dehydrogenases
 - Location within SEQ ID NO 1176: from 69 to 163 aa.
- (D) Related Amino Acid Sequences
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1177
 - Ceres seq_id 1499788
 - Location of start within SEQ ID NO 1174: at 170 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
 - Alignment No. 9263
 - Zinc-binding dehydrogenases
 - Location within SEQ ID NO 1177: from 33 to 127 aa.
- (D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 249388

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1178
- Ceres seq_id 1499789

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1179
- Ceres seq_id 1499790
- Location of start within SEQ ID NO 1178: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9264
- Merozoite Surface Antigen 2 (MSA-2) family
- Location within SEQ ID NO 1179: from 110 to 240 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1180
- Ceres seq_id 1499791
- Location of start within SEQ ID NO 1178: at 120 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9265
- Merozoite Surface Antigen 2 (MSA-2) family
- Location within SEQ ID NO 1180: from 71 to 201 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 249485

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1181
- Ceres seq_id 1499792

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1182
- Ceres seq_id 1499793
- Location of start within SEQ ID NO 1181: at 154 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9266
- Dehydrogenase E1 component
- Location within SEQ ID NO 1182: from 73 to 377 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9267
- gi No. 2454182
- % Identity 98.9
- Alignment Length 366
- Location of Alignment in SEQ ID NO 1182: from 47 to 412

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1183
- Ceres seq_id 1499794
- Location of start within SEQ ID NO 1181: at 163 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9268

- Dehydrogenase E1 component
- Location within SEQ ID NO 1183: from 70 to 374 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9269
- gi No. 2454182
- % Identity 98.9
- Alignment Length 366
- Location of Alignment in SEQ ID NO 1183: from 44 to 409

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1184
- Ceres seq_id 1499795
- Location of start within SEQ ID NO 1181: at 376 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9270
- Dehydrogenase E1 component
- Location within SEQ ID NO 1184: from 1 to 303 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9271
- gi No. 2454182
- % Identity 98.9
- Alignment Length 366
- Location of Alignment in SEQ ID NO 1184: from 1 to 338

Maximum Length Sequence corresponding to clone ID 249591

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1185
- Ceres seq_id 1499800

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1186
- Ceres seq_id 1499801
- Location of start within SEQ ID NO 1185: at 335 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9272
- gi No. 2708751
- % Identity 83.1
- Alignment Length 267
- Location of Alignment in SEQ ID NO 1186: from 32 to 292

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1187
- Ceres seq_id 1499802
- Location of start within SEQ ID NO 1185: at 338 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9273
- gi No. 2708751
- % Identity 83.1
- Alignment Length 267
- Location of Alignment in SEQ ID NO 1187: from 31 to 291

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1188
- Ceres seq_id 1499803
- Location of start within SEQ ID NO 1185: at 362 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9274
- gi No. 2708751
- % Identity 83.1
- Alignment Length 267
- Location of Alignment in SEQ ID NO 1188: from 23 to 283

Maximum Length Sequence corresponding to clone ID 249631

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1189
- Ceres seq_id 1499811

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1190
- Ceres seq_id 1499812
- Location of start within SEQ ID NO 1189: at 381 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9275
- Phosphoglycerate mutase family
- Location within SEQ ID NO 1190: from 1 to 78 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9276
- gi No. 4539345
- % Identity 99.2
- Alignment Length 124
- Location of Alignment in SEQ ID NO 1190: from 1 to 123

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1191
- Ceres seq_id 1499813
- Location of start within SEQ ID NO 1189: at 384 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9277
- Phosphoglycerate mutase family
- Location within SEQ ID NO 1191: from 1 to 77 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9278
- gi No. 4539345
- % Identity 99.2
- Alignment Length 124
- Location of Alignment in SEQ ID NO 1191: from 1 to 122

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1192
- Ceres seq_id 1499814
- Location of start within SEQ ID NO 1189: at 483 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9279
- gi No. 4539345
- % Identity 99.2
- Alignment Length 124
- Location of Alignment in SEQ ID NO 1192: from 1 to 89

Maximum Length Sequence corresponding to clone ID 249747

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1193
 - Ceres seq_id 1499823
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1194
 - Ceres seq_id 1499824
 - Location of start within SEQ ID NO 1193: at 131 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9280
- Tropomyosins
- Location within SEQ ID NO 1194: from 126 to 244 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9281
- gi No. 2832682
- % Identity 96.3
- Alignment Length 244
- Location of Alignment in SEQ ID NO 1194: from 1 to 244

Maximum Length Sequence corresponding to clone ID 249756

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1195
 - Ceres seq_id 1499825
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1196
 - Ceres seq_id 1499826
 - Location of start within SEQ ID NO 1195: at 208 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9282
- Protein phosphatase 2C
- Location within SEQ ID NO 1196: from 243 to 317 aa.

- Alignment No. 9283
- Protein phosphatase 2C
- Location within SEQ ID NO 1196: from 309 to 452 aa.

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1197
 - Ceres seq_id 1499827
 - Location of start within SEQ ID NO 1195: at 535 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9284
- Protein phosphatase 2C
- Location within SEQ ID NO 1197: from 134 to 208 aa.

- Alignment No. 9285

- Protein phosphatase 2C
- Location within SEQ ID NO 1197: from 200 to 343 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1198
- Ceres seq_id 1499828
- Location of start within SEQ ID NO 1195: at 607 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9286
- Protein phosphatase 2C
- Location within SEQ ID NO 1198: from 110 to 184 aa.
- Alignment No. 9287
- Protein phosphatase 2C
- Location within SEQ ID NO 1198: from 176 to 319 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 249769

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1199
- Ceres seq_id 1499829

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1200
- Ceres seq_id 1499830
- Location of start within SEQ ID NO 1199: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9288
- gi No. 4914402
- % Identity 99.6
- Alignment Length 515
- Location of Alignment in SEQ ID NO 1200: from 17 to 531

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1201
- Ceres seq_id 1499831
- Location of start within SEQ ID NO 1199: at 50 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9289
- gi No. 4914402
- % Identity 99.6
- Alignment Length 515
- Location of Alignment in SEQ ID NO 1201: from 1 to 515

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1202
- Ceres seq_id 1499832
- Location of start within SEQ ID NO 1199: at 338 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 9290
 - gi No. 4914402
 - % Identity 99.6
 - Alignment Length 515
 - Location of Alignment in SEQ ID NO 1202: from 1 to 419

Maximum Length Sequence corresponding to clone ID 249772

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1203
 - Ceres seq_id 1499833
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1204
 - Ceres seq_id 1499834
 - Location of start within SEQ ID NO 1203: at 70 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9291
- Mitochondrial carrier proteins
- Location within SEQ ID NO 1204: from 121 to 388 aa.

- (D) Related Amino Acid Sequences
 - Alignment No. 9292
 - gi No. 3068714
 - % Identity 75.5
 - Alignment Length 343
 - Location of Alignment in SEQ ID NO 1204: from 64 to 405

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1205
 - Ceres seq_id 1499835
 - Location of start within SEQ ID NO 1203: at 496 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9293
- Mitochondrial carrier proteins
- Location within SEQ ID NO 1205: from 1 to 246 aa.

- (D) Related Amino Acid Sequences
 - Alignment No. 9294
 - gi No. 3068714
 - % Identity 75.5
 - Alignment Length 343
 - Location of Alignment in SEQ ID NO 1205: from 1 to 263

Maximum Length Sequence corresponding to clone ID 249844

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1206
 - Ceres seq_id 1499844
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1207
 - Ceres seq_id 1499845
 - Location of start within SEQ ID NO 1206: at 174 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9295
- Tropomyosins
- Location within SEQ ID NO 1207: from 122 to 242 aa.

- (D) Related Amino Acid Sequences
 - Alignment No. 9296
 - gi No. 2832682
 - % Identity 96.7
 - Alignment Length 242
 - Location of Alignment in SEQ ID NO 1207: from 1 to 242

Maximum Length Sequence corresponding to clone ID 250092

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1208
 - Ceres seq_id 1499850
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1209
 - Ceres seq_id 1499851
 - Location of start within SEQ ID NO 1208: at 78 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1210
 - Ceres seq_id 1499852
 - Location of start within SEQ ID NO 1208: at 190 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 9297
 - gi No. 4097571
 - % Identity 76.9
 - Alignment Length 13
 - Location of Alignment in SEQ ID NO 1210: from 91 to 103

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1211
 - Ceres seq_id 1499853
 - Location of start within SEQ ID NO 1208: at 362 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 250127

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1212
 - Ceres seq_id 1499854
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1213
 - Ceres seq_id 1499855
 - Location of start within SEQ ID NO 1212: at 135 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9298
- Zinc finger, C3HC4 type (RING finger)
- Location within SEQ ID NO 1213: from 113 to 153 aa.

- (D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 1214
 - Ceres seq_id 1499856
 - Location of start within SEQ ID NO 1212: at 330 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9299
- Zinc finger, C3HC4 type (RING finger)
- Location within SEQ ID NO 1214: from 48 to 88 aa.

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 1215
 - Ceres seq_id 1499857
 - Location of start within SEQ ID NO 1212: at 357 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9300
- Zinc finger, C3HC4 type (RING finger)
- Location within SEQ ID NO 1215: from 39 to 79 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 250751

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1216
- Ceres seq_id 1499875

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1217
- Ceres seq_id 1499876
- Location of start within SEQ ID NO 1216: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9301
- gi No. 1698582
- % Identity 74.2
- Alignment Length 376
- Location of Alignment in SEQ ID NO 1217: from 62 to 435

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1218
- Ceres seq_id 1499877
- Location of start within SEQ ID NO 1216: at 35 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9302
- gi No. 1698582
- % Identity 74.2
- Alignment Length 376
- Location of Alignment in SEQ ID NO 1218: from 51 to 424

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1219
- Ceres seq_id 1499878

- Location of start within SEQ ID NO 1216: at 404 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 9303
 - gi No. 1698582
 - % Identity 74.2
 - Alignment Length 376
 - Location of Alignment in SEQ ID NO 1219: from 1 to 301

Maximum Length Sequence corresponding to clone ID 251247

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1220
- Ceres seq_id 1499899

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1221
- Ceres seq_id 1499900
- Location of start within SEQ ID NO 1220: at 96 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9304
- Response regulator receiver domain
- Location within SEQ ID NO 1221: from 22 to 136 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9305
- gi No. 3687688
- % Identity 78.9
- Alignment Length 142
- Location of Alignment in SEQ ID NO 1221: from 1 to 142

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1222
- Ceres seq_id 1499901
- Location of start within SEQ ID NO 1220: at 210 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9306
- Response regulator receiver domain
- Location within SEQ ID NO 1222: from 1 to 98 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9307
- gi No. 3687688
- % Identity 78.9
- Alignment Length 142
- Location of Alignment in SEQ ID NO 1222: from 1 to 104

Maximum Length Sequence corresponding to clone ID 251438

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1223
- Ceres seq_id 1499902

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1224
- Ceres seq_id 1499903
- Location of start within SEQ ID NO 1223: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 9308
- alpha/beta hydrolase fold
- Location within SEQ ID NO 1224: from 73 to 136 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1225
- Ceres seq_id 1499904
- Location of start within SEQ ID NO 1223: at 70 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 9309
- alpha/beta hydrolase fold
- Location within SEQ ID NO 1225: from 50 to 113 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1226
- Ceres seq_id 1499905
- Location of start within SEQ ID NO 1223: at 163 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 9310
- alpha/beta hydrolase fold
- Location within SEQ ID NO 1226: from 19 to 82 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 251466

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1227
- Ceres seq_id 1499906

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1228
- Ceres seq_id 1499907
- Location of start within SEQ ID NO 1227: at 53 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 9311
- AP2 domain
- Location within SEQ ID NO 1228: from 62 to 112 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9312
- gi No. 1246403
- % Identity 74.5
- Alignment Length 55
- Location of Alignment in SEQ ID NO 1228: from 59 to 112
- Alignment No. 9313
- gi No. 3643601
- % Identity 70
- Alignment Length 50
- Location of Alignment in SEQ ID NO 1228: from 64 to 112

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1229
 - Ceres seq_id 1499908
 - Location of start within SEQ ID NO 1227: at 490 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 251549

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1230
- Ceres seq_id 1499909

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1231
- Ceres seq_id 1499910
- Location of start within SEQ ID NO 1230: at 430 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences

- Alignment No. 9314
- gi No. 4982498
- % Identity 100
- Alignment Length 154
- Location of Alignment in SEQ ID NO 1231: from 6 to 159

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1232
- Ceres seq_id 1499911
- Location of start within SEQ ID NO 1230: at 439 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences

- Alignment No. 9315
- gi No. 4982498
- % Identity 100
- Alignment Length 154
- Location of Alignment in SEQ ID NO 1232: from 3 to 156

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1233
- Ceres seq_id 1499912
- Location of start within SEQ ID NO 1230: at 466 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences

- Alignment No. 9316
- gi No. 4982498
- % Identity 100
- Alignment Length 154
- Location of Alignment in SEQ ID NO 1233: from 1 to 147

Maximum Length Sequence corresponding to clone ID 251841

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1234
- Ceres seq_id 1499924

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1235
- Ceres seq_id 1499925
- Location of start within SEQ ID NO 1234: at 21 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9317
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 1235: from 46 to 113 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9318
- gi No. 2827657
- % Identity 96.3
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1235: from 46 to 152

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1236
- Ceres seq_id 1499926
- Location of start within SEQ ID NO 1234: at 147 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9319
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 1236: from 4 to 71 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9320
- gi No. 2827657
- % Identity 96.3
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1236: from 4 to 110

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1237
- Ceres seq_id 1499927
- Location of start within SEQ ID NO 1234: at 249 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9321
- gi No. 2827657
- % Identity 96.3
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1237: from 1 to 76

Maximum Length Sequence corresponding to clone ID 251906

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1238
- Ceres seq_id 1499928

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1239
- Ceres seq_id 1499929
- Location of start within SEQ ID NO 1238: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9322

- Pollen proteins Ole e I family
- Location within SEQ ID NO 1239: from 48 to 108 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1240
- Ceres seq_id 1499930
- Location of start within SEQ ID NO 1238: at 51 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9323
- Pollen proteins Ole e I family
- Location within SEQ ID NO 1240: from 32 to 92 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1241
- Ceres seq_id 1499931
- Location of start within SEQ ID NO 1238: at 66 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9324
- Pollen proteins Ole e I family
- Location within SEQ ID NO 1241: from 27 to 87 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 252299

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1242
- Ceres seq_id 1499935

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1243
- Ceres seq_id 1499936
- Location of start within SEQ ID NO 1242: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9325
- Chlorophyll A-B binding proteins
- Location within SEQ ID NO 1243: from 62 to 114 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9326
- gi No. 100607
- % Identity 95
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1243: from 94 to 113

- Alignment No. 9327
- gi No. 1084336
- % Identity 87.5
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1243: from 20 to 114

- Alignment No. 9328
- gi No. 115764

- % Identity 70.4
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1243: from 87 to 113

- Alignment No. 9329
- gi No. 115833
- % Identity 95
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1243: from 94 to 113

- Alignment No. 9330
- gi No. 115834
- % Identity 100
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1243: from 94 to 113

- Alignment No. 9331
- gi No. 2326947
- % Identity 74.2
- Alignment Length 31
- Location of Alignment in SEQ ID NO 1243: from 83 to 113

- Alignment No. 9332
- gi No. 2498362
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1243: from 98 to 112

- Alignment No. 9333
- gi No. 282865
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1243: from 87 to 113

- Alignment No. 9334
- gi No. 322377
- % Identity 94.1
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1243: from 96 to 112

- Alignment No. 9335
- gi No. 322380
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1243: from 84 to 110

- Alignment No. 9336
- gi No. 322392
- % Identity 73.1
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1243: from 87 to 112

- Alignment No. 9337
- gi No. 322393
- % Identity 73.1
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1243: from 87 to 112

- Alignment No. 9338
- gi No. 543939
- % Identity 100

- Alignment Length 20
- Location of Alignment in SEQ ID NO 1243: from 94 to 113
- Alignment No. 9339
- gi No. 625547
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1243: from 87 to 113
- Alignment No. 9340
- gi No. 82078
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1243: from 87 to 113
- Alignment No. 9341
- gi No. 82079
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1243: from 87 to 113
- Alignment No. 9342
- gi No. 99485
- % Identity 70.4
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1243: from 87 to 113
- Alignment No. 9343
- gi No. 99488
- % Identity 70.4
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1243: from 87 to 113

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1244
- Ceres seq_id 1499937
- Location of start within SEQ ID NO 1242: at 11 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9344
- Chlorophyll A-B binding proteins
- Location within SEQ ID NO 1244: from 59 to 111 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9345
- gi No. 100607
- % Identity 95
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1244: from 91 to 110
- Alignment No. 9346
- gi No. 1084336
- % Identity 87.5
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1244: from 17 to 111
- Alignment No. 9347
- gi No. 115764
- % Identity 70.4
- Alignment Length 27

- Location of Alignment in SEQ ID NO 1244: from 84 to 110
- Alignment No. 9348
 - gi No. 115833
 - % Identity 95
 - Alignment Length 20
- Location of Alignment in SEQ ID NO 1244: from 91 to 110
- Alignment No. 9349
 - gi No. 115834
 - % Identity 100
 - Alignment Length 20
- Location of Alignment in SEQ ID NO 1244: from 91 to 110
- Alignment No. 9350
 - gi No. 2326947
 - % Identity 74.2
 - Alignment Length 31
- Location of Alignment in SEQ ID NO 1244: from 80 to 110
- Alignment No. 9351
 - gi No. 2498362
 - % Identity 73.3
 - Alignment Length 15
- Location of Alignment in SEQ ID NO 1244: from 95 to 109
- Alignment No. 9352
 - gi No. 282865
 - % Identity 74.1
 - Alignment Length 27
- Location of Alignment in SEQ ID NO 1244: from 84 to 110
- Alignment No. 9353
 - gi No. 322377
 - % Identity 94.1
 - Alignment Length 17
- Location of Alignment in SEQ ID NO 1244: from 93 to 109
- Alignment No. 9354
 - gi No. 322380
 - % Identity 74.1
 - Alignment Length 27
- Location of Alignment in SEQ ID NO 1244: from 81 to 107
- Alignment No. 9355
 - gi No. 322392
 - % Identity 73.1
 - Alignment Length 26
- Location of Alignment in SEQ ID NO 1244: from 84 to 109
- Alignment No. 9356
 - gi No. 322393
 - % Identity 73.1
 - Alignment Length 26
- Location of Alignment in SEQ ID NO 1244: from 84 to 109
- Alignment No. 9357
 - gi No. 543939
 - % Identity 100
 - Alignment Length 20
- Location of Alignment in SEQ ID NO 1244: from 91 to 110

- Alignment No. 9358
- gi No. 625547
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1244: from 84 to 110

- Alignment No. 9359
- gi No. 82078
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1244: from 84 to 110

- Alignment No. 9360
- gi No. 82079
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1244: from 84 to 110

- Alignment No. 9361
- gi No. 99485
- % Identity 70.4
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1244: from 84 to 110

- Alignment No. 9362
- gi No. 99488
- % Identity 70.4
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1244: from 84 to 110

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1245
- Ceres seq_id 1499938
- Location of start within SEQ ID NO 1242: at 532 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9363
- Chlorophyll A-B binding proteins
- Location within SEQ ID NO 1245: from 1 to 111 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9364
- gi No. 1084336
- % Identity 97.2
- Alignment Length 143
- Location of Alignment in SEQ ID NO 1245: from 1 to 113

Maximum Length Sequence corresponding to clone ID 252372

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1246
- Ceres seq_id 1499939

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1247
- Ceres seq_id 1499940
- Location of start within SEQ ID NO 1246: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9365
- gi No. 3169182
- % Identity 83.3
- Alignment Length 78
- Location of Alignment in SEQ ID NO 1247: from 46 to 122
- Alignment No. 9366
- gi No. 3860323
- % Identity 87.2
- Alignment Length 78
- Location of Alignment in SEQ ID NO 1247: from 46 to 122

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1248
- Ceres seq_id 1499941
- Location of start within SEQ ID NO 1246: at 138 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9367
- gi No. 3169182
- % Identity 83.3
- Alignment Length 78
- Location of Alignment in SEQ ID NO 1248: from 1 to 77
- Alignment No. 9368
- gi No. 3860323
- % Identity 87.2
- Alignment Length 78
- Location of Alignment in SEQ ID NO 1248: from 1 to 77

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1249
- Ceres seq_id 1499942
- Location of start within SEQ ID NO 1246: at 168 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9369
- gi No. 3169182
- % Identity 83.3
- Alignment Length 78
- Location of Alignment in SEQ ID NO 1249: from 1 to 67
- Alignment No. 9370
- gi No. 3860323
- % Identity 87.2
- Alignment Length 78
- Location of Alignment in SEQ ID NO 1249: from 1 to 67

Maximum Length Sequence corresponding to clone ID 252497

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1250
- Ceres seq_id 1499943

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1251
- Ceres seq_id 1499944
- Location of start within SEQ ID NO 1250: at 89 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9371
- Core histone H2A/H2B/H3/H4
- Location within SEQ ID NO 1251: from 17 to 128 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9372
- gi No. 10253
- % Identity 88.3
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9373
- gi No. 103198
- % Identity 90.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9374
- gi No. 104698
- % Identity 88
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1251: from 2 to 26

- Alignment No. 9375
- gi No. 1053045
- % Identity 94.5
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 1 to 127

- Alignment No. 9376
- gi No. 1053047
- % Identity 94.5
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 1 to 127

- Alignment No. 9377
- gi No. 1053053
- % Identity 89.8
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 1 to 127

- Alignment No. 9378
- gi No. 1053055
- % Identity 82.8
- Alignment Length 29
- Location of Alignment in SEQ ID NO 1251: from 1 to 29

- Alignment No. 9379
- gi No. 1053057
- % Identity 94.5
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 1 to 127

- Alignment No. 9380
- gi No. 1053059
- % Identity 92.9
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 1 to 127

- Alignment No. 9381
- gi No. 1076583
- % Identity 95
- Alignment Length 60
- Location of Alignment in SEQ ID NO 1251: from 1 to 60
- Alignment No. 9382
- gi No. 1079199
- % Identity 90.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9383
- gi No. 1085857
- % Identity 91.6
- Alignment Length 83
- Location of Alignment in SEQ ID NO 1251: from 34 to 116
- Alignment No. 9384
- gi No. 1085858
- % Identity 92.8
- Alignment Length 83
- Location of Alignment in SEQ ID NO 1251: from 34 to 116
- Alignment No. 9385
- gi No. 108593
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1251: from 112 to 128
- Alignment No. 9386
- gi No. 109977
- % Identity 88.6
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1251: from 2 to 36
- Alignment No. 9387
- gi No. 1166436
- % Identity 81.4
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1251: from 36 to 94
- Alignment No. 9388
- gi No. 1197519
- % Identity 82.8
- Alignment Length 116
- Location of Alignment in SEQ ID NO 1251: from 13 to 128
- Alignment No. 9389
- gi No. 1208642
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80
- Alignment No. 9390
- gi No. 1208644
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80
- Alignment No. 9391

- gi No. 1208646
- % Identity 98.2
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80

- Alignment No. 9392
- gi No. 1208656
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80

- Alignment No. 9393
- gi No. 1208658
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80

- Alignment No. 9394
- gi No. 1208664
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80

- Alignment No. 9395
- gi No. 1208668
- % Identity 94.6
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80

- Alignment No. 9396
- gi No. 1208699
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80

- Alignment No. 9397
- gi No. 1208701
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80

- Alignment No. 9398
- gi No. 1208707
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80

- Alignment No. 9399
- gi No. 1208715
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80

- Alignment No. 9400
- gi No. 1208725
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80

- Alignment No. 9401
- gi No. 1208727

- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80

- Alignment No. 9402
- gi No. 1213291
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80

- Alignment No. 9403
- gi No. 1213307
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80

- Alignment No. 9404
- gi No. 1213313
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80

- Alignment No. 9405
- gi No. 1213315
- % Identity 89.3
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1251: from 25 to 80

- Alignment No. 9406
- gi No. 122065
- % Identity 87.5
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9407
- gi No. 122066
- % Identity 83.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9408
- gi No. 122068
- % Identity 91.4
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9409
- gi No. 122070
- % Identity 90.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9410
- gi No. 122071
- % Identity 82.9
- Alignment Length 41
- Location of Alignment in SEQ ID NO 1251: from 1 to 41

- Alignment No. 9411
- gi No. 122072
- % Identity 78

- Alignment Length 41
- Location of Alignment in SEQ ID NO 1251: from 1 to 41

- Alignment No. 9412
- gi No. 122074
- % Identity 87.5
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9413
- gi No. 122076
- % Identity 86.7
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9414
- gi No. 122077
- % Identity 84.3
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 1 to 127

- Alignment No. 9415
- gi No. 122078
- % Identity 77.3
- Alignment Length 132
- Location of Alignment in SEQ ID NO 1251: from 1 to 132

- Alignment No. 9416
- gi No. 122079
- % Identity 91.4
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9417
- gi No. 122080
- % Identity 85.2
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9418
- gi No. 122081
- % Identity 89.8
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9419
- gi No. 122082
- % Identity 89.8
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9420
- gi No. 122083
- % Identity 91.3
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 2 to 128

- Alignment No. 9421
- gi No. 122084
- % Identity 95.8
- Alignment Length 72

- Location of Alignment in SEQ ID NO 1251: from 57 to 128
- Alignment No. 9422
 - gi No. 122085
 - % Identity 92.2
 - Alignment Length 128
 - Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9423
 - gi No. 122086
 - % Identity 84.4
 - Alignment Length 128
 - Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9424
 - gi No. 122087
 - % Identity 92.2
 - Alignment Length 128
 - Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9425
 - gi No. 122088
 - % Identity 90.6
 - Alignment Length 128
 - Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9426
 - gi No. 122089
 - % Identity 89.8
 - Alignment Length 128
 - Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9427
 - gi No. 122090
 - % Identity 92.2
 - Alignment Length 128
 - Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9428
 - gi No. 122091
 - % Identity 84.4
 - Alignment Length 128
 - Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9429
 - gi No. 1360625
 - % Identity 78.6
 - Alignment Length 131
 - Location of Alignment in SEQ ID NO 1251: from 1 to 129
- Alignment No. 9430
 - gi No. 1360627
 - % Identity 76.5
 - Alignment Length 98
 - Location of Alignment in SEQ ID NO 1251: from 1 to 96
- Alignment No. 9431
 - gi No. 1362108
 - % Identity 92.1
 - Alignment Length 127
 - Location of Alignment in SEQ ID NO 1251: from 1 to 127

- Alignment No. 9432
- gi No. 1362171
- % Identity 95.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1251: from 105 to 128
- Alignment No. 9433
- gi No. 159967
- % Identity 89.1
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9434
- gi No. 161319
- % Identity 89.8
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9435
- gi No. 166384
- % Identity 91.4
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9436
- gi No. 1708108
- % Identity 92.2
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9437
- gi No. 1708109
- % Identity 90.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9438
- gi No. 171637
- % Identity 84.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1251: from 3 to 35
- Alignment No. 9439
- gi No. 1723293
- % Identity 90.4
- Alignment Length 83
- Location of Alignment in SEQ ID NO 1251: from 46 to 128
- Alignment No. 9440
- gi No. 1731925
- % Identity 90.4
- Alignment Length 115
- Location of Alignment in SEQ ID NO 1251: from 3 to 117
- Alignment No. 9441
- gi No. 1762791
- % Identity 71.2
- Alignment Length 132
- Location of Alignment in SEQ ID NO 1251: from 4 to 128

- Alignment No. 9442
- gi No. 1763308
- % Identity 84.4
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9443
- gi No. 1870700
- % Identity 89.2
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1251: from 1 to 111

- Alignment No. 9444
- gi No. 1881589
- % Identity 87.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1251: from 89 to 128

- Alignment No. 9445
- gi No. 1881594
- % Identity 91
- Alignment Length 89
- Location of Alignment in SEQ ID NO 1251: from 1 to 87

- Alignment No. 9446
- gi No. 1881601
- % Identity 93.1
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1251: from 1 to 87

- Alignment No. 9447
- gi No. 19611
- % Identity 92.2
- Alignment Length 115
- Location of Alignment in SEQ ID NO 1251: from 14 to 128

- Alignment No. 9448
- gi No. 19614
- % Identity 90
- Alignment Length 50
- Location of Alignment in SEQ ID NO 1251: from 79 to 128

- Alignment No. 9449
- gi No. 208463
- % Identity 84.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1251: from 3 to 35

- Alignment No. 9450
- gi No. 2116601
- % Identity 89.8
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9451
- gi No. 211855
- % Identity 90.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9452

- gi No. 2119011
- % Identity 90.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9453
- gi No. 2119012
- % Identity 90.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9454
- gi No. 2119013
- % Identity 92.1
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 1 to 127

- Alignment No. 9455
- gi No. 2119014
- % Identity 91.2
- Alignment Length 68
- Location of Alignment in SEQ ID NO 1251: from 61 to 128

- Alignment No. 9456
- gi No. 2119018
- % Identity 91.4
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9457
- gi No. 2135356
- % Identity 88.9
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1251: from 1 to 27

- Alignment No. 9458
- gi No. 2136686
- % Identity 89.7
- Alignment Length 29
- Location of Alignment in SEQ ID NO 1251: from 2 to 30

- Alignment No. 9459
- gi No. 2147399
- % Identity 89.7
- Alignment Length 39
- Location of Alignment in SEQ ID NO 1251: from 1 to 39

- Alignment No. 9460
- gi No. 2252516
- % Identity 89.5
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1251: from 1 to 38

- Alignment No. 9461
- gi No. 2253166
- % Identity 87.3
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1251: from 1 to 63

- Alignment No. 9462
- gi No. 2253615

- % Identity 78.6
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9463
- gi No. 2909431
- % Identity 80.4
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1251: from 13 to 122

- Alignment No. 9464
- gi No. 2995216
- % Identity 77.8
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1251: from 1 to 36

- Alignment No. 9465
- gi No. 2995219
- % Identity 75
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1251: from 1 to 36

- Alignment No. 9466
- gi No. 2995225
- % Identity 83.3
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1251: from 1 to 36

- Alignment No. 9467
- gi No. 2995264
- % Identity 80.6
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1251: from 1 to 36

- Alignment No. 9468
- gi No. 3002595
- % Identity 90.1
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1251: from 15 to 105

- Alignment No. 9469
- gi No. 3002597
- % Identity 89
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1251: from 15 to 105

- Alignment No. 9470
- gi No. 3002603
- % Identity 87
- Alignment Length 92
- Location of Alignment in SEQ ID NO 1251: from 15 to 105

- Alignment No. 9471
- gi No. 3002613
- % Identity 87.9
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1251: from 15 to 105

- Alignment No. 9472
- gi No. 3002621
- % Identity 86.8

- Alignment Length 91
- Location of Alignment in SEQ ID NO 1251: from 15 to 105

- Alignment No. 9473
- gi No. 3002633
- % Identity 89
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1251: from 15 to 105

- Alignment No. 9474
- gi No. 3002635
- % Identity 89
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1251: from 15 to 105

- Alignment No. 9475
- gi No. 3002637
- % Identity 88.9
- Alignment Length 90
- Location of Alignment in SEQ ID NO 1251: from 16 to 105

- Alignment No. 9476
- gi No. 3002643
- % Identity 89
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1251: from 15 to 105

- Alignment No. 9477
- gi No. 3002647
- % Identity 90
- Alignment Length 90
- Location of Alignment in SEQ ID NO 1251: from 15 to 104

- Alignment No. 9478
- gi No. 3002649
- % Identity 87.6
- Alignment Length 89
- Location of Alignment in SEQ ID NO 1251: from 15 to 103

- Alignment No. 9479
- gi No. 3002657
- % Identity 89
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1251: from 15 to 105

- Alignment No. 9480
- gi No. 3002663
- % Identity 87.9
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1251: from 15 to 105

- Alignment No. 9481
- gi No. 3219788
- % Identity 84.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1251: from 13 to 122

- Alignment No. 9482
- gi No. 3219789
- % Identity 82.1
- Alignment Length 112

- Location of Alignment in SEQ ID NO 1251: from 13 to 122
- Alignment No. 9483
- gi No. 3219790
- % Identity 85.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1251: from 13 to 122
- Alignment No. 9484
- gi No. 3219791
- % Identity 83.9
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1251: from 13 to 122
- Alignment No. 9485
- gi No. 3219792
- % Identity 83.9
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1251: from 13 to 122
- Alignment No. 9486
- gi No. 3219803
- % Identity 81.3
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1251: from 13 to 122
- Alignment No. 9487
- gi No. 3219805
- % Identity 82.9
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1251: from 13 to 122
- Alignment No. 9488
- gi No. 352175
- % Identity 83.5
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 2 to 128
- Alignment No. 9489
- gi No. 3745758
- % Identity 91.7
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1251: from 21 to 128
- Alignment No. 9490
- gi No. 386772
- % Identity 91.4
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9491
- gi No. 3875420
- % Identity 82.8
- Alignment Length 116
- Location of Alignment in SEQ ID NO 1251: from 13 to 128
- Alignment No. 9492
- gi No. 3875421
- % Identity 76.4
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 1 to 127

- Alignment No. 9493
 - gi No. 3880527
 - % Identity 87.5
 - Alignment Length 128
 - Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9494
 - gi No. 3880606
 - % Identity 83.3
 - Alignment Length 72
 - Location of Alignment in SEQ ID NO 1251: from 57 to 128
- Alignment No. 9495
 - gi No. 3979986
 - % Identity 92.2
 - Alignment Length 128
 - Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9496
 - gi No. 404466
 - % Identity 89.8
 - Alignment Length 128
 - Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9497
 - gi No. 4139869
 - % Identity 90.6
 - Alignment Length 85
 - Location of Alignment in SEQ ID NO 1251: from 44 to 128
- Alignment No. 9498
 - gi No. 417103
 - % Identity 95.3
 - Alignment Length 128
 - Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9499
 - gi No. 422605
 - % Identity 87.5
 - Alignment Length 128
 - Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9500
 - gi No. 422606
 - % Identity 90.6
 - Alignment Length 128
 - Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9501
 - gi No. 4388695
 - % Identity 89.7
 - Alignment Length 68
 - Location of Alignment in SEQ ID NO 1251: from 61 to 128
- Alignment No. 9502
 - gi No. 4504279
 - % Identity 91.4
 - Alignment Length 128
 - Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9503
- gi No. 4504281
- % Identity 91.4
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9504
- gi No. 4504283
- % Identity 90.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9505
- gi No. 4504299
- % Identity 88.3
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9506
- gi No. 4574208
- % Identity 97.2
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1251: from 22 to 128

- Alignment No. 9507
- gi No. 4761212
- % Identity 91.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1251: from 8 to 119

- Alignment No. 9508
- gi No. 484441
- % Identity 90.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9509
- gi No. 484530
- % Identity 90.6
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 2 to 128

- Alignment No. 9510
- gi No. 484531
- % Identity 90.6
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 2 to 128

- Alignment No. 9511
- gi No. 4883733
- % Identity 89.6
- Alignment Length 106
- Location of Alignment in SEQ ID NO 1251: from 11 to 116

- Alignment No. 9512
- gi No. 4883734
- % Identity 90.7
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1251: from 10 to 116

- Alignment No. 9513

- gi No. 4883735
- % Identity 90.8
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1251: from 9 to 117

- Alignment No. 9514
- gi No. 4883736
- % Identity 89.5
- Alignment Length 105
- Location of Alignment in SEQ ID NO 1251: from 11 to 115

- Alignment No. 9515
- gi No. 4883737
- % Identity 90.3
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1251: from 13 to 115

- Alignment No. 9516
- gi No. 4883738
- % Identity 87.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1251: from 17 to 109

- Alignment No. 9517
- gi No. 4883739
- % Identity 90.4
- Alignment Length 104
- Location of Alignment in SEQ ID NO 1251: from 13 to 116

- Alignment No. 9518
- gi No. 4883740
- % Identity 89.3
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1251: from 13 to 115

- Alignment No. 9519
- gi No. 4883741
- % Identity 90.7
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1251: from 9 to 116

- Alignment No. 9520
- gi No. 4883743
- % Identity 88.1
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1251: from 9 to 117

- Alignment No. 9521
- gi No. 4883744
- % Identity 89.9
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1251: from 9 to 117

- Alignment No. 9522
- gi No. 4883745
- % Identity 90.7
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1251: from 9 to 116

- Alignment No. 9523
- gi No. 4883746

- % Identity 88.9
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1251: from 9 to 116
- Alignment No. 9524
- gi No. 4883747
- % Identity 89.9
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1251: from 9 to 117
- Alignment No. 9525
- gi No. 4883748
- % Identity 89.9
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1251: from 9 to 117
- Alignment No. 9526
- gi No. 4883749
- % Identity 91.4
- Alignment Length 105
- Location of Alignment in SEQ ID NO 1251: from 13 to 117
- Alignment No. 9527
- gi No. 4883751
- % Identity 89.8
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1251: from 9 to 116
- Alignment No. 9528
- gi No. 4883752
- % Identity 89.8
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1251: from 10 to 117
- Alignment No. 9529
- gi No. 4883753
- % Identity 89.9
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1251: from 9 to 117
- Alignment No. 9530
- gi No. 4883754
- % Identity 88.8
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1251: from 9 to 115
- Alignment No. 9531
- gi No. 4883755
- % Identity 91.3
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1251: from 13 to 115
- Alignment No. 9532
- gi No. 4883756
- % Identity 89.9
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1251: from 9 to 117
- Alignment No. 9533
- gi No. 4883758
- % Identity 91.2

- Alignment Length 102
- Location of Alignment in SEQ ID NO 1251: from 13 to 114
- Alignment No. 9534
- gi No. 4883759
- % Identity 89
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1251: from 9 to 117
- Alignment No. 9535
- gi No. 4883760
- % Identity 88.1
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1251: from 9 to 117
- Alignment No. 9536
- gi No. 4883762
- % Identity 88.9
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1251: from 9 to 116
- Alignment No. 9537
- gi No. 488571
- % Identity 95
- Alignment Length 119
- Location of Alignment in SEQ ID NO 1251: from 10 to 128
- Alignment No. 9538
- gi No. 488573
- % Identity 95.7
- Alignment Length 116
- Location of Alignment in SEQ ID NO 1251: from 13 to 128
- Alignment No. 9539
- gi No. 529954
- % Identity 82.6
- Alignment Length 132
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9540
- gi No. 539427
- % Identity 91.7
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1251: from 2 to 49
- Alignment No. 9541
- gi No. 556612
- % Identity 84.4
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9542
- gi No. 559807
- % Identity 89.1
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128
- Alignment No. 9543
- gi No. 578470
- % Identity 88.2
- Alignment Length 68

- Location of Alignment in SEQ ID NO 1251: from 61 to 128
- Alignment No. 9544
 - gi No. 630475
 - % Identity 85.5
 - Alignment Length 76
 - Location of Alignment in SEQ ID NO 1251: from 1 to 76
- Alignment No. 9545
 - gi No. 630476
 - % Identity 85.7
 - Alignment Length 63
 - Location of Alignment in SEQ ID NO 1251: from 1 to 63
- Alignment No. 9546
 - gi No. 631693
 - % Identity 88
 - Alignment Length 50
 - Location of Alignment in SEQ ID NO 1251: from 79 to 128
- Alignment No. 9547
 - gi No. 70743
 - % Identity 91.3
 - Alignment Length 127
 - Location of Alignment in SEQ ID NO 1251: from 2 to 128
- Alignment No. 9548
 - gi No. 70747
 - % Identity 90.6
 - Alignment Length 127
 - Location of Alignment in SEQ ID NO 1251: from 2 to 128
- Alignment No. 9549
 - gi No. 70748
 - % Identity 89.8
 - Alignment Length 127
 - Location of Alignment in SEQ ID NO 1251: from 2 to 128
- Alignment No. 9550
 - gi No. 70749
 - % Identity 91.3
 - Alignment Length 127
 - Location of Alignment in SEQ ID NO 1251: from 2 to 128
- Alignment No. 9551
 - gi No. 70753
 - % Identity 92.1
 - Alignment Length 127
 - Location of Alignment in SEQ ID NO 1251: from 2 to 128
- Alignment No. 9552
 - gi No. 70755
 - % Identity 87.4
 - Alignment Length 127
 - Location of Alignment in SEQ ID NO 1251: from 2 to 128
- Alignment No. 9553
 - gi No. 70760
 - % Identity 77.1
 - Alignment Length 131
 - Location of Alignment in SEQ ID NO 1251: from 2 to 132

- Alignment No. 9554
- gi No. 729676
- % Identity 84.4
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9555
- gi No. 729677
- % Identity 82.8
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9556
- gi No. 81850
- % Identity 95.5
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1251: from 18 to 128

- Alignment No. 9557
- gi No. 84300
- % Identity 80.5
- Alignment Length 41
- Location of Alignment in SEQ ID NO 1251: from 1 to 41

- Alignment No. 9558
- gi No. 84329
- % Identity 84.3
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1251: from 2 to 128

- Alignment No. 9559
- gi No. 85000
- % Identity 91.3
- Alignment Length 115
- Location of Alignment in SEQ ID NO 1251: from 2 to 116

- Alignment No. 9560
- gi No. 85001
- % Identity 89.8
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9561
- gi No. 90622
- % Identity 90.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1251: from 1 to 128

- Alignment No. 9562
- gi No. 995959
- % Identity 82.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1251: from 1 to 40

- Alignment No. 9563
- gi No. 99980
- % Identity 90.6
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1251: from 85 to 116

- Alignment No. 9564
- gi No. 99980
- % Identity 88.6
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1251: from 2 to 45
- Alignment No. 9565
- gi No. 99981
- % Identity 78.1
- Alignment Length 64
- Location of Alignment in SEQ ID NO 1251: from 2 to 65

Maximum Length Sequence corresponding to clone ID 253173

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1252
- Ceres seq_id 1499960

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1253
- Ceres seq_id 1499961
- Location of start within SEQ ID NO 1252: at 121 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9566
- O-methyltransferase
- Location within SEQ ID NO 1253: from 97 to 338 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9567
- gi No. 1169009
- % Identity 76.6
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1253: from 1 to 361
- Alignment No. 9568
- gi No. 116908
- % Identity 77
- Alignment Length 365
- Location of Alignment in SEQ ID NO 1253: from 1 to 363
- Alignment No. 9569
- gi No. 1184041
- % Identity 78.4
- Alignment Length 343
- Location of Alignment in SEQ ID NO 1253: from 21 to 363
- Alignment No. 9570
- gi No. 1236980
- % Identity 74.4
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1253: from 1 to 362
- Alignment No. 9571
- gi No. 1582580
- % Identity 73.9
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1253: from 1 to 362
- Alignment No. 9572
- gi No. 170277
- % Identity 81.6

- Alignment Length 114
- Location of Alignment in SEQ ID NO 1253: from 231 to 344
- Alignment No. 9573
- gi No. 1791352
- % Identity 76.5
- Alignment Length 349
- Location of Alignment in SEQ ID NO 1253: from 15 to 361
- Alignment No. 9574
- gi No. 231757
- % Identity 79.4
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1253: from 1 to 362
- Alignment No. 9575
- gi No. 252735
- % Identity 90
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1253: from 163 to 182
- Alignment No. 9576
- gi No. 2781394
- % Identity 99.7
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1253: from 1 to 363
- Alignment No. 9577
- gi No. 3421382
- % Identity 71.5
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1253: from 1 to 361
- Alignment No. 9578
- gi No. 3913289
- % Identity 77.2
- Alignment Length 368
- Location of Alignment in SEQ ID NO 1253: from 1 to 361
- Alignment No. 9579
- gi No. 3913295
- % Identity 79.7
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1253: from 1 to 362
- Alignment No. 9580
- gi No. 444327
- % Identity 78.8
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1253: from 1 to 361
- Alignment No. 9581
- gi No. 4468044
- % Identity 77.1
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1253: from 222 to 361
- Alignment No. 9582
- gi No. 4468046
- % Identity 76.4
- Alignment Length 365

- Location of Alignment in SEQ ID NO 1253: from 1 to 363
- Alignment No. 9583
- gi No. 4468048
- % Identity 74.1
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1253: from 1 to 361
- Alignment No. 9584
- gi No. 4468050
- % Identity 80.1
- Alignment Length 226
- Location of Alignment in SEQ ID NO 1253: from 136 to 361
- Alignment No. 9585
- gi No. 480082
- % Identity 77.5
- Alignment Length 346
- Location of Alignment in SEQ ID NO 1253: from 1 to 344
- Alignment No. 9586
- gi No. 480083
- % Identity 76.9
- Alignment Length 346
- Location of Alignment in SEQ ID NO 1253: from 1 to 344
- Alignment No. 9587
- gi No. 4808522
- % Identity 70.6
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1253: from 1 to 361
- Alignment No. 9588
- gi No. 4808524
- % Identity 71.8
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1253: from 1 to 361
- Alignment No. 9589
- gi No. 4808526
- % Identity 71.5
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1253: from 1 to 361
- Alignment No. 9590
- gi No. 4808528
- % Identity 70.6
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1253: from 1 to 361
- Alignment No. 9591
- gi No. 4808530
- % Identity 72.1
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1253: from 1 to 361
- Alignment No. 9592
- gi No. 5031492
- % Identity 74.8
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1253: from 1 to 361

- Alignment No. 9593
- gi No. 5031494
- % Identity 75.1
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1253: from 1 to 361

- Alignment No. 9594
- gi No. 642952
- % Identity 70.2
- Alignment Length 350
- Location of Alignment in SEQ ID NO 1253: from 16 to 361

- Alignment No. 9595
- gi No. 762870
- % Identity 78.6
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1253: from 1 to 362

- Alignment No. 9596
- gi No. 762872
- % Identity 74.7
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1253: from 1 to 362

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1254
- Ceres seq_id 1499962
- Location of start within SEQ ID NO 1252: at 190 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9597
- O-methyltransferase
- Location within SEQ ID NO 1254: from 74 to 315 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9598
- gi No. 1169009
- % Identity 76.6
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1254: from 1 to 338

- Alignment No. 9599
- gi No. 116908
- % Identity 77
- Alignment Length 365
- Location of Alignment in SEQ ID NO 1254: from 1 to 340

- Alignment No. 9600
- gi No. 1184041
- % Identity 78.4
- Alignment Length 343
- Location of Alignment in SEQ ID NO 1254: from 1 to 340

- Alignment No. 9601
- gi No. 1236980
- % Identity 74.4
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1254: from 1 to 339

- Alignment No. 9602
- gi No. 1582580
- % Identity 73.9
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1254: from 1 to 339

- Alignment No. 9603
- gi No. 170277
- % Identity 81.6
- Alignment Length 114
- Location of Alignment in SEQ ID NO 1254: from 208 to 321

- Alignment No. 9604
- gi No. 1791352
- % Identity 76.5
- Alignment Length 349
- Location of Alignment in SEQ ID NO 1254: from 1 to 338

- Alignment No. 9605
- gi No. 231757
- % Identity 79.4
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1254: from 1 to 339

- Alignment No. 9606
- gi No. 252735
- % Identity 90
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1254: from 140 to 159

- Alignment No. 9607
- gi No. 2781394
- % Identity 99.7
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1254: from 1 to 340

- Alignment No. 9608
- gi No. 3421382
- % Identity 71.5
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1254: from 1 to 338

- Alignment No. 9609
- gi No. 3913289
- % Identity 77.2
- Alignment Length 368
- Location of Alignment in SEQ ID NO 1254: from 1 to 338

- Alignment No. 9610
- gi No. 3913295
- % Identity 79.7
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1254: from 1 to 339

- Alignment No. 9611
- gi No. 444327
- % Identity 78.8
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1254: from 1 to 338

- Alignment No. 9612

- gi No. 4468044
- % Identity 77.1
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1254: from 199 to 338

- Alignment No. 9613
- gi No. 4468046
- % Identity 76.4
- Alignment Length 365
- Location of Alignment in SEQ ID NO 1254: from 1 to 340

- Alignment No. 9614
- gi No. 4468048
- % Identity 74.1
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1254: from 1 to 338

- Alignment No. 9615
- gi No. 4468050
- % Identity 80.1
- Alignment Length 226
- Location of Alignment in SEQ ID NO 1254: from 113 to 338

- Alignment No. 9616
- gi No. 480082
- % Identity 77.5
- Alignment Length 346
- Location of Alignment in SEQ ID NO 1254: from 1 to 321

- Alignment No. 9617
- gi No. 480083
- % Identity 76.9
- Alignment Length 346
- Location of Alignment in SEQ ID NO 1254: from 1 to 321

- Alignment No. 9618
- gi No. 4808522
- % Identity 70.6
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1254: from 1 to 338

- Alignment No. 9619
- gi No. 4808524
- % Identity 71.8
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1254: from 1 to 338

- Alignment No. 9620
- gi No. 4808526
- % Identity 71.5
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1254: from 1 to 338

- Alignment No. 9621
- gi No. 4808528
- % Identity 70.6
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1254: from 1 to 338

- Alignment No. 9622
- gi No. 4808530

- % Identity 72.1
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1254: from 1 to 338
- Alignment No. 9623
- gi No. 5031492
- % Identity 74.8
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1254: from 1 to 338
- Alignment No. 9624
- gi No. 5031494
- % Identity 75.1
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1254: from 1 to 338
- Alignment No. 9625
- gi No. 642952
- % Identity 70.2
- Alignment Length 350
- Location of Alignment in SEQ ID NO 1254: from 1 to 338
- Alignment No. 9626
- gi No. 762870
- % Identity 78.6
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1254: from 1 to 339
- Alignment No. 9627
- gi No. 762872
- % Identity 74.7
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1254: from 1 to 339

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1255
- Ceres seq_id 1499963
- Location of start within SEQ ID NO 1252: at 220 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9628
- O-methyltransferase
- Location within SEQ ID NO 1255: from 64 to 305 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9629
- gi No. 1169009
- % Identity 76.6
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1255: from 1 to 328
- Alignment No. 9630
- gi No. 116908
- % Identity 77
- Alignment Length 365
- Location of Alignment in SEQ ID NO 1255: from 1 to 330
- Alignment No. 9631
- gi No. 1184041
- % Identity 78.4

- Alignment Length 343
- Location of Alignment in SEQ ID NO 1255: from 1 to 330

- Alignment No. 9632
- gi No. 1236980
- % Identity 74.4
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1255: from 1 to 329

- Alignment No. 9633
- gi No. 1582580
- % Identity 73.9
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1255: from 1 to 329

- Alignment No. 9634
- gi No. 170277
- % Identity 81.6
- Alignment Length 114
- Location of Alignment in SEQ ID NO 1255: from 198 to 311

- Alignment No. 9635
- gi No. 1791352
- % Identity 76.5
- Alignment Length 349
- Location of Alignment in SEQ ID NO 1255: from 1 to 328

- Alignment No. 9636
- gi No. 231757
- % Identity 79.4
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1255: from 1 to 329

- Alignment No. 9637
- gi No. 252735
- % Identity 90
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1255: from 130 to 149

- Alignment No. 9638
- gi No. 2781394
- % Identity 99.7
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1255: from 1 to 330

- Alignment No. 9639
- gi No. 3421382
- % Identity 71.5
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1255: from 1 to 328

- Alignment No. 9640
- gi No. 3913289
- % Identity 77.2
- Alignment Length 368
- Location of Alignment in SEQ ID NO 1255: from 1 to 328

- Alignment No. 9641
- gi No. 3913295
- % Identity 79.7
- Alignment Length 364

- Location of Alignment in SEQ ID NO 1255: from 1 to 329

- Alignment No. 9642
- gi No. 444327
- % Identity 78.8
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1255: from 1 to 328

- Alignment No. 9643
- gi No. 4468044
- % Identity 77.1
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1255: from 189 to 328

- Alignment No. 9644
- gi No. 4468046
- % Identity 76.4
- Alignment Length 365
- Location of Alignment in SEQ ID NO 1255: from 1 to 330

- Alignment No. 9645
- gi No. 4468048
- % Identity 74.1
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1255: from 1 to 328

- Alignment No. 9646
- gi No. 4468050
- % Identity 80.1
- Alignment Length 226
- Location of Alignment in SEQ ID NO 1255: from 103 to 328

- Alignment No. 9647
- gi No. 480082
- % Identity 77.5
- Alignment Length 346
- Location of Alignment in SEQ ID NO 1255: from 1 to 311

- Alignment No. 9648
- gi No. 480083
- % Identity 76.9
- Alignment Length 346
- Location of Alignment in SEQ ID NO 1255: from 1 to 311

- Alignment No. 9649
- gi No. 4808522
- % Identity 70.6
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1255: from 1 to 328

- Alignment No. 9650
- gi No. 4808524
- % Identity 71.8
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1255: from 1 to 328

- Alignment No. 9651
- gi No. 4808526
- % Identity 71.5
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1255: from 1 to 328

- Alignment No. 9652
- gi No. 4808528
- % Identity 70.6
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1255: from 1 to 328

- Alignment No. 9653
- gi No. 4808530
- % Identity 72.1
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1255: from 1 to 328

- Alignment No. 9654
- gi No. 5031492
- % Identity 74.8
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1255: from 1 to 328

- Alignment No. 9655
- gi No. 5031494
- % Identity 75.1
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1255: from 1 to 328

- Alignment No. 9656
- gi No. 642952
- % Identity 70.2
- Alignment Length 350
- Location of Alignment in SEQ ID NO 1255: from 1 to 328

- Alignment No. 9657
- gi No. 762870
- % Identity 78.6
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1255: from 1 to 329

- Alignment No. 9658
- gi No. 762872
- % Identity 74.7
- Alignment Length 364
- Location of Alignment in SEQ ID NO 1255: from 1 to 329

Maximum Length Sequence corresponding to clone ID 253258

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1256
- Ceres seq_id 1499964

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1257
- Ceres seq_id 1499965
- Location of start within SEQ ID NO 1256: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9659
- gi No. 3785990
- % Identity 84.7
- Alignment Length 157
- Location of Alignment in SEQ ID NO 1257: from 15 to 99

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1258
 - Ceres seq_id 1499966
 - Location of start within SEQ ID NO 1256: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1259
 - Ceres seq_id 1499967
 - Location of start within SEQ ID NO 1256: at 434 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9660
- gi No. 3785990
- % Identity 98.9
- Alignment Length 95
- Location of Alignment in SEQ ID NO 1259: from 1 to 92

Maximum Length Sequence corresponding to clone ID 253262

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1260
- Ceres seq_id 1499968

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1261
- Ceres seq_id 1499969
- Location of start within SEQ ID NO 1260: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9661
- gi No. 3152605
- % Identity 98.8
- Alignment Length 83
- Location of Alignment in SEQ ID NO 1261: from 4 to 84

- Alignment No. 9662
- gi No. 4006889
- % Identity 83.1
- Alignment Length 83
- Location of Alignment in SEQ ID NO 1261: from 4 to 84

Maximum Length Sequence corresponding to clone ID 253359

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1262
- Ceres seq_id 1499970

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1263
- Ceres seq_id 1499971
- Location of start within SEQ ID NO 1262: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9663
- Hsp90 protein
- Location within SEQ ID NO 1263: from 36 to 110 aa.

- Alignment No. 9664
- Hsp90 protein
- Location within SEQ ID NO 1263: from 39 to 138 aa.
- Alignment No. 9665
- Hsp90 protein
- Location within SEQ ID NO 1263: from 131 to 181 aa.
- Alignment No. 9666
- 11-S plant seed storage protein
- Location within SEQ ID NO 1263: from 14 to 95 aa.
- Alignment No. 9667
- Troponin
- Location within SEQ ID NO 1263: from 25 to 123 aa.
- Alignment No. 9668
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 1263: from 7 to 85 aa.
- Alignment No. 9669
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 1263: from 7 to 88 aa.
- Alignment No. 9670
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 1263: from 9 to 86 aa.
- Alignment No. 9671
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 1263: from 17 to 133 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 253404

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1264
- Ceres seq_id 1499972

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1265
- Ceres seq_id 1499973
- Location of start within SEQ ID NO 1264: at 131 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9672
- Glycosyl hydrolase family 9
- Location within SEQ ID NO 1265: from 58 to 514 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1266
- Ceres seq_id 1499974
- Location of start within SEQ ID NO 1264: at 479 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9673
- Glycosyl hydrolase family 9

- Location within SEQ ID NO 1266: from 1 to 398 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1267
- Ceres seq_id 1499975
- Location of start within SEQ ID NO 1264: at 533 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9674
- Glycosyl hydrolase family 9
- Location within SEQ ID NO 1267: from 1 to 380 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 253420

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1268
- Ceres seq_id 1499976

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1269
- Ceres seq_id 1499977
- Location of start within SEQ ID NO 1268: at 159 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9675
- gi No. 3928150
- % Identity 78.6
- Alignment Length 28
- Location of Alignment in SEQ ID NO 1269: from 1 to 28

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1270
- Ceres seq_id 1499978
- Location of start within SEQ ID NO 1268: at 563 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1271
- Ceres seq_id 1499979
- Location of start within SEQ ID NO 1268: at 638 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 253499

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1272
- Ceres seq_id 1499984

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1273
- Ceres seq_id 1499985
- Location of start within SEQ ID NO 1272: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9676
- alpha/beta hydrolase fold
- Location within SEQ ID NO 1273: from 96 to 318 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1274
- Ceres seq_id 1499986
- Location of start within SEQ ID NO 1272: at 30 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9677
- alpha/beta hydrolase fold
- Location within SEQ ID NO 1274: from 87 to 309 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 253505

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1275
- Ceres seq_id 1499989

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1276
- Ceres seq_id 1499990
- Location of start within SEQ ID NO 1275: at 206 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9678
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1276: from 83 to 360 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9679
- gi No. 2351097
- % Identity 99.5
- Alignment Length 391
- Location of Alignment in SEQ ID NO 1276: from 1 to 391

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1277
- Ceres seq_id 1499991
- Location of start within SEQ ID NO 1275: at 356 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9680
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1277: from 33 to 310 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9681
- gi No. 2351097
- % Identity 99.5
- Alignment Length 391
- Location of Alignment in SEQ ID NO 1277: from 1 to 341

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1278
 - Ceres seq_id 1499992
 - Location of start within SEQ ID NO 1275: at 422 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9682
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1278: from 11 to 288 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9683
- gi No. 2351097
- % Identity 99.5
- Alignment Length 391
- Location of Alignment in SEQ ID NO 1278: from 1 to 319

Maximum Length Sequence corresponding to clone ID 253633

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1279
- Ceres seq_id 1499993

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1280
- Ceres seq_id 1499994
- Location of start within SEQ ID NO 1279: at 198 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9684
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1280: from 3 to 125 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 253648

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1281
- Ceres seq_id 1499995

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1282
- Ceres seq_id 1499996
- Location of start within SEQ ID NO 1281: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1283
- Ceres seq_id 1499997
- Location of start within SEQ ID NO 1281: at 60 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9685
- gi No. 1209262
- % Identity 71
- Alignment Length 63

- Location of Alignment in SEQ ID NO 1283: from 5 to 66
- Alignment No. 9686
- gi No. 125408
- % Identity 92.4
- Alignment Length 66
- Location of Alignment in SEQ ID NO 1283: from 1 to 66
- Alignment No. 9687
- gi No. 167146
- % Identity 71
- Alignment Length 62
- Location of Alignment in SEQ ID NO 1283: from 5 to 66
- Alignment No. 9688
- gi No. 399298
- % Identity 100
- Alignment Length 66
- Location of Alignment in SEQ ID NO 1283: from 1 to 66
- Alignment No. 9689
- gi No. 4493273
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1283: from 27 to 63
- Alignment No. 9690
- gi No. 4493276
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1283: from 27 to 63
- Alignment No. 9691
- gi No. 4494076
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1283: from 27 to 63
- Alignment No. 9692
- gi No. 4538893
- % Identity 91.9
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1283: from 27 to 63

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1284
- Ceres seq_id 1499998
- Location of start within SEQ ID NO 1281: at 79 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 253653

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1285
- Ceres seq_id 1499999

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1286
- Ceres seq_id 1500000
- Location of start within SEQ ID NO 1285: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9693
- Plant lipid transfer protein family
- Location within SEQ ID NO 1286: from 45 to 76 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1287
- Ceres seq_id 1500001
- Location of start within SEQ ID NO 1285: at 37 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9694
- Plant lipid transfer protein family
- Location within SEQ ID NO 1287: from 33 to 64 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1288
- Ceres seq_id 1500002
- Location of start within SEQ ID NO 1285: at 85 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9695
- Plant lipid transfer protein family
- Location within SEQ ID NO 1288: from 17 to 48 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 253679

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1289
- Ceres seq_id 1500003

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1290
- Ceres seq_id 1500004
- Location of start within SEQ ID NO 1289: at 603 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9696
- gi No. 4455227
- % Identity 100
- Alignment Length 178
- Location of Alignment in SEQ ID NO 1290: from 37 to 214

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1291
- Ceres seq_id 1500005
- Location of start within SEQ ID NO 1289: at 606 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9697
- gi No. 4455227
- % Identity 100
- Alignment Length 178
- Location of Alignment in SEQ ID NO 1291: from 36 to 213

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1292
- Ceres seq_id 1500006
- Location of start within SEQ ID NO 1289: at 711 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9698
- gi No. 4455227
- % Identity 100
- Alignment Length 178
- Location of Alignment in SEQ ID NO 1292: from 1 to 178

Maximum Length Sequence corresponding to clone ID 253698

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1293
- Ceres seq_id 1500007

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1294
- Ceres seq_id 1500008
- Location of start within SEQ ID NO 1293: at 20 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9699
- Cytochrome P450
- Location within SEQ ID NO 1294: from 31 to 481 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9700
- gi No. 4006850
- % Identity 83.3
- Alignment Length 180
- Location of Alignment in SEQ ID NO 1294: from 314 to 492

- Alignment No. 9701
- gi No. 4006851
- % Identity 73.8
- Alignment Length 500
- Location of Alignment in SEQ ID NO 1294: from 1 to 494

- Alignment No. 9702
- gi No. 4468802
- % Identity 76.1
- Alignment Length 494
- Location of Alignment in SEQ ID NO 1294: from 1 to 492

- Alignment No. 9703
- gi No. 4468803
- % Identity 98.8
- Alignment Length 494
- Location of Alignment in SEQ ID NO 1294: from 1 to 494

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1295
- Ceres seq_id 1500009
- Location of start within SEQ ID NO 1293: at 365 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9704
- Cytochrome P450
- Location within SEQ ID NO 1295: from 1 to 366 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9705
- gi No. 4006850
- % Identity 83.3
- Alignment Length 180
- Location of Alignment in SEQ ID NO 1295: from 199 to 377
- Alignment No. 9706
- gi No. 4006851
- % Identity 73.8
- Alignment Length 500
- Location of Alignment in SEQ ID NO 1295: from 1 to 379
- Alignment No. 9707
- gi No. 4468802
- % Identity 76.1
- Alignment Length 494
- Location of Alignment in SEQ ID NO 1295: from 1 to 377
- Alignment No. 9708
- gi No. 4468803
- % Identity 98.8
- Alignment Length 494
- Location of Alignment in SEQ ID NO 1295: from 1 to 379

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1296
- Ceres seq_id 1500010
- Location of start within SEQ ID NO 1293: at 536 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9709
- Cytochrome P450
- Location within SEQ ID NO 1296: from 1 to 309 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9710
- gi No. 4006850
- % Identity 83.3
- Alignment Length 180
- Location of Alignment in SEQ ID NO 1296: from 142 to 320
- Alignment No. 9711
- gi No. 4006851
- % Identity 73.8
- Alignment Length 500
- Location of Alignment in SEQ ID NO 1296: from 1 to 322
- Alignment No. 9712
- gi No. 4468802

- % Identity 76.1
- Alignment Length 494
- Location of Alignment in SEQ ID NO 1296: from 1 to 320
- Alignment No. 9713
- gi No. 4468803
- % Identity 98.8
- Alignment Length 494
- Location of Alignment in SEQ ID NO 1296: from 1 to 322

Maximum Length Sequence corresponding to clone ID 253770

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1297
- Ceres seq_id 1500011

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1298
- Ceres seq_id 1500012
- Location of start within SEQ ID NO 1297: at 95 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9714
- Inositol monophosphatase family
- Location within SEQ ID NO 1298: from 122 to 327 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9715
- gi No. 1354510
- % Identity 100
- Alignment Length 373
- Location of Alignment in SEQ ID NO 1298: from 1 to 373
- Alignment No. 9716
- gi No. 2736075
- % Identity 99.5
- Alignment Length 373
- Location of Alignment in SEQ ID NO 1298: from 1 to 373

Maximum Length Sequence corresponding to clone ID 253849

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1299
- Ceres seq_id 1500017

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1300
- Ceres seq_id 1500018
- Location of start within SEQ ID NO 1299: at 106 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9717
- Zinc finger, C3HC4 type (RING finger)
- Location within SEQ ID NO 1300: from 201 to 241 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9718
- gi No. 2642154
- % Identity 96.3
- Alignment Length 354
- Location of Alignment in SEQ ID NO 1300: from 1 to 354

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1301
- Ceres seq_id 1500019
- Location of start within SEQ ID NO 1299: at 325 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9719
- Zinc finger, C3HC4 type (RING finger)
- Location within SEQ ID NO 1301: from 128 to 168 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9720
- gi No. 2642154
- % Identity 96.3
- Alignment Length 354
- Location of Alignment in SEQ ID NO 1301: from 1 to 281

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1302
- Ceres seq_id 1500020
- Location of start within SEQ ID NO 1299: at 472 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9721
- Zinc finger, C3HC4 type (RING finger)
- Location within SEQ ID NO 1302: from 79 to 119 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9722
- gi No. 2642154
- % Identity 96.3
- Alignment Length 354
- Location of Alignment in SEQ ID NO 1302: from 1 to 232

Maximum Length Sequence corresponding to clone ID 254111

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1303
- Ceres seq_id 1500025

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1304
- Ceres seq_id 1500026
- Location of start within SEQ ID NO 1303: at 381 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9723
- gi No. 5541682
- % Identity 98.7
- Alignment Length 157
- Location of Alignment in SEQ ID NO 1304: from 18 to 174

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1305
- Ceres seq_id 1500027
- Location of start within SEQ ID NO 1303: at 522 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9724
- gi No. 5541682
- % Identity 98.7
- Alignment Length 157
- Location of Alignment in SEQ ID NO 1305: from 1 to 127

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1306
- Ceres seq_id 1500028
- Location of start within SEQ ID NO 1303: at 528 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9725
- gi No. 5541682
- % Identity 98.7
- Alignment Length 157
- Location of Alignment in SEQ ID NO 1306: from 1 to 125

Maximum Length Sequence corresponding to clone ID 254513

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1307
- Ceres seq_id 1500036

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1308
- Ceres seq_id 1500037
- Location of start within SEQ ID NO 1307: at 613 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9726
- gi No. 4006920
- % Identity 99.3
- Alignment Length 400
- Location of Alignment in SEQ ID NO 1308: from 1 to 373

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1309
- Ceres seq_id 1500038
- Location of start within SEQ ID NO 1307: at 718 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9727
- gi No. 4006920
- % Identity 99.3
- Alignment Length 400
- Location of Alignment in SEQ ID NO 1309: from 1 to 338

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1310
- Ceres seq_id 1500039
- Location of start within SEQ ID NO 1307: at 868 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9728

- gi No. 4006920
- % Identity 99.3
- Alignment Length 400
- Location of Alignment in SEQ ID NO 1310: from 1 to 288

Maximum Length Sequence corresponding to clone ID 254633

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1311
- Ceres seq_id 1500040

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1312
- Ceres seq_id 1500041
- Location of start within SEQ ID NO 1311: at 98 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9729
- gi No. 2935529
- % Identity 76
- Alignment Length 217
- Location of Alignment in SEQ ID NO 1312: from 101 to 317

- Alignment No. 9730
- gi No. 3687238
- % Identity 100
- Alignment Length 234
- Location of Alignment in SEQ ID NO 1312: from 76 to 309

- Alignment No. 9731
- gi No. 4539422
- % Identity 73.9
- Alignment Length 319
- Location of Alignment in SEQ ID NO 1312: from 1 to 317

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1313
- Ceres seq_id 1500042
- Location of start within SEQ ID NO 1311: at 242 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 9732
- gi No. 2935529
- % Identity 76
- Alignment Length 217
- Location of Alignment in SEQ ID NO 1313: from 53 to 269

- Alignment No. 9733
- gi No. 3687238
- % Identity 100
- Alignment Length 234
- Location of Alignment in SEQ ID NO 1313: from 28 to 261

- Alignment No. 9734
- gi No. 4539422
- % Identity 73.9
- Alignment Length 319
- Location of Alignment in SEQ ID NO 1313: from 1 to 269

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1314
 - Ceres seq_id 1500043
 - Location of start within SEQ ID NO 1311: at 323 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 9735
 - gi No. 2935529
 - % Identity 76
 - Alignment Length 217
 - Location of Alignment in SEQ ID NO 1314: from 26 to 242
- Alignment No. 9736
 - gi No. 3687238
 - % Identity 100
 - Alignment Length 234
 - Location of Alignment in SEQ ID NO 1314: from 1 to 234
- Alignment No. 9737
 - gi No. 4539422
 - % Identity 73.9
 - Alignment Length 319
 - Location of Alignment in SEQ ID NO 1314: from 1 to 242

Maximum Length Sequence corresponding to clone ID 254758

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1315
- Ceres seq_id 1500050

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1316
- Ceres seq_id 1500051
- Location of start within SEQ ID NO 1315: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9738
- TBC domain
- Location within SEQ ID NO 1316: from 156 to 275 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9739
- gi No. 2880048
- % Identity 96.9
- Alignment Length 254
- Location of Alignment in SEQ ID NO 1316: from 143 to 275

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1317
- Ceres seq_id 1500052
- Location of start within SEQ ID NO 1315: at 51 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9740
- TBC domain
- Location within SEQ ID NO 1317: from 140 to 259 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9741

- gi No. 2880048
- % Identity 96.9
- Alignment Length 254
- Location of Alignment in SEQ ID NO 1317: from 127 to 259

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1318
- Ceres seq_id 1500053
- Location of start within SEQ ID NO 1315: at 408 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9742
- TBC domain
- Location within SEQ ID NO 1318: from 21 to 140 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9743
- gi No. 2880048
- % Identity 96.9
- Alignment Length 254
- Location of Alignment in SEQ ID NO 1318: from 8 to 140

Maximum Length Sequence corresponding to clone ID 254801

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1319
- Ceres seq_id 1500054

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1320
- Ceres seq_id 1500055
- Location of start within SEQ ID NO 1319: at 401 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 9744
- Ubiquitin family
- Location within SEQ ID NO 1320: from 1 to 76 aa.
- Alignment No. 9745
- Ubiquitin family
- Location within SEQ ID NO 1320: from 77 to 146 aa.

(D) Related Amino Acid Sequences

- Alignment No. 9746
- gi No. 100490
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9747
- gi No. 100490
- % Identity 100
- Alignment Length 137
- Location of Alignment in SEQ ID NO 1320: from 10 to 146
- Alignment No. 9748
- gi No. 100490
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9749
- gi No. 100490
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9750
- gi No. 100524
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9751
- gi No. 100524
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9752
- gi No. 100524
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9753
- gi No. 100524
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9754
- gi No. 100524
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9755
- gi No. 100524
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9756
- gi No. 100525
- % Identity 100
- Alignment Length 106
- Location of Alignment in SEQ ID NO 1320: from 1 to 106
- Alignment No. 9757
- gi No. 100525
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9758
- gi No. 100525
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9759

- gi No. 100525
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9760
- gi No. 100598
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 9761
- gi No. 100598
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 9762
- gi No. 100599
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 9763
- gi No. 100599
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 9764
- gi No. 100812
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 9765
- gi No. 100812
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 9766
- gi No. 100934
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 9767
- gi No. 100934
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9768
- gi No. 100934
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9769
- gi No. 100934

- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9770
- gi No. 100934
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9771
- gi No. 100934
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9772
- gi No. 100934
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9773
- gi No. 100981
- % Identity 100
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1320: from 113 to 146

- Alignment No. 9774
- gi No. 100981
- % Identity 100
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1320: from 37 to 76

- Alignment No. 9775
- gi No. 102062
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 9776
- gi No. 102062
- % Identity 92.2
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 9777
- gi No. 102278
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 9778
- gi No. 102278
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9779
- gi No. 102278
- % Identity 94.5

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9780
- gi No. 102278
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9781
- gi No. 102278
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9782
- gi No. 102278
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9783
- gi No. 102278
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9784
- gi No. 102279
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 9785
- gi No. 102279
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9786
- gi No. 102279
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9787
- gi No. 102280
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 9788
- gi No. 102280
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9789
- gi No. 102280
- % Identity 93.2
- Alignment Length 146

- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9790
- gi No. 102280
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9791
- gi No. 102280
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9792
- gi No. 102281
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9793
- gi No. 102281
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9794
- gi No. 102281
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9795
- gi No. 102281
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9796
- gi No. 102281
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9797
- gi No. 102389
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 9798
- gi No. 102389
- % Identity 85.2
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1320: from 1 to 87
- Alignment No. 9799
- gi No. 103436
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 9800
- gi No. 103436
- % Identity 94.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 9801
- gi No. 1044940
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 9802
- gi No. 1044940
- % Identity 98.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 9803
- gi No. 104829
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 9804
- gi No. 104829
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9805
- gi No. 104829
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9806
- gi No. 1050930
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 9807
- gi No. 1050930
- % Identity 95
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1320: from 1 to 100

- Alignment No. 9808
- gi No. 10673
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 9809
- gi No. 10673
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1320: from 1 to 87

- Alignment No. 9810
- gi No. 1070590
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9811
- gi No. 1070590
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9812
- gi No. 1070590
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9813
- gi No. 1070591
- % Identity 94.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
- Alignment No. 9814
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9815
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9816
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9817
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9818
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9819
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9820

- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9821
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9822
- gi No. 1076678
- % Identity 98.7
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 9823
- gi No. 1076678
- % Identity 79.2
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1320: from 54 to 146

- Alignment No. 9824
- gi No. 1076708
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 9825
- gi No. 1076708
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9826
- gi No. 1076708
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9827
- gi No. 1076708
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9828
- gi No. 1078777
- % Identity 87.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 9829
- gi No. 1078777
- % Identity 88.2
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 9830
- gi No. 1078813

- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 9831
- gi No. 1078813
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9832
- gi No. 1078813
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9833
- gi No. 1083758
- % Identity 88
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1320: from 1 to 108

- Alignment No. 9834
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9835
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9836
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9837
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9838
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9839
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9840
- gi No. 1083758
- % Identity 95.9

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9841
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9842
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9843
- gi No. 1101011
- % Identity 84.2
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 9844
- gi No. 1101011
- % Identity 87.3
- Alignment Length 79
- Location of Alignment in SEQ ID NO 1320: from 68 to 146

- Alignment No. 9845
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9846
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9847
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9848
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9849
- gi No. 1101011
- % Identity 84.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9850
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146

- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9851
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9852
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9853
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9854
- gi No. 1101013
- % Identity 85
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1320: from 7 to 46
- Alignment No. 9855
- gi No. 1101013
- % Identity 85
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1320: from 83 to 122
- Alignment No. 9856
- gi No. 1101015
- % Identity 85
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1320: from 7 to 46
- Alignment No. 9857
- gi No. 1101015
- % Identity 85
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1320: from 83 to 122
- Alignment No. 9858
- gi No. 1101019
- % Identity 80
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1320: from 7 to 46
- Alignment No. 9859
- gi No. 1101019
- % Identity 80
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1320: from 83 to 122
- Alignment No. 9860
- gi No. 1101021
- % Identity 87
- Alignment Length 46
- Location of Alignment in SEQ ID NO 1320: from 1 to 46

- Alignment No. 9861
- gi No. 1101021
- % Identity 84.4
- Alignment Length 64
- Location of Alignment in SEQ ID NO 1320: from 83 to 146
- Alignment No. 9862
- gi No. 1101021
- % Identity 86.2
- Alignment Length 116
- Location of Alignment in SEQ ID NO 1320: from 7 to 122
- Alignment No. 9863
- gi No. 1101023
- % Identity 87.9
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1320: from 114 to 146
- Alignment No. 9864
- gi No. 1101023
- % Identity 92
- Alignment Length 50
- Location of Alignment in SEQ ID NO 1320: from 38 to 87
- Alignment No. 9865
- gi No. 1107481
- % Identity 97.9
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1320: from 1 to 96
- Alignment No. 9866
- gi No. 1107481
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9867
- gi No. 1143188
- % Identity 94.5
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1320: from 77 to 149
- Alignment No. 9868
- gi No. 1143188
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9869
- gi No. 1143188
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9870
- gi No. 1143188
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9871
- gi No. 1167510
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 9872
- gi No. 1167510
- % Identity 91.3
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1320: from 1 to 103

- Alignment No. 9873
- gi No. 1174858
- % Identity 74.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 9874
- gi No. 1174858
- % Identity 76.3
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 9875
- gi No. 1174859
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 9876
- gi No. 1174859
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 9877
- gi No. 1174860
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 9878
- gi No. 1174860
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 9879
- gi No. 1174861
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 9880
- gi No. 1174861
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 9881

- gi No. 1184755
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 9882
- gi No. 1184755
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9883
- gi No. 1197093
- % Identity 94.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
- Alignment No. 9884
- gi No. 1197093
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9885
- gi No. 1197093
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9886
- gi No. 1197093
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9887
- gi No. 1304128
- % Identity 96.2
- Alignment Length 79
- Location of Alignment in SEQ ID NO 1320: from 1 to 79
- Alignment No. 9888
- gi No. 1304128
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9889
- gi No. 1304128
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9890
- gi No. 1304128
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9891
- gi No. 1304128

- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9892
- gi No. 1304128
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9893
- gi No. 1304128
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9894
- gi No. 1304128
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9895
- gi No. 1304357
- % Identity 81.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 9896
- gi No. 1304357
- % Identity 82.9
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 9897
- gi No. 1321735
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 9898
- gi No. 1321735
- % Identity 95.7
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1320: from 1 to 139

- Alignment No. 9899
- gi No. 1326021
- % Identity 96.3
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1320: from 120 to 146

- Alignment No. 9900
- gi No. 1326021
- % Identity 97
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1320: from 44 to 76

- Alignment No. 9901
- gi No. 1326022
- % Identity 96.1

- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9902
- gi No. 1326022
- % Identity 97.2
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1320: from 39 to 146
- Alignment No. 9903
- gi No. 1326022
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9904
- gi No. 1332579
- % Identity 97.4
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
- Alignment No. 9905
- gi No. 1332579
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9906
- gi No. 1332579
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9907
- gi No. 1332579
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9908
- gi No. 1332579
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9909
- gi No. 1332579
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9910
- gi No. 1332579
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9911
- gi No. 1332579
- % Identity 100
- Alignment Length 146

- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9912
- gi No. 1332579
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9913
- gi No. 1332579
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9914
- gi No. 1351348
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 9915
- gi No. 1351348
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9916
- gi No. 1351349
- % Identity 90
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 9917
- gi No. 1351349
- % Identity 90.8
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9918
- gi No. 1353755
- % Identity 95.2
- Alignment Length 83
- Location of Alignment in SEQ ID NO 1320: from 1 to 83
- Alignment No. 9919
- gi No. 1353755
- % Identity 95.2
- Alignment Length 105
- Location of Alignment in SEQ ID NO 1320: from 42 to 146
- Alignment No. 9920
- gi No. 1353757
- % Identity 93.5
- Alignment Length 46
- Location of Alignment in SEQ ID NO 1320: from 1 to 46
- Alignment No. 9921
- gi No. 1353757
- % Identity 94.2
- Alignment Length 69
- Location of Alignment in SEQ ID NO 1320: from 78 to 146

- Alignment No. 9922
 - gi No. 1353757
 - % Identity 94.2
 - Alignment Length 121
 - Location of Alignment in SEQ ID NO 1320: from 2 to 122
- Alignment No. 9923
 - gi No. 1362008
 - % Identity 97.4
 - Alignment Length 76
 - Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9924
 - gi No. 1362008
 - % Identity 92.5
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9925
 - gi No. 1362008
 - % Identity 92.5
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9926
 - gi No. 1362008
 - % Identity 86.3
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9927
 - gi No. 1362008
 - % Identity 92.5
 - Alignment Length 159
 - Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9928
 - gi No. 1362009
 - % Identity 79.7
 - Alignment Length 148
 - Location of Alignment in SEQ ID NO 1320: from 1 to 148
- Alignment No. 9929
 - gi No. 1362010
 - % Identity 92.2
 - Alignment Length 77
 - Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9930
 - gi No. 1362010
 - % Identity 96.6
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9931
 - gi No. 1362010
 - % Identity 88.4
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9932
- gi No. 1362010
- % Identity 92.5
- Alignment Length 147
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9933
- gi No. 1362012
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9934
- gi No. 1362012
- % Identity 76.2
- Alignment Length 149
- Location of Alignment in SEQ ID NO 1320: from 1 to 147
- Alignment No. 9935
- gi No. 1362012
- % Identity 79.6
- Alignment Length 152
- Location of Alignment in SEQ ID NO 1320: from 1 to 145
- Alignment No. 9936
- gi No. 1362012
- % Identity 71.1
- Alignment Length 167
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9937
- gi No. 136665
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 9938
- gi No. 136665
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9939
- gi No. 136666
- % Identity 98.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 9940
- gi No. 136666
- % Identity 98.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9941
- gi No. 136667
- % Identity 98.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 9942

- gi No. 136667
- % Identity 98.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 9943
- gi No. 136668
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 9944
- gi No. 136668
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 9945
- gi No. 136669
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 9946
- gi No. 136669
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 9947
- gi No. 136670
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 9948
- gi No. 136670
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 9949
- gi No. 136671
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 9950
- gi No. 136671
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 9951
- gi No. 136672
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 9952
- gi No. 136672

- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 9953
- gi No. 136673
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 9954
- gi No. 136673
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 9955
- gi No. 136674
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 9956
- gi No. 136674
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 9957
- gi No. 136675
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 9958
- gi No. 136675
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 9959
- gi No. 136676
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 9960
- gi No. 136676
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 9961
- gi No. 136677
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 9962
- gi No. 136677
- % Identity 97.4

- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 9963
- gi No. 136678
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 9964
- gi No. 136678
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 9965
- gi No. 1421797
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 9966
- gi No. 1421797
- % Identity 96.2
- Alignment Length 79
- Location of Alignment in SEQ ID NO 1320: from 1 to 79

- Alignment No. 9967
- gi No. 1480012
- % Identity 96.3
- Alignment Length 54
- Location of Alignment in SEQ ID NO 1320: from 93 to 146

- Alignment No. 9968
- gi No. 1480012
- % Identity 95.1
- Alignment Length 61
- Location of Alignment in SEQ ID NO 1320: from 17 to 77

- Alignment No. 9969
- gi No. 156480
- % Identity 94.6
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1320: from 1 to 37

- Alignment No. 9970
- gi No. 156480
- % Identity 94.6
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1320: from 77 to 113

- Alignment No. 9971
- gi No. 158759
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 9972
- gi No. 158759
- % Identity 94.7
- Alignment Length 76

- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9973
- gi No. 158763
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 9974
- gi No. 158763
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9975
- gi No. 158765
- % Identity 91.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 9976
- gi No. 158765
- % Identity 92.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9977
- gi No. 158767
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 9978
- gi No. 158767
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9979
- gi No. 158769
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 9980
- gi No. 158769
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9981
- gi No. 158771
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 9982
- gi No. 158771
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 9983
- gi No. 161281
- % Identity 94.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1320: from 77 to 147

- Alignment No. 9984
- gi No. 161281
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 9985
- gi No. 163575
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 9986
- gi No. 163575
- % Identity 96.3
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1320: from 66 to 146

- Alignment No. 9987
- gi No. 163575
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9988
- gi No. 166336
- % Identity 96.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 9989
- gi No. 166336
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9990
- gi No. 166336
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9991
- gi No. 166336
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9992
- gi No. 166336
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 9993
- gi No. 166336
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 9994
- gi No. 1666175
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 9995
- gi No. 1666175
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9996
- gi No. 1675359
- % Identity 92.7
- Alignment Length 41
- Location of Alignment in SEQ ID NO 1320: from 1 to 41
- Alignment No. 9997
- gi No. 1675359
- % Identity 92.7
- Alignment Length 41
- Location of Alignment in SEQ ID NO 1320: from 77 to 117
- Alignment No. 9998
- gi No. 167935
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 9999
- gi No. 167935
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10000
- gi No. 167935
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10001
- gi No. 167935
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10002
- gi No. 167935
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10003

- gi No. 167941
- % Identity 92.8
- Alignment Length 69
- Location of Alignment in SEQ ID NO 1320: from 78 to 146

- Alignment No. 10004
- gi No. 167941
- % Identity 93.3
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1320: from 2 to 76

- Alignment No. 10005
- gi No. 167945
- % Identity 93.5
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 10006
- gi No. 167945
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10007
- gi No. 167945
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10008
- gi No. 167947
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10009
- gi No. 167947
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10010
- gi No. 167947
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10011
- gi No. 167947
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10012
- gi No. 167947
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10013
- gi No. 167947

- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10014
- gi No. 167947
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10015
- gi No. 167949
- % Identity 93.5
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
- Alignment No. 10016
- gi No. 167949
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10017
- gi No. 167949
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10018
- gi No. 167949
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10019
- gi No. 167949
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10020
- gi No. 1684855
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10021
- gi No. 1684855
- % Identity 81.7
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1320: from 16 to 146
- Alignment No. 10022
- gi No. 1684855
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10023
- gi No. 1684855
- % Identity 100

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
-
- Alignment No. 10024
- gi No. 1684855
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
-
- Alignment No. 10025
- gi No. 1684857
- % Identity 98.7
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
-
- Alignment No. 10026
- gi No. 1684857
- % Identity 100
- Alignment Length 132
- Location of Alignment in SEQ ID NO 1320: from 15 to 146
-
- Alignment No. 10027
- gi No. 1684857
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
-
- Alignment No. 10028
- gi No. 170352
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
-
- Alignment No. 10029
- gi No. 170352
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
-
- Alignment No. 10030
- gi No. 170352
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
-
- Alignment No. 10031
- gi No. 170352
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
-
- Alignment No. 10032
- gi No. 170352
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
-
- Alignment No. 10033
- gi No. 170352
- % Identity 100
- Alignment Length 146

- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10034
 - gi No. 170354
 - % Identity 100
 - Alignment Length 76
 - Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10035
 - gi No. 170354
 - % Identity 100
 - Alignment Length 142
 - Location of Alignment in SEQ ID NO 1320: from 5 to 146
- Alignment No. 10036
 - gi No. 170354
 - % Identity 100
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10037
 - gi No. 170354
 - % Identity 100
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10038
 - gi No. 170354
 - % Identity 100
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10039
 - gi No. 1762374
 - % Identity 95.7
 - Alignment Length 70
 - Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10040
 - gi No. 1762374
 - % Identity 95.8
 - Alignment Length 71
 - Location of Alignment in SEQ ID NO 1320: from 1 to 71
- Alignment No. 10041
 - gi No. 1762935
 - % Identity 98.6
 - Alignment Length 70
 - Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10042
 - gi No. 1762935
 - % Identity 98.7
 - Alignment Length 76
 - Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10043
 - gi No. 1763015
 - % Identity 95.7
 - Alignment Length 70
 - Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10044
- gi No. 1763015
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10045
- gi No. 1771780
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10046
- gi No. 1771780
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10047
- gi No. 1778712
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10048
- gi No. 1778712
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10049
- gi No. 1778712
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10050
- gi No. 1778712
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10051
- gi No. 1778712
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10052
- gi No. 1800281
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10053
- gi No. 1800281
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10054
 - gi No. 1800281
 - % Identity 100
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10055
 - gi No. 1800281
 - % Identity 99.3
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10056
 - gi No. 1800281
 - % Identity 99.3
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10057
 - gi No. 1805696
 - % Identity 95.2
 - Alignment Length 63
 - Location of Alignment in SEQ ID NO 1320: from 84 to 146
- Alignment No. 10058
 - gi No. 1805696
 - % Identity 95.4
 - Alignment Length 65
 - Location of Alignment in SEQ ID NO 1320: from 1 to 65
- Alignment No. 10059
 - gi No. 1805696
 - % Identity 95.5
 - Alignment Length 134
 - Location of Alignment in SEQ ID NO 1320: from 8 to 141
- Alignment No. 10060
 - gi No. 1839584
 - % Identity 100
 - Alignment Length 38
 - Location of Alignment in SEQ ID NO 1320: from 1 to 38
- Alignment No. 10061
 - gi No. 1839584
 - % Identity 100
 - Alignment Length 38
 - Location of Alignment in SEQ ID NO 1320: from 77 to 114
- Alignment No. 10062
 - gi No. 1841849
 - % Identity 100
 - Alignment Length 16
 - Location of Alignment in SEQ ID NO 1320: from 1 to 16
- Alignment No. 10063
 - gi No. 1841849
 - % Identity 100
 - Alignment Length 35
 - Location of Alignment in SEQ ID NO 1320: from 112 to 146
- Alignment No. 10064

- gi No. 1841849
- % Identity 100
- Alignment Length 57
- Location of Alignment in SEQ ID NO 1320: from 36 to 92

- Alignment No. 10065
- gi No. 208558
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10066
- gi No. 208558
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10067
- gi No. 208560
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10068
- gi No. 208560
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10069
- gi No. 208562
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10070
- gi No. 208562
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10071
- gi No. 208564
- % Identity 91.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10072
- gi No. 208564
- % Identity 92.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10073
- gi No. 208566
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10074
- gi No. 208566

- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10075
- gi No. 208568
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10076
- gi No. 208568
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10077
- gi No. 208891
- % Identity 96
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1320: from 72 to 146

- Alignment No. 10078
- gi No. 208891
- % Identity 93.9
- Alignment Length 98
- Location of Alignment in SEQ ID NO 1320: from 1 to 98

- Alignment No. 10079
- gi No. 209603
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10080
- gi No. 209603
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10081
- gi No. 2118958
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10082
- gi No. 2118958
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10083
- gi No. 2118958
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10084
- gi No. 2118958
- % Identity 95.9

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10085
- gi No. 2118958
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10086
- gi No. 2118959
- % Identity 85.7
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1320: from 1 to 112

- Alignment No. 10087
- gi No. 2118959
- % Identity 84.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10088
- gi No. 2118959
- % Identity 83.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10089
- gi No. 2118960
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10090
- gi No. 2118960
- % Identity 96.5
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1320: from 62 to 146

- Alignment No. 10091
- gi No. 2118960
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10092
- gi No. 2118961
- % Identity 94.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1320: from 73 to 146

- Alignment No. 10093
- gi No. 2118961
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10094
- gi No. 2118961
- % Identity 95.2
- Alignment Length 146

- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10095
- gi No. 2118962
- % Identity 95.9
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1320: from 73 to 146

- Alignment No. 10096
- gi No. 2118962
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10097
- gi No. 2118962
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10098
- gi No. 2118963
- % Identity 89.3
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1320: from 1 to 75

- Alignment No. 10099
- gi No. 2118963
- % Identity 91
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1320: from 36 to 146

- Alignment No. 10100
- gi No. 2118964
- % Identity 94.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 10101
- gi No. 2118964
- % Identity 96.4
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1320: from 37 to 146

- Alignment No. 10102
- gi No. 2118964
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10103
- gi No. 2118964
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10104
- gi No. 2118965
- % Identity 94.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 10105
- gi No. 2118965
- % Identity 96.3
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1320: from 66 to 146

- Alignment No. 10106
- gi No. 2118965
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10107
- gi No. 2118965
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10108
- gi No. 2129452
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10109
- gi No. 2129452
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10110
- gi No. 2129452
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10111
- gi No. 2129452
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10112
- gi No. 2129452
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10113
- gi No. 2129452
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10114
- gi No. 2133278
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10115
- gi No. 2133278
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10116
- gi No. 2133549
- % Identity 96.3
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1320: from 120 to 146
- Alignment No. 10117
- gi No. 2133549
- % Identity 95.8
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1320: from 1 to 48
- Alignment No. 10118
- gi No. 2133549
- % Identity 96
- Alignment Length 50
- Location of Alignment in SEQ ID NO 1320: from 97 to 146
- Alignment No. 10119
- gi No. 2133549
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1320: from 21 to 76
- Alignment No. 10120
- gi No. 2133549
- % Identity 96.3
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1320: from 44 to 124
- Alignment No. 10121
- gi No. 2144011
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10122
- gi No. 2144011
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10123
- gi No. 2144275
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10124
- gi No. 2144275
- % Identity 92.2
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
- Alignment No. 10125

- gi No. 2144734
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1320: from 1 to 87

- Alignment No. 10126
- gi No. 2144734
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10127
- gi No. 2144734
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10128
- gi No. 2144734
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10129
- gi No. 2149467
- % Identity 87.7
- Alignment Length 83
- Location of Alignment in SEQ ID NO 1320: from 68 to 146

- Alignment No. 10130
- gi No. 2149467
- % Identity 83.3
- Alignment Length 90
- Location of Alignment in SEQ ID NO 1320: from 1 to 85

- Alignment No. 10131
- gi No. 2209091
- % Identity 93.5
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 10132
- gi No. 2209091
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10133
- gi No. 223061
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10134
- gi No. 223061
- % Identity 94.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1320: from 1 to 75

- Alignment No. 10135
- gi No. 224321

- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10136
- gi No. 224321
- % Identity 97.2
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1320: from 39 to 146

- Alignment No. 10137
- gi No. 224321
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10138
- gi No. 225317
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 1 to 70

- Alignment No. 10139
- gi No. 225317
- % Identity 89.6
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 77 to 153

- Alignment No. 10140
- gi No. 225319
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 1 to 70

- Alignment No. 10141
- gi No. 225319
- % Identity 89.6
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 77 to 153

- Alignment No. 10142
- gi No. 225320
- % Identity 91.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 1 to 70

- Alignment No. 10143
- gi No. 225320
- % Identity 87
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 77 to 153

- Alignment No. 10144
- gi No. 2281952
- % Identity 95.2
- Alignment Length 62
- Location of Alignment in SEQ ID NO 1320: from 8 to 69

- Alignment No. 10145
- gi No. 2281952
- % Identity 95.2

- Alignment Length 62
- Location of Alignment in SEQ ID NO 1320: from 84 to 145
- Alignment No. 10146
- gi No. 2281954
- % Identity 93.5
- Alignment Length 62
- Location of Alignment in SEQ ID NO 1320: from 8 to 69
- Alignment No. 10147
- gi No. 2281954
- % Identity 93.5
- Alignment Length 62
- Location of Alignment in SEQ ID NO 1320: from 84 to 145
- Alignment No. 10148
- gi No. 2281955
- % Identity 88.9
- Alignment Length 45
- Location of Alignment in SEQ ID NO 1320: from 8 to 52
- Alignment No. 10149
- gi No. 2281955
- % Identity 88.9
- Alignment Length 45
- Location of Alignment in SEQ ID NO 1320: from 84 to 128
- Alignment No. 10150
- gi No. 2281959
- % Identity 90.6
- Alignment Length 64
- Location of Alignment in SEQ ID NO 1320: from 83 to 146
- Alignment No. 10151
- gi No. 2281959
- % Identity 90.8
- Alignment Length 65
- Location of Alignment in SEQ ID NO 1320: from 7 to 71
- Alignment No. 10152
- gi No. 2330875
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10153
- gi No. 2330875
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10154
- gi No. 2350864
- % Identity 75.9
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1320: from 6 to 63
- Alignment No. 10155
- gi No. 2350864
- % Identity 75.9
- Alignment Length 58

- Location of Alignment in SEQ ID NO 1320: from 82 to 139
- Alignment No. 10156
- gi No. 2408009
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10157
- gi No. 2408009
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1320: from 1 to 87
- Alignment No. 10158
- gi No. 2437825
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10159
- gi No. 2437825
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10160
- gi No. 2437825
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10161
- gi No. 2437825
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10162
- gi No. 247308
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10163
- gi No. 247308
- % Identity 90.8
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10164
- gi No. 248865
- % Identity 95
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1320: from 1 to 20
- Alignment No. 10165
- gi No. 248865
- % Identity 95
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1320: from 77 to 96

- Alignment No. 10166
- gi No. 2558539
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10167
- gi No. 2558539
- % Identity 94.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 10168
- gi No. 2627129
- % Identity 94.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 10169
- gi No. 2627129
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10170
- gi No. 2627129
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10171
- gi No. 2627129
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10172
- gi No. 2627129
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10173
- gi No. 2627129
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10174
- gi No. 2627129
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10175
- gi No. 2627129
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10176
- gi No. 2627131
- % Identity 89.8
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1320: from 1 to 108
- Alignment No. 10177
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10178
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10179
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10180
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10181
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10182
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10183
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10184
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10185
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10186

- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10187
- gi No. 2627133
- % Identity 89.8
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1320: from 1 to 108

- Alignment No. 10188
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10189
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10190
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10191
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10192
- gi No. 2627133
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10193
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10194
- gi No. 2627133
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10195
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10196
- gi No. 2627133

- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10197
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10198
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10199
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10200
- gi No. 2641213
- % Identity 98.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10201
- gi No. 2641213
- % Identity 98.6
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1320: from 1 to 139

- Alignment No. 10202
- gi No. 2654141
- % Identity 92.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10203
- gi No. 2654141
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10204
- gi No. 2654141
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10205
- gi No. 2654141
- % Identity 89
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10206
- gi No. 2654141
- % Identity 89.7

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10207
- gi No. 2707837
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10208
- gi No. 2707837
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10209
- gi No. 2707837
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10210
- gi No. 2707837
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10211
- gi No. 2739333
- % Identity 97.4
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
- Alignment No. 10212
- gi No. 2739333
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10213
- gi No. 2739333
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10214
- gi No. 2739333
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10215
- gi No. 2760345
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10216
- gi No. 2760345
- % Identity 100
- Alignment Length 146

- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10217
- gi No. 2760345
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10218
- gi No. 2760345
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10219
- gi No. 2760347
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10220
- gi No. 2760347
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10221
- gi No. 2760347
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10222
- gi No. 2760347
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10223
- gi No. 2760347
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10224
- gi No. 2760347
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10225
- gi No. 2760349
- % Identity 98.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10226
- gi No. 2760349
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10227
- gi No. 2760349
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10228
- gi No. 2760349
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10229
- gi No. 2760349
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10230
- gi No. 279635
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10231
- gi No. 279635
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10232
- gi No. 279636
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10233
- gi No. 279636
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10234
- gi No. 280386
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10235
- gi No. 280386
- % Identity 98.7
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 10236
- gi No. 281276
- % Identity 90
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1320: from 1 to 20

- Alignment No. 10237
- gi No. 281276
- % Identity 90
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1320: from 77 to 96
- Alignment No. 10238
- gi No. 283496
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10239
- gi No. 283496
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10240
- gi No. 283496
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10241
- gi No. 283496
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10242
- gi No. 283496
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10243
- gi No. 2894304
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10244
- gi No. 2894304
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10245
- gi No. 2894304
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10246
- gi No. 2894304
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10247

- gi No. 2894306
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10248
- gi No. 2894306
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10249
- gi No. 2894308
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10250
- gi No. 2894308
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10251
- gi No. 2894308
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10252
- gi No. 2894308
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10253
- gi No. 2894308
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10254
- gi No. 2995277
- % Identity 100
- Alignment Length 23
- Location of Alignment in SEQ ID NO 1320: from 124 to 146

- Alignment No. 10255
- gi No. 2995277
- % Identity 96.7
- Alignment Length 30
- Location of Alignment in SEQ ID NO 1320: from 48 to 77

- Alignment No. 10256
- gi No. 2995949
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10257
- gi No. 2995949

- % Identity 100
- Alignment Length 104
- Location of Alignment in SEQ ID NO 1320: from 43 to 146

- Alignment No. 10258
- gi No. 3047314
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10259
- gi No. 3047314
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1320: from 1 to 87

- Alignment No. 10260
- gi No. 3047316
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10261
- gi No. 3047316
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10262
- gi No. 3047318
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10263
- gi No. 3047318
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10264
- gi No. 3047318
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10265
- gi No. 3047318
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10266
- gi No. 3047318
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10267
- gi No. 3091264
- % Identity 98.7

- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10268
- gi No. 3091264
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10269
- gi No. 3091264
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10270
- gi No. 3091264
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10271
- gi No. 3126967
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10272
- gi No. 3126967
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10273
- gi No. 3126967
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10274
- gi No. 3126967
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10275
- gi No. 3126967
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10276
- gi No. 3126967
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10277
- gi No. 3152950
- % Identity 97.1
- Alignment Length 70

- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10278
 - gi No. 3152950
 - % Identity 97.4
 - Alignment Length 76
 - Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10279
 - gi No. 3158372
 - % Identity 100
 - Alignment Length 98
 - Location of Alignment in SEQ ID NO 1320: from 49 to 146
- Alignment No. 10280
 - gi No. 3158372
 - % Identity 99.1
 - Alignment Length 109
 - Location of Alignment in SEQ ID NO 1320: from 1 to 109
- Alignment No. 10281
 - gi No. 320608
 - % Identity 100
 - Alignment Length 76
 - Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10282
 - gi No. 320608
 - % Identity 100
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10283
 - gi No. 320608
 - % Identity 100
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10284
 - gi No. 320608
 - % Identity 100
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10285
 - gi No. 322750
 - % Identity 100
 - Alignment Length 70
 - Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10286
 - gi No. 322750
 - % Identity 98.7
 - Alignment Length 77
 - Location of Alignment in SEQ ID NO 1320: from 1 to 77
- Alignment No. 10287
 - gi No. 323071
 - % Identity 84.3
 - Alignment Length 70
 - Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10288
- gi No. 323071
- % Identity 85.5
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10289
- gi No. 323157
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10290
- gi No. 323157
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10291
- gi No. 323157
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10292
- gi No. 323157
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10293
- gi No. 323157
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10294
- gi No. 323157
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10295
- gi No. 323208
- % Identity 88.2
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1320: from 1 to 85

- Alignment No. 10296
- gi No. 323208
- % Identity 82.5
- Alignment Length 144
- Location of Alignment in SEQ ID NO 1320: from 4 to 146

- Alignment No. 10297
- gi No. 323230
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10298
- gi No. 323230
- % Identity 83.7
- Alignment Length 86
- Location of Alignment in SEQ ID NO 1320: from 1 to 85
- Alignment No. 10299
- gi No. 3265058
- % Identity 98.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10300
- gi No. 3265058
- % Identity 98.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10301
- gi No. 3319208
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10302
- gi No. 3319208
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10303
- gi No. 3335355
- % Identity 100
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1320: from 132 to 146
- Alignment No. 10304
- gi No. 3335355
- % Identity 100
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1320: from 56 to 76
- Alignment No. 10305
- gi No. 3335355
- % Identity 97.7
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1320: from 1 to 129
- Alignment No. 10306
- gi No. 3335355
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10307
- gi No. 3335355
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10308

- gi No. 340062
- % Identity 95.5
- Alignment Length 66
- Location of Alignment in SEQ ID NO 1320: from 81 to 146

- Alignment No. 10309
- gi No. 340062
- % Identity 95.8
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1320: from 5 to 76

- Alignment No. 10310
- gi No. 3452083
- % Identity 93.1
- Alignment Length 29
- Location of Alignment in SEQ ID NO 1320: from 1 to 29

- Alignment No. 10311
- gi No. 3452083
- % Identity 97.9
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1320: from 99 to 146

- Alignment No. 10312
- gi No. 3452083
- % Identity 96.4
- Alignment Length 83
- Location of Alignment in SEQ ID NO 1320: from 23 to 105

- Alignment No. 10313
- gi No. 348148
- % Identity 96.3
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1320: from 120 to 146

- Alignment No. 10314
- gi No. 348148
- % Identity 95.8
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1320: from 1 to 48

- Alignment No. 10315
- gi No. 348148
- % Identity 96.3
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1320: from 44 to 124

- Alignment No. 10316
- gi No. 348149
- % Identity 96
- Alignment Length 50
- Location of Alignment in SEQ ID NO 1320: from 97 to 146

- Alignment No. 10317
- gi No. 348149
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1320: from 21 to 76

- Alignment No. 10318
- gi No. 3603456

- % Identity 98.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10319
- gi No. 3603456
- % Identity 100
- Alignment Length 106
- Location of Alignment in SEQ ID NO 1320: from 41 to 146

- Alignment No. 10320
- gi No. 3603456
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10321
- gi No. 3603456
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10322
- gi No. 3687425
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10323
- gi No. 3687425
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10324
- gi No. 3687425
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10325
- gi No. 3738185
- % Identity 96.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 10326
- gi No. 3738185
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10327
- gi No. 3738185
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10328
- gi No. 3738185
- % Identity 97.3

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10329
- gi No. 3738185
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10330
- gi No. 3776536
- % Identity 96.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 10331
- gi No. 3776536
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10332
- gi No. 3776536
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10333
- gi No. 3776536
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10334
- gi No. 3776536
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10335
- gi No. 3776536
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10336
- gi No. 3776536
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10337
- gi No. 3776536
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10338
- gi No. 3789940
- % Identity 100
- Alignment Length 76

- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10339
- gi No. 3789940
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10340
- gi No. 3789940
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10341
- gi No. 3789940
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10342
- gi No. 3789942
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10343
- gi No. 3789942
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10344
- gi No. 3789942
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10345
- gi No. 3789942
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10346
- gi No. 3789942
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10347
- gi No. 3822277
- % Identity 75.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10348
- gi No. 3822277
- % Identity 77.6
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10349
- gi No. 385076
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10350
- gi No. 385076
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10351
- gi No. 3882081
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10352
- gi No. 3882081
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10353
- gi No. 3882081
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10354
- gi No. 3885463
- % Identity 94
- Alignment Length 67
- Location of Alignment in SEQ ID NO 1320: from 80 to 146

- Alignment No. 10355
- gi No. 3885463
- % Identity 86.6
- Alignment Length 82
- Location of Alignment in SEQ ID NO 1320: from 4 to 85

- Alignment No. 10356
- gi No. 3892189
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10357
- gi No. 3892189
- % Identity 84.1
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1320: from 1 to 87

- Alignment No. 10358
- gi No. 402242
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10359
- gi No. 402242
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10360
- gi No. 4049712
- % Identity 85.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10361
- gi No. 4049712
- % Identity 84.6
- Alignment Length 78
- Location of Alignment in SEQ ID NO 1320: from 1 to 78

- Alignment No. 10362
- gi No. 4102845
- % Identity 86.2
- Alignment Length 65
- Location of Alignment in SEQ ID NO 1320: from 82 to 146

- Alignment No. 10363
- gi No. 4102845
- % Identity 87.3
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1320: from 6 to 76

- Alignment No. 10364
- gi No. 4105408
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10365
- gi No. 4105408
- % Identity 95.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 1320: from 10 to 146

- Alignment No. 10366
- gi No. 4105408
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10367
- gi No. 4105408
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10368
- gi No. 4115337
- % Identity 98.7
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 10369

- gi No. 4115337
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10370
- gi No. 4115337
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10371
- gi No. 4115337
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10372
- gi No. 4115337
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10373
- gi No. 4115337
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10374
- gi No. 4150898
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10375
- gi No. 4150898
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10376
- gi No. 4150898
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10377
- gi No. 4150898
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10378
- gi No. 4150912
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10379
- gi No. 4150912

- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10380
- gi No. 4150912
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10381
- gi No. 4150912
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10382
- gi No. 4150912
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10383
- gi No. 4150914
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10384
- gi No. 4150914
- % Identity 95.7
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1320: from 7 to 146

- Alignment No. 10385
- gi No. 4151082
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10386
- gi No. 4151082
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10387
- gi No. 418854
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10388
- gi No. 418854
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10389
- gi No. 418854
- % Identity 100

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10390
- gi No. 418854
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10391
- gi No. 418854
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10392
- gi No. 418854
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10393
- gi No. 421735
- % Identity 94.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1320: from 1 to 19

- Alignment No. 10394
- gi No. 421735
- % Identity 94.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1320: from 77 to 95

- Alignment No. 10395
- gi No. 421867
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10396
- gi No. 421867
- % Identity 98.7
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 10397
- gi No. 421929
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10398
- gi No. 421929
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10399
- gi No. 421929
- % Identity 99.3
- Alignment Length 146

- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10400
- gi No. 421929
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10401
- gi No. 421929
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10402
- gi No. 421929
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10403
- gi No. 421929
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10404
- gi No. 422248
- % Identity 97.4
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
- Alignment No. 10405
- gi No. 422248
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10406
- gi No. 422248
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10407
- gi No. 422248
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10408
- gi No. 422248
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10409
- gi No. 422269
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10410
- gi No. 422269
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10411
- gi No. 422270
- % Identity 90
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10412
- gi No. 422270
- % Identity 89.6
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 10413
- gi No. 422271
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10414
- gi No. 422271
- % Identity 92.2
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 10415
- gi No. 433970
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10416
- gi No. 433970
- % Identity 95.5
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1320: from 36 to 146

- Alignment No. 10417
- gi No. 433970
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10418
- gi No. 433970
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10419
- gi No. 433970
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10420
- gi No. 433970
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10421
- gi No. 444791
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10422
- gi No. 444791
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10423
- gi No. 444791
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10424
- gi No. 444791
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10425
- gi No. 4506713
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10426
- gi No. 4506713
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10427
- gi No. 4507761
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10428
- gi No. 4507761
- % Identity 94.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
- Alignment No. 10429
- gi No. 4510359
- % Identity 100
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1320: from 112 to 146
- Alignment No. 10430

- gi No. 4510359
- % Identity 97.6
- Alignment Length 42
- Location of Alignment in SEQ ID NO 1320: from 36 to 77

- Alignment No. 10431
- gi No. 456779
- % Identity 92
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1320: from 1 to 25

- Alignment No. 10432
- gi No. 456779
- % Identity 92
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1320: from 77 to 101

- Alignment No. 10433
- gi No. 4586594
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10434
- gi No. 4586594
- % Identity 100
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1320: from 1 to 108

- Alignment No. 10435
- gi No. 4587232
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10436
- gi No. 4587232
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10437
- gi No. 4587234
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10438
- gi No. 4587234
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10439
- gi No. 4587236
- % Identity 96.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 10440
- gi No. 4587236

- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10441
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10442
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10443
- gi No. 4587236
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10444
- gi No. 4587236
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10445
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10446
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10447
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10448
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10449
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10450
- gi No. 4587236
- % Identity 95.9

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10451
- gi No. 4587534
- % Identity 75.3
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1320: from 1 to 73
- Alignment No. 10452
- gi No. 4589760
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10453
- gi No. 4589760
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10454
- gi No. 463363
- % Identity 84.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10455
- gi No. 463363
- % Identity 85.5
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10456
- gi No. 463365
- % Identity 90
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10457
- gi No. 463365
- % Identity 90.8
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10458
- gi No. 463367
- % Identity 88.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10459
- gi No. 463367
- % Identity 89.5
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10460
- gi No. 463369
- % Identity 91.4
- Alignment Length 70

- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10461
- gi No. 463369
- % Identity 92.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10462
- gi No. 463371
- % Identity 87.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10463
- gi No. 463371
- % Identity 88.2
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10464
- gi No. 463373
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10465
- gi No. 463373
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10466
- gi No. 463375
- % Identity 91.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10467
- gi No. 463375
- % Identity 92.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10468
- gi No. 464989
- % Identity 78.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10469
- gi No. 464989
- % Identity 80.3
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10470
- gi No. 464990
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10471
- gi No. 464990
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10472
- gi No. 468272
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10473
- gi No. 468272
- % Identity 94.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 10474
- gi No. 4737
- % Identity 95.7
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1320: from 1 to 47

- Alignment No. 10475
- gi No. 4737
- % Identity 95.7
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1320: from 77 to 123

- Alignment No. 10476
- gi No. 477437
- % Identity 76
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1320: from 3 to 27

- Alignment No. 10477
- gi No. 477437
- % Identity 76
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1320: from 79 to 103

- Alignment No. 10478
- gi No. 477630
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10479
- gi No. 477630
- % Identity 94.4
- Alignment Length 126
- Location of Alignment in SEQ ID NO 1320: from 21 to 146

- Alignment No. 10480
- gi No. 477815
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10481
- gi No. 477815
- % Identity 93.5
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
- Alignment No. 10482
- gi No. 478811
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10483
- gi No. 478811
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10484
- gi No. 478811
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10485
- gi No. 478811
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10486
- gi No. 4809266
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10487
- gi No. 4809266
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10488
- gi No. 4809266
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10489
- gi No. 4809266
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10490
- gi No. 4809266
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10491

- gi No. 481477
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10492
- gi No. 481477
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10493
- gi No. 481477
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10494
- gi No. 481477
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10495
- gi No. 481477
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10496
- gi No. 481477
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10497
- gi No. 485427
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 1 to 70

- Alignment No. 10498
- gi No. 485427
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10499
- gi No. 485518
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10500
- gi No. 485518
- % Identity 98.7
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 10501
- gi No. 49586

- % Identity 95.8
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1320: from 1 to 71

- Alignment No. 10502
- gi No. 49586
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10503
- gi No. 49586
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10504
- gi No. 510473
- % Identity 85.4
- Alignment Length 89
- Location of Alignment in SEQ ID NO 1320: from 1 to 89

- Alignment No. 10505
- gi No. 510473
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10506
- gi No. 510473
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10507
- gi No. 510473
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10508
- gi No. 510473
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10509
- gi No. 510473
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10510
- gi No. 510473
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10511
- gi No. 510473
- % Identity 95.9

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10512
- gi No. 510473
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10513
- gi No. 510476
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10514
- gi No. 510476
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10515
- gi No. 5107695
- % Identity 85.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10516
- gi No. 5107695
- % Identity 86.8
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10517
- gi No. 539404
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10518
- gi No. 539404
- % Identity 85.2
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1320: from 1 to 87
- Alignment No. 10519
- gi No. 539935
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10520
- gi No. 539935
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10521
- gi No. 539935
- % Identity 95.9
- Alignment Length 146

- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10522
- gi No. 539935
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10523
- gi No. 541546
- % Identity 97.4
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
- Alignment No. 10524
- gi No. 541546
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10525
- gi No. 541546
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10526
- gi No. 541546
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10527
- gi No. 541546
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10528
- gi No. 541953
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10529
- gi No. 541953
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10530
- gi No. 541954
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10531
- gi No. 541954
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10532
- gi No. 542395
- % Identity 97.9
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1320: from 99 to 146

- Alignment No. 10533
- gi No. 542395
- % Identity 98.1
- Alignment Length 54
- Location of Alignment in SEQ ID NO 1320: from 23 to 76

- Alignment No. 10534
- gi No. 5441519
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10535
- gi No. 5441519
- % Identity 94.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 10536
- gi No. 552237
- % Identity 97.1
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1320: from 112 to 146

- Alignment No. 10537
- gi No. 552237
- % Identity 91.7
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1320: from 1 to 36

- Alignment No. 10538
- gi No. 552237
- % Identity 94.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 36 to 112

- Alignment No. 10539
- gi No. 5523967
- % Identity 88.2
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1320: from 1 to 85

- Alignment No. 10540
- gi No. 5523967
- % Identity 96.6
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1320: from 60 to 146

- Alignment No. 10541
- gi No. 5523969
- % Identity 95.1
- Alignment Length 82
- Location of Alignment in SEQ ID NO 1320: from 65 to 146

- Alignment No. 10542
- gi No. 5523969
- % Identity 88.2
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1320: from 1 to 85
- Alignment No. 10543
- gi No. 5523969
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10544
- gi No. 5523971
- % Identity 88.2
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1320: from 1 to 85
- Alignment No. 10545
- gi No. 5523971
- % Identity 95.5
- Alignment Length 89
- Location of Alignment in SEQ ID NO 1320: from 58 to 146
- Alignment No. 10546
- gi No. 5523973
- % Identity 88.2
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1320: from 1 to 85
- Alignment No. 10547
- gi No. 5523973
- % Identity 87.6
- Alignment Length 121
- Location of Alignment in SEQ ID NO 1320: from 26 to 146
- Alignment No. 10548
- gi No. 5523975
- % Identity 95.9
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1320: from 74 to 146
- Alignment No. 10549
- gi No. 5523975
- % Identity 88.2
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1320: from 1 to 85
- Alignment No. 10550
- gi No. 5523977
- % Identity 88.2
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1320: from 1 to 85
- Alignment No. 10551
- gi No. 5523977
- % Identity 95.6
- Alignment Length 114
- Location of Alignment in SEQ ID NO 1320: from 33 to 146
- Alignment No. 10552

- gi No. 5523979
- % Identity 88.2
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1320: from 1 to 85

- Alignment No. 10553
- gi No. 5523979
- % Identity 72.2
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1320: from 39 to 146

- Alignment No. 10554
- gi No. 5523979
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10555
- gi No. 5523981
- % Identity 88.2
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1320: from 1 to 85

- Alignment No. 10556
- gi No. 5523981
- % Identity 89.7
- Alignment Length 97
- Location of Alignment in SEQ ID NO 1320: from 50 to 146

- Alignment No. 10557
- gi No. 5523983
- % Identity 94.1
- Alignment Length 68
- Location of Alignment in SEQ ID NO 1320: from 79 to 146

- Alignment No. 10558
- gi No. 5523983
- % Identity 86.7
- Alignment Length 83
- Location of Alignment in SEQ ID NO 1320: from 3 to 85

- Alignment No. 10559
- gi No. 5523985
- % Identity 87.1
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1320: from 1 to 85

- Alignment No. 10560
- gi No. 5523985
- % Identity 94.9
- Alignment Length 118
- Location of Alignment in SEQ ID NO 1320: from 29 to 146

- Alignment No. 10561
- gi No. 5523987
- % Identity 88.2
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1320: from 1 to 85

- Alignment No. 10562
- gi No. 5523987

- % Identity 96.6
- Alignment Length 118
- Location of Alignment in SEQ ID NO 1320: from 29 to 146

- Alignment No. 10563
- gi No. 5531273
- % Identity 96.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 10564
- gi No. 5531273
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10565
- gi No. 5531273
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10566
- gi No. 5531273
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10567
- gi No. 5531273
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10568
- gi No. 5531278
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10569
- gi No. 5531278
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1320: from 1 to 87

- Alignment No. 10570
- gi No. 5531281
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10571
- gi No. 5531281
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10572
- gi No. 554564
- % Identity 93.2

- Alignment Length 73
- Location of Alignment in SEQ ID NO 1320: from 74 to 146
- Alignment No. 10573
- gi No. 554564
- % Identity 94.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
- Alignment No. 10574
- gi No. 567767
- % Identity 88.2
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1320: from 1 to 85
- Alignment No. 10575
- gi No. 567767
- % Identity 84
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1320: from 47 to 146
- Alignment No. 10576
- gi No. 567767
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10577
- gi No. 571519
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10578
- gi No. 571519
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10579
- gi No. 571519
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10580
- gi No. 571519
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10581
- gi No. 571519
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10582
- gi No. 571519
- % Identity 95.9
- Alignment Length 146

- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10583
- gi No. 576773
- % Identity 98.7
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
- Alignment No. 10584
- gi No. 576773
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10585
- gi No. 576773
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10586
- gi No. 576773
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10587
- gi No. 576773
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10588
- gi No. 576775
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10589
- gi No. 576775
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1320: from 1 to 87
- Alignment No. 10590
- gi No. 578545
- % Identity 89.3
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1320: from 1 to 75
- Alignment No. 10591
- gi No. 578545
- % Identity 89
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10592
- gi No. 578545
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10593
- gi No. 578545
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10594
- gi No. 578545
- % Identity 84.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10595
- gi No. 578546
- % Identity 85.3
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1320: from 1 to 75

- Alignment No. 10596
- gi No. 578546
- % Identity 87
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10597
- gi No. 578546
- % Identity 84.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10598
- gi No. 578546
- % Identity 87
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10599
- gi No. 578546
- % Identity 83.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10600
- gi No. 578549
- % Identity 81.3
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1320: from 1 to 75

- Alignment No. 10601
- gi No. 578549
- % Identity 85.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10602
- gi No. 578549
- % Identity 84.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10603
- gi No. 578549
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10604
- gi No. 578551
- % Identity 89.3
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1320: from 1 to 75

- Alignment No. 10605
- gi No. 578551
- % Identity 86.8
- Alignment Length 144
- Location of Alignment in SEQ ID NO 1320: from 3 to 146

- Alignment No. 10606
- gi No. 578551
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10607
- gi No. 578551
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10608
- gi No. 578551
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10609
- gi No. 600539
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10610
- gi No. 600539
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10611
- gi No. 602076
- % Identity 100
- Alignment Length 113
- Location of Alignment in SEQ ID NO 1320: from 1 to 113

- Alignment No. 10612
- gi No. 602076
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10613

- gi No. 602076
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10614
- gi No. 602076
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10615
- gi No. 625174
- % Identity 86.7
- Alignment Length 90
- Location of Alignment in SEQ ID NO 1320: from 1 to 89

- Alignment No. 10616
- gi No. 625174
- % Identity 95.3
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1320: from 18 to 146

- Alignment No. 10617
- gi No. 625174
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10618
- gi No. 625509
- % Identity 100
- Alignment Length 90
- Location of Alignment in SEQ ID NO 1320: from 57 to 146

- Alignment No. 10619
- gi No. 625509
- % Identity 97.7
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1320: from 1 to 129

- Alignment No. 10620
- gi No. 625509
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10621
- gi No. 625509
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10622
- gi No. 630455
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10623
- gi No. 630455

- % Identity 96.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 10624
- gi No. 630479
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10625
- gi No. 630479
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10626
- gi No. 630479
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10627
- gi No. 630479
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10628
- gi No. 630479
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10629
- gi No. 70636
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10630
- gi No. 70636
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10631
- gi No. 70637
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10632
- gi No. 70637
- % Identity 95.9
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1320: from 1 to 74

- Alignment No. 10633
- gi No. 70639
- % Identity 97.4

- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10634
- gi No. 70639
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10635
- gi No. 70639
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10636
- gi No. 70639
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10637
- gi No. 70640
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10638
- gi No. 70640
- % Identity 97.4
- Alignment Length 78
- Location of Alignment in SEQ ID NO 1320: from 1 to 78
- Alignment No. 10639
- gi No. 70642
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10640
- gi No. 70642
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10641
- gi No. 70642
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10642
- gi No. 70642
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10643
- gi No. 70642
- % Identity 100
- Alignment Length 146

- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10644
 - gi No. 70643
 - % Identity 100
 - Alignment Length 76
 - Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10645
 - gi No. 70643
 - % Identity 100
 - Alignment Length 81
 - Location of Alignment in SEQ ID NO 1320: from 66 to 146
- Alignment No. 10646
 - gi No. 70644
 - % Identity 100
 - Alignment Length 76
 - Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10647
 - gi No. 70644
 - % Identity 100
 - Alignment Length 99
 - Location of Alignment in SEQ ID NO 1320: from 48 to 146
- Alignment No. 10648
 - gi No. 70644
 - % Identity 100
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10649
 - gi No. 70644
 - % Identity 100
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10650
 - gi No. 70644
 - % Identity 100
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10651
 - gi No. 70644
 - % Identity 100
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10652
 - gi No. 70645
 - % Identity 100
 - Alignment Length 76
 - Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10653
 - gi No. 70645
 - % Identity 100
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10654
- gi No. 70645
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10655
- gi No. 70645
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10656
- gi No. 70645
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10657
- gi No. 70646
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10658
- gi No. 70646
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10659
- gi No. 70647
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10660
- gi No. 70647
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10661
- gi No. 70647
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10662
- gi No. 70648
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10663
- gi No. 70648
- % Identity 93.5
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 10664
- gi No. 70650
- % Identity 74.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10665
- gi No. 70650
- % Identity 76.3
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10666
- gi No. 70653
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10667
- gi No. 70653
- % Identity 92.3
- Alignment Length 78
- Location of Alignment in SEQ ID NO 1320: from 1 to 78
- Alignment No. 10668
- gi No. 70654
- % Identity 98.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10669
- gi No. 70654
- % Identity 97.4
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
- Alignment No. 10670
- gi No. 70657
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10671
- gi No. 70657
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10672
- gi No. 70658
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10673
- gi No. 70658
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10674

- gi No. 70659
- % Identity 96.9
- Alignment Length 65
- Location of Alignment in SEQ ID NO 1320: from 82 to 146
- Alignment No. 10675
- gi No. 70659
- % Identity 97.2
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1320: from 6 to 76
- Alignment No. 10676
- gi No. 70660
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10677
- gi No. 70660
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10678
- gi No. 726391
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10679
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10680
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10681
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10682
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10683
- gi No. 726391
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10684
- gi No. 726391

- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10685
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10686
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10687
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10688
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10689
- gi No. 82040
- % Identity 99.1
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1320: from 36 to 146

- Alignment No. 10690
- gi No. 82040
- % Identity 100
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1320: from 1 to 112

- Alignment No. 10691
- gi No. 82040
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10692
- gi No. 82040
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10693
- gi No. 82284
- % Identity 100
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1320: from 1 to 56

- Alignment No. 10694
- gi No. 82284
- % Identity 100

- Alignment Length 56
- Location of Alignment in SEQ ID NO 1320: from 77 to 132
- Alignment No. 10695
- gi No. 82286
- % Identity 100
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1320: from 133 to 146
- Alignment No. 10696
- gi No. 82286
- % Identity 100
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1320: from 57 to 76
- Alignment No. 10697
- gi No. 82287
- % Identity 100
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1320: from 1 to 48
- Alignment No. 10698
- gi No. 82287
- % Identity 100
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1320: from 77 to 124
- Alignment No. 10699
- gi No. 82288
- % Identity 100
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1320: from 113 to 146
- Alignment No. 10700
- gi No. 82288
- % Identity 100
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1320: from 37 to 76
- Alignment No. 10701
- gi No. 82426
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10702
- gi No. 82426
- % Identity 100
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1320: from 59 to 146
- Alignment No. 10703
- gi No. 82426
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10704
- gi No. 82512
- % Identity 98.7
- Alignment Length 77

- Location of Alignment in SEQ ID NO 1320: from 1 to 77
- Alignment No. 10705
- gi No. 82512
- % Identity 100
- Alignment Length 106
- Location of Alignment in SEQ ID NO 1320: from 41 to 146
- Alignment No. 10706
- gi No. 82512
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10707
- gi No. 825728
- % Identity 96.8
- Alignment Length 31
- Location of Alignment in SEQ ID NO 1320: from 116 to 146
- Alignment No. 10708
- gi No. 825728
- % Identity 94.7
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1320: from 40 to 77
- Alignment No. 10709
- gi No. 82733
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10710
- gi No. 82733
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10711
- gi No. 82734
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10712
- gi No. 82734
- % Identity 100
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1320: from 35 to 146
- Alignment No. 10713
- gi No. 82734
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10714
- gi No. 82734
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10715
- gi No. 829173
- % Identity 93.1
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1320: from 89 to 146
- Alignment No. 10716
- gi No. 829173
- % Identity 90.9
- Alignment Length 66
- Location of Alignment in SEQ ID NO 1320: from 13 to 78
- Alignment No. 10717
- gi No. 83594
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10718
- gi No. 83594
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1320: from 1 to 87
- Alignment No. 10719
- gi No. 83596
- % Identity 97.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10720
- gi No. 83596
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10721
- gi No. 83596
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10722
- gi No. 83596
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10723
- gi No. 83596
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10724
- gi No. 84151
- % Identity 93.5
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77

- Alignment No. 10725
- gi No. 84151
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10726
- gi No. 84151
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10727
- gi No. 84152
- % Identity 93.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10728
- gi No. 84152
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10729
- gi No. 84152
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10730
- gi No. 84152
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10731
- gi No. 84152
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10732
- gi No. 84336
- % Identity 94.2
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1320: from 95 to 146
- Alignment No. 10733
- gi No. 84336
- % Identity 93.3
- Alignment Length 60
- Location of Alignment in SEQ ID NO 1320: from 19 to 78
- Alignment No. 10734
- gi No. 84337
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10735

- gi No. 84337
- % Identity 93.7
- Alignment Length 95
- Location of Alignment in SEQ ID NO 1320: from 1 to 95

- Alignment No. 10736
- gi No. 84478
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10737
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10738
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10739
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10740
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10741
- gi No. 84478
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10742
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10743
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10744
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10745
- gi No. 84478

- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10746
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10747
- gi No. 84834
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10748
- gi No. 84834
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10749
- gi No. 84834
- % Identity 96.7
- Alignment Length 92
- Location of Alignment in SEQ ID NO 1320: from 1 to 92

- Alignment No. 10750
- gi No. 84834
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1320: from 54 to 146

- Alignment No. 10751
- gi No. 85106
- % Identity 94.9
- Alignment Length 78
- Location of Alignment in SEQ ID NO 1320: from 1 to 78

- Alignment No. 10752
- gi No. 85106
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10753
- gi No. 85106
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10754
- gi No. 86473
- % Identity 96.2
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1320: from 121 to 146

- Alignment No. 10755
- gi No. 86473
- % Identity 93.8

- Alignment Length 32
- Location of Alignment in SEQ ID NO 1320: from 45 to 76
- Alignment No. 10756
- gi No. 86474
- % Identity 94.4
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1320: from 60 to 77
- Alignment No. 10757
- gi No. 870794
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10758
- gi No. 870794
- % Identity 75.5
- Alignment Length 149
- Location of Alignment in SEQ ID NO 1320: from 1 to 147
- Alignment No. 10759
- gi No. 870794
- % Identity 79.6
- Alignment Length 152
- Location of Alignment in SEQ ID NO 1320: from 1 to 145
- Alignment No. 10760
- gi No. 870794
- % Identity 70.5
- Alignment Length 167
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10761
- gi No. 89311
- % Identity 96.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10762
- gi No. 89311
- % Identity 95.8
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1320: from 51 to 146
- Alignment No. 10763
- gi No. 89311
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10764
- gi No. 89311
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10765
- gi No. 899115
- % Identity 100
- Alignment Length 70

- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10766
- gi No. 899115
- % Identity 100
- Alignment Length 99
- Location of Alignment in SEQ ID NO 1320: from 1 to 99
- Alignment No. 10767
- gi No. 899608
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10768
- gi No. 899608
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10769
- gi No. 899608
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10770
- gi No. 899608
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10771
- gi No. 899608
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10772
- gi No. 902525
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10773
- gi No. 902525
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10774
- gi No. 902584
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10775
- gi No. 902584
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10776
- gi No. 902584
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10777
- gi No. 902584
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10778
- gi No. 902584
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10779
- gi No. 902584
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10780
- gi No. 902584
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10781
- gi No. 902586
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76
- Alignment No. 10782
- gi No. 902586
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10783
- gi No. 902586
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10784
- gi No. 902586
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10785
- gi No. 902586
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10786
- gi No. 91870
- % Identity 96
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1320: from 72 to 146
- Alignment No. 10787
- gi No. 91870
- % Identity 93.9
- Alignment Length 98
- Location of Alignment in SEQ ID NO 1320: from 1 to 98
- Alignment No. 10788
- gi No. 91871
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146
- Alignment No. 10789
- gi No. 91871
- % Identity 94.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1320: from 1 to 77
- Alignment No. 10790
- gi No. 9295
- % Identity 85.7
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1320: from 84 to 146
- Alignment No. 10791
- gi No. 9295
- % Identity 87
- Alignment Length 69
- Location of Alignment in SEQ ID NO 1320: from 8 to 76
- Alignment No. 10792
- gi No. 940395
- % Identity 88.9
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1320: from 1 to 108
- Alignment No. 10793
- gi No. 940395
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10794
- gi No. 940395
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10795
- gi No. 940395
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146
- Alignment No. 10796

- gi No. 940395
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10797
- gi No. 940395
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10798
- gi No. 940395
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10799
- gi No. 940395
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1320: from 1 to 146

- Alignment No. 10800
- gi No. 967985
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10801
- gi No. 967985
- % Identity 94.7
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10802
- gi No. 99469
- % Identity 100
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1320: from 114 to 146

- Alignment No. 10803
- gi No. 99469
- % Identity 100
- Alignment Length 42
- Location of Alignment in SEQ ID NO 1320: from 38 to 79

- Alignment No. 10804
- gi No. 99771
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10805
- gi No. 99771
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10806
- gi No. 99772

- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10807
- gi No. 99772
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

- Alignment No. 10808
- gi No. 99975
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1320: from 77 to 146

- Alignment No. 10809
- gi No. 99975
- % Identity 100
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1320: from 1 to 76

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1321
- Ceres seq_id 1500056
- Location of start within SEQ ID NO 1319: at 629 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 10810
- Ubiquitin family
- Location within SEQ ID NO 1321: from 1 to 70 aa.

(D) Related Amino Acid Sequences

- Alignment No. 10811
- gi No. 100490
- % Identity 100
- Alignment Length 137
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10812
- gi No. 100490
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10813
- gi No. 100490
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10814
- gi No. 100524
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10815
- gi No. 100524
- % Identity 100

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10816
- gi No. 100524
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10817
- gi No. 100524
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10818
- gi No. 100524
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10819
- gi No. 100525
- % Identity 100
- Alignment Length 106
- Location of Alignment in SEQ ID NO 1321: from 1 to 30
- Alignment No. 10820
- gi No. 100525
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10821
- gi No. 100525
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10822
- gi No. 100525
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10823
- gi No. 100598
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10824
- gi No. 100599
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10825
- gi No. 100812
- % Identity 100
- Alignment Length 70

- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10826
 - gi No. 100934
 - % Identity 100
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10827
 - gi No. 100934
 - % Identity 100
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10828
 - gi No. 100934
 - % Identity 100
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10829
 - gi No. 100934
 - % Identity 100
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10830
 - gi No. 100934
 - % Identity 100
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10831
 - gi No. 100934
 - % Identity 100
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10832
 - gi No. 100981
 - % Identity 100
 - Alignment Length 34
 - Location of Alignment in SEQ ID NO 1321: from 37 to 70
- Alignment No. 10833
 - gi No. 102062
 - % Identity 92.9
 - Alignment Length 70
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10834
 - gi No. 102278
 - % Identity 94.5
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10835
 - gi No. 102278
 - % Identity 94.5
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10836
- gi No. 102278
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10837
- gi No. 102278
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10838
- gi No. 102278
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10839
- gi No. 102278
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10840
- gi No. 102279
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10841
- gi No. 102279
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10842
- gi No. 102280
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10843
- gi No. 102280
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10844
- gi No. 102280
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10845
- gi No. 102280
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10846
- gi No. 102281
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10847
- gi No. 102281
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10848
- gi No. 102281
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10849
- gi No. 102281
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10850
- gi No. 102389
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10851
- gi No. 102389
- % Identity 85.2
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1321: from 1 to 11
- Alignment No. 10852
- gi No. 103436
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10853
- gi No. 1044940
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10854
- gi No. 104829
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10855
- gi No. 104829
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10856

- gi No. 1050930
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10857
- gi No. 1050930
- % Identity 95
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1321: from 1 to 24

- Alignment No. 10858
- gi No. 10673
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10859
- gi No. 10673
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1321: from 1 to 11

- Alignment No. 10860
- gi No. 1070590
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10861
- gi No. 1070590
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10862
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10863
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10864
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10865
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10866
- gi No. 1070591

- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10867
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10868
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10869
- gi No. 1070591
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10870
- gi No. 1076678
- % Identity 79.2
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10871
- gi No. 1076708
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10872
- gi No. 1076708
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10873
- gi No. 1076708
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10874
- gi No. 1078777
- % Identity 87.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10875
- gi No. 1078813
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10876
- gi No. 1078813
- % Identity 95.9

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10877
- gi No. 1083758
- % Identity 88
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1321: from 1 to 32

- Alignment No. 10878
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10879
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10880
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10881
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10882
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10883
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10884
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10885
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10886
- gi No. 1083758
- % Identity 95.9
- Alignment Length 146

- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10887
- gi No. 1101011
- % Identity 87.3
- Alignment Length 79
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10888
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10889
- gi No. 1101011
- % Identity 84.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10890
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10891
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10892
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10893
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10894
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10895
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10896
- gi No. 1101011
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10897
- gi No. 1101013
- % Identity 85
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1321: from 7 to 46

- Alignment No. 10898
- gi No. 1101015
- % Identity 85
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1321: from 7 to 46

- Alignment No. 10899
- gi No. 1101019
- % Identity 80
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1321: from 7 to 46

- Alignment No. 10900
- gi No. 1101021
- % Identity 84.4
- Alignment Length 64
- Location of Alignment in SEQ ID NO 1321: from 7 to 70

- Alignment No. 10901
- gi No. 1101021
- % Identity 86.2
- Alignment Length 116
- Location of Alignment in SEQ ID NO 1321: from 1 to 46

- Alignment No. 10902
- gi No. 1101023
- % Identity 87.9
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1321: from 38 to 70

- Alignment No. 10903
- gi No. 1101023
- % Identity 92
- Alignment Length 50
- Location of Alignment in SEQ ID NO 1321: from 1 to 11

- Alignment No. 10904
- gi No. 1107481
- % Identity 97.9
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1321: from 1 to 20

- Alignment No. 10905
- gi No. 1107481
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10906
- gi No. 1143188
- % Identity 94.5
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1321: from 1 to 73

- Alignment No. 10907
- gi No. 1143188
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10908
- gi No. 1143188
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10909
- gi No. 1167510
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10910
- gi No. 1167510
- % Identity 91.3
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1321: from 1 to 27

- Alignment No. 10911
- gi No. 1174858
- % Identity 74.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10912
- gi No. 1174859
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10913
- gi No. 1174860
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10914
- gi No. 1174861
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10915
- gi No. 1184755
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10916
- gi No. 1197093
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10917

- gi No. 1197093
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10918
- gi No. 1197093
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10919
- gi No. 1304128
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10920
- gi No. 1304128
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10921
- gi No. 1304128
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10922
- gi No. 1304128
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10923
- gi No. 1304128
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10924
- gi No. 1304128
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10925
- gi No. 1304128
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10926
- gi No. 1304357
- % Identity 81.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10927
- gi No. 1321735

- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10928
- gi No. 1321735
- % Identity 95.7
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1321: from 1 to 63

- Alignment No. 10929
- gi No. 1326021
- % Identity 96.3
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1321: from 44 to 70

- Alignment No. 10930
- gi No. 1326022
- % Identity 97.2
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10931
- gi No. 1326022
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10932
- gi No. 1332579
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10933
- gi No. 1332579
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10934
- gi No. 1332579
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10935
- gi No. 1332579
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10936
- gi No. 1332579
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10937
- gi No. 1332579
- % Identity 98.6

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10938
- gi No. 1332579
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10939
- gi No. 1332579
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10940
- gi No. 1332579
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10941
- gi No. 1351348
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10942
- gi No. 1351349
- % Identity 90
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10943
- gi No. 1353755
- % Identity 95.2
- Alignment Length 105
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10944
- gi No. 1353757
- % Identity 94.2
- Alignment Length 69
- Location of Alignment in SEQ ID NO 1321: from 2 to 70

- Alignment No. 10945
- gi No. 1353757
- % Identity 94.2
- Alignment Length 121
- Location of Alignment in SEQ ID NO 1321: from 1 to 46

- Alignment No. 10946
- gi No. 1362008
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10947
- gi No. 1362008
- % Identity 92.5
- Alignment Length 146

- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10948
- gi No. 1362008
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10949
- gi No. 1362008
- % Identity 92.5
- Alignment Length 159
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10950
- gi No. 1362009
- % Identity 79.7
- Alignment Length 148
- Location of Alignment in SEQ ID NO 1321: from 1 to 72
- Alignment No. 10951
- gi No. 1362010
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10952
- gi No. 1362010
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10953
- gi No. 1362010
- % Identity 92.5
- Alignment Length 147
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10954
- gi No. 1362012
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10955
- gi No. 1362012
- % Identity 76.2
- Alignment Length 149
- Location of Alignment in SEQ ID NO 1321: from 1 to 71
- Alignment No. 10956
- gi No. 1362012
- % Identity 79.6
- Alignment Length 152
- Location of Alignment in SEQ ID NO 1321: from 1 to 69
- Alignment No. 10957
- gi No. 1362012
- % Identity 71.1
- Alignment Length 167
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10958
- gi No. 136665
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10959
- gi No. 136666
- % Identity 98.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10960
- gi No. 136667
- % Identity 98.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10961
- gi No. 136668
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10962
- gi No. 136669
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10963
- gi No. 136670
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10964
- gi No. 136671
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10965
- gi No. 136672
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10966
- gi No. 136673
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10967
- gi No. 136674
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10968
 - gi No. 136675
 - % Identity 94.3
 - Alignment Length 70
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10969
 - gi No. 136676
 - % Identity 94.3
 - Alignment Length 70
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10970
 - gi No. 136677
 - % Identity 97.1
 - Alignment Length 70
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10971
 - gi No. 136678
 - % Identity 97.1
 - Alignment Length 70
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10972
 - gi No. 1421797
 - % Identity 95.7
 - Alignment Length 70
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10973
 - gi No. 1480012
 - % Identity 96.3
 - Alignment Length 54
 - Location of Alignment in SEQ ID NO 1321: from 17 to 70
- Alignment No. 10974
 - gi No. 156480
 - % Identity 94.6
 - Alignment Length 37
 - Location of Alignment in SEQ ID NO 1321: from 1 to 37
- Alignment No. 10975
 - gi No. 158759
 - % Identity 94.3
 - Alignment Length 70
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10976
 - gi No. 158763
 - % Identity 94.3
 - Alignment Length 70
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10977
 - gi No. 158765
 - % Identity 91.4
 - Alignment Length 70
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 10978

- gi No. 158767
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10979
- gi No. 158769
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10980
- gi No. 158771
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10981
- gi No. 161281
- % Identity 94.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1321: from 1 to 71

- Alignment No. 10982
- gi No. 163575
- % Identity 96.3
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10983
- gi No. 163575
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10984
- gi No. 166336
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10985
- gi No. 166336
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10986
- gi No. 166336
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10987
- gi No. 166336
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10988
- gi No. 166336

- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10989
- gi No. 1666175
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10990
- gi No. 1675359
- % Identity 92.7
- Alignment Length 41
- Location of Alignment in SEQ ID NO 1321: from 1 to 41

- Alignment No. 10991
- gi No. 167935
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10992
- gi No. 167935
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10993
- gi No. 167935
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10994
- gi No. 167935
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10995
- gi No. 167941
- % Identity 92.8
- Alignment Length 69
- Location of Alignment in SEQ ID NO 1321: from 2 to 70

- Alignment No. 10996
- gi No. 167945
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10997
- gi No. 167945
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10998
- gi No. 167947
- % Identity 94.5

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 10999
- gi No. 167947
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11000
- gi No. 167947
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11001
- gi No. 167947
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11002
- gi No. 167947
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11003
- gi No. 167947
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11004
- gi No. 167949
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11005
- gi No. 167949
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11006
- gi No. 167949
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11007
- gi No. 167949
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11008
- gi No. 1684855
- % Identity 81.7
- Alignment Length 131

- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11009
- gi No. 1684855
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11010
- gi No. 1684855
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11011
- gi No. 1684855
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11012
- gi No. 1684857
- % Identity 100
- Alignment Length 132
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11013
- gi No. 1684857
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11014
- gi No. 170352
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11015
- gi No. 170352
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11016
- gi No. 170352
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11017
- gi No. 170352
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11018
- gi No. 170352
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11019
- gi No. 170354
- % Identity 100
- Alignment Length 142
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11020
- gi No. 170354
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11021
- gi No. 170354
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11022
- gi No. 170354
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11023
- gi No. 1762374
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11024
- gi No. 1762935
- % Identity 98.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11025
- gi No. 1763015
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11026
- gi No. 1771780
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11027
- gi No. 1778712
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11028
- gi No. 1778712
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11029
- gi No. 1778712
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11030
- gi No. 1778712
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11031
- gi No. 1800281
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11032
- gi No. 1800281
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11033
- gi No. 1800281
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11034
- gi No. 1800281
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11035
- gi No. 1805696
- % Identity 95.2
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1321: from 8 to 70

- Alignment No. 11036
- gi No. 1805696
- % Identity 95.5
- Alignment Length 134
- Location of Alignment in SEQ ID NO 1321: from 1 to 65

- Alignment No. 11037
- gi No. 1839584
- % Identity 100
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1321: from 1 to 38

- Alignment No. 11038
- gi No. 1841849
- % Identity 100
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1321: from 36 to 70

- Alignment No. 11039

- gi No. 1841849
- % Identity 100
- Alignment Length 57
- Location of Alignment in SEQ ID NO 1321: from 1 to 16

- Alignment No. 11040
- gi No. 208558
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11041
- gi No. 208560
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11042
- gi No. 208562
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11043
- gi No. 208564
- % Identity 91.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11044
- gi No. 208566
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11045
- gi No. 208568
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11046
- gi No. 208891
- % Identity 96
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11047
- gi No. 208891
- % Identity 93.9
- Alignment Length 98
- Location of Alignment in SEQ ID NO 1321: from 1 to 22

- Alignment No. 11048
- gi No. 209603
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11049
- gi No. 2118958

- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11050
- gi No. 2118958
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11051
- gi No. 2118958
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11052
- gi No. 2118958
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11053
- gi No. 2118959
- % Identity 85.7
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1321: from 1 to 36

- Alignment No. 11054
- gi No. 2118959
- % Identity 84.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11055
- gi No. 2118959
- % Identity 83.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11056
- gi No. 2118960
- % Identity 96.5
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11057
- gi No. 2118960
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11058
- gi No. 2118961
- % Identity 94.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11059
- gi No. 2118961
- % Identity 95.2

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11060
- gi No. 2118962
- % Identity 95.9
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11061
- gi No. 2118962
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11062
- gi No. 2118963
- % Identity 91
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11063
- gi No. 2118964
- % Identity 96.4
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11064
- gi No. 2118964
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11065
- gi No. 2118964
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11066
- gi No. 2118965
- % Identity 96.3
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11067
- gi No. 2118965
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11068
- gi No. 2118965
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11069
- gi No. 2129452
- % Identity 95.9
- Alignment Length 146

- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11070
 - gi No. 2129452
 - % Identity 95.9
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11071
 - gi No. 2129452
 - % Identity 95.2
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11072
 - gi No. 2129452
 - % Identity 95.2
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11073
 - gi No. 2129452
 - % Identity 95.9
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11074
 - gi No. 2133278
 - % Identity 94.3
 - Alignment Length 70
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11075
 - gi No. 2133549
 - % Identity 96.3
 - Alignment Length 27
 - Location of Alignment in SEQ ID NO 1321: from 44 to 70
- Alignment No. 11076
 - gi No. 2133549
 - % Identity 96
 - Alignment Length 50
 - Location of Alignment in SEQ ID NO 1321: from 21 to 70
- Alignment No. 11077
 - gi No. 2133549
 - % Identity 96.3
 - Alignment Length 81
 - Location of Alignment in SEQ ID NO 1321: from 1 to 48
- Alignment No. 11078
 - gi No. 2144011
 - % Identity 95.7
 - Alignment Length 70
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11079
 - gi No. 2144275
 - % Identity 92.9
 - Alignment Length 70
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11080
- gi No. 2144734
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1321: from 1 to 11
- Alignment No. 11081
- gi No. 2144734
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11082
- gi No. 2144734
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11083
- gi No. 2144734
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11084
- gi No. 2149467
- % Identity 87.7
- Alignment Length 83
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11085
- gi No. 2209091
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11086
- gi No. 223061
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11087
- gi No. 224321
- % Identity 97.2
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11088
- gi No. 224321
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11089
- gi No. 225317
- % Identity 89.6
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1321: from 1 to 77

- Alignment No. 11090
- gi No. 225319
- % Identity 89.6
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1321: from 1 to 77

- Alignment No. 11091
- gi No. 225320
- % Identity 87
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1321: from 1 to 77

- Alignment No. 11092
- gi No. 2281952
- % Identity 95.2
- Alignment Length 62
- Location of Alignment in SEQ ID NO 1321: from 8 to 69

- Alignment No. 11093
- gi No. 2281954
- % Identity 93.5
- Alignment Length 62
- Location of Alignment in SEQ ID NO 1321: from 8 to 69

- Alignment No. 11094
- gi No. 2281955
- % Identity 88.9
- Alignment Length 45
- Location of Alignment in SEQ ID NO 1321: from 8 to 52

- Alignment No. 11095
- gi No. 2281959
- % Identity 90.6
- Alignment Length 64
- Location of Alignment in SEQ ID NO 1321: from 7 to 70

- Alignment No. 11096
- gi No. 2330875
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11097
- gi No. 2350864
- % Identity 75.9
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1321: from 6 to 63

- Alignment No. 11098
- gi No. 2408009
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11099
- gi No. 2408009
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1321: from 1 to 11

- Alignment No. 11100

- gi No. 2437825
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11101
- gi No. 2437825
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11102
- gi No. 2437825
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11103
- gi No. 247308
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11104
- gi No. 248865
- % Identity 95
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1321: from 1 to 20

- Alignment No. 11105
- gi No. 2558539
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11106
- gi No. 2627129
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11107
- gi No. 2627129
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11108
- gi No. 2627129
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11109
- gi No. 2627129
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11110
- gi No. 2627129

- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11111
- gi No. 2627129
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11112
- gi No. 2627129
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11113
- gi No. 2627131
- % Identity 89.8
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1321: from 1 to 32

- Alignment No. 11114
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11115
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11116
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11117
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11118
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11119
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11120
- gi No. 2627131
- % Identity 95.9

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11121
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11122
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11123
- gi No. 2627131
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11124
- gi No. 2627133
- % Identity 89.8
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1321: from 1 to 32

- Alignment No. 11125
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11126
- gi No. 2627133
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11127
- gi No. 2627133
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11128
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11129
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11130
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146

- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11131
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11132
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11133
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11134
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11135
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11136
- gi No. 2627133
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11137
- gi No. 2641213
- % Identity 98.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11138
- gi No. 2641213
- % Identity 98.6
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1321: from 1 to 63
- Alignment No. 11139
- gi No. 2654141
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11140
- gi No. 2654141
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11141
- gi No. 2654141
- % Identity 89
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11142
- gi No. 2654141
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11143
- gi No. 2707837
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11144
- gi No. 2707837
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11145
- gi No. 2707837
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11146
- gi No. 2739333
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11147
- gi No. 2739333
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11148
- gi No. 2739333
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11149
- gi No. 2760345
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11150
- gi No. 2760345
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11151
- gi No. 2760345
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11152
- gi No. 2760347
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11153
- gi No. 2760347
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11154
- gi No. 2760347
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11155
- gi No. 2760347
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11156
- gi No. 2760347
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11157
- gi No. 2760349
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11158
- gi No. 2760349
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11159
- gi No. 2760349
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11160
- gi No. 2760349
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11161

- gi No. 279635
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11162
- gi No. 279636
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11163
- gi No. 280386
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11164
- gi No. 281276
- % Identity 90
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1321: from 1 to 20

- Alignment No. 11165
- gi No. 283496
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11166
- gi No. 283496
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11167
- gi No. 283496
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11168
- gi No. 283496
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11169
- gi No. 2894304
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11170
- gi No. 2894304
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11171
- gi No. 2894304

- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11172
- gi No. 2894306
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11173
- gi No. 2894308
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11174
- gi No. 2894308
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11175
- gi No. 2894308
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11176
- gi No. 2894308
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11177
- gi No. 2995277
- % Identity 100
- Alignment Length 23
- Location of Alignment in SEQ ID NO 1321: from 48 to 70

- Alignment No. 11178
- gi No. 2995949
- % Identity 100
- Alignment Length 104
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11179
- gi No. 3047314
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11180
- gi No. 3047314
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1321: from 1 to 11

- Alignment No. 11181
- gi No. 3047316
- % Identity 97.1

- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11182
- gi No. 3047318
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11183
- gi No. 3047318
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11184
- gi No. 3047318
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11185
- gi No. 3047318
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11186
- gi No. 3091264
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11187
- gi No. 3091264
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11188
- gi No. 3091264
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11189
- gi No. 3126967
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11190
- gi No. 3126967
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11191
- gi No. 3126967
- % Identity 100
- Alignment Length 146

- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11192
- gi No. 3126967
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11193
- gi No. 3126967
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11194
- gi No. 3152950
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11195
- gi No. 3158372
- % Identity 100
- Alignment Length 98
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11196
- gi No. 3158372
- % Identity 99.1
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1321: from 1 to 33
- Alignment No. 11197
- gi No. 320608
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11198
- gi No. 320608
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11199
- gi No. 320608
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11200
- gi No. 322750
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11201
- gi No. 323071
- % Identity 84.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11202
- gi No. 323157
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11203
- gi No. 323157
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11204
- gi No. 323157
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11205
- gi No. 323157
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11206
- gi No. 323157
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11207
- gi No. 323208
- % Identity 82.5
- Alignment Length 144
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11208
- gi No. 323230
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11209
- gi No. 3265058
- % Identity 98.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11210
- gi No. 3319208
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11211
- gi No. 3335355
- % Identity 100
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1321: from 56 to 70

- Alignment No. 11212
- gi No. 3335355
- % Identity 97.7
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1321: from 1 to 53
- Alignment No. 11213
- gi No. 3335355
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11214
- gi No. 3335355
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11215
- gi No. 340062
- % Identity 95.5
- Alignment Length 66
- Location of Alignment in SEQ ID NO 1321: from 5 to 70
- Alignment No. 11216
- gi No. 3452083
- % Identity 97.9
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1321: from 23 to 70
- Alignment No. 11217
- gi No. 3452083
- % Identity 96.4
- Alignment Length 83
- Location of Alignment in SEQ ID NO 1321: from 1 to 29
- Alignment No. 11218
- gi No. 348148
- % Identity 96.3
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1321: from 44 to 70
- Alignment No. 11219
- gi No. 348148
- % Identity 96.3
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1321: from 1 to 48
- Alignment No. 11220
- gi No. 348149
- % Identity 96
- Alignment Length 50
- Location of Alignment in SEQ ID NO 1321: from 21 to 70
- Alignment No. 11221
- gi No. 3603456
- % Identity 100
- Alignment Length 106
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11222

- gi No. 3603456
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11223
- gi No. 3603456
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11224
- gi No. 3687425
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11225
- gi No. 3687425
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11226
- gi No. 3738185
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11227
- gi No. 3738185
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11228
- gi No. 3738185
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11229
- gi No. 3738185
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11230
- gi No. 3776536
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11231
- gi No. 3776536
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11232
- gi No. 3776536

- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11233
- gi No. 3776536
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11234
- gi No. 3776536
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11235
- gi No. 3776536
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11236
- gi No. 3776536
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11237
- gi No. 3789940
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11238
- gi No. 3789940
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11239
- gi No. 3789940
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11240
- gi No. 3789942
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11241
- gi No. 3789942
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11242
- gi No. 3789942
- % Identity 98.6

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11243
- gi No. 3789942
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11244
- gi No. 3822277
- % Identity 75.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11245
- gi No. 385076
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11246
- gi No. 3882081
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11247
- gi No. 3882081
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11248
- gi No. 3885463
- % Identity 94
- Alignment Length 67
- Location of Alignment in SEQ ID NO 1321: from 4 to 70

- Alignment No. 11249
- gi No. 3892189
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11250
- gi No. 3892189
- % Identity 84.1
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1321: from 1 to 11

- Alignment No. 11251
- gi No. 402242
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11252
- gi No. 4049712
- % Identity 85.7
- Alignment Length 70

- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11253
- gi No. 4102845
- % Identity 86.2
- Alignment Length 65
- Location of Alignment in SEQ ID NO 1321: from 6 to 70
- Alignment No. 11254
- gi No. 4105408
- % Identity 95.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11255
- gi No. 4105408
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11256
- gi No. 4105408
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11257
- gi No. 4115337
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11258
- gi No. 4115337
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11259
- gi No. 4115337
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11260
- gi No. 4115337
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11261
- gi No. 4115337
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11262
- gi No. 4150898
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11263
- gi No. 4150898
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11264
- gi No. 4150898
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11265
- gi No. 4150912
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11266
- gi No. 4150912
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11267
- gi No. 4150912
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11268
- gi No. 4150912
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11269
- gi No. 4150914
- % Identity 95.7
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11270
- gi No. 4151082
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11271
- gi No. 418854
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11272
- gi No. 418854
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11273
- gi No. 418854
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11274
- gi No. 418854
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11275
- gi No. 418854
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11276
- gi No. 421735
- % Identity 94.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1321: from 1 to 19
- Alignment No. 11277
- gi No. 421867
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11278
- gi No. 421929
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11279
- gi No. 421929
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11280
- gi No. 421929
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11281
- gi No. 421929
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11282
- gi No. 421929
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11283

- gi No. 421929
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11284
- gi No. 422248
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11285
- gi No. 422248
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11286
- gi No. 422248
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11287
- gi No. 422248
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11288
- gi No. 422269
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11289
- gi No. 422270
- % Identity 90
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11290
- gi No. 422271
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11291
- gi No. 433970
- % Identity 95.5
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11292
- gi No. 433970
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11293
- gi No. 433970

- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11294
- gi No. 433970
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11295
- gi No. 433970
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11296
- gi No. 444791
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11297
- gi No. 444791
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11298
- gi No. 444791
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11299
- gi No. 4506713
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11300
- gi No. 4507761
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11301
- gi No. 4510359
- % Identity 100
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1321: from 36 to 70

- Alignment No. 11302
- gi No. 456779
- % Identity 92
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1321: from 1 to 25

- Alignment No. 11303
- gi No. 4586594
- % Identity 100

- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11304
- gi No. 4586594
- % Identity 100
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1321: from 1 to 32

- Alignment No. 11305
- gi No. 4587232
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11306
- gi No. 4587234
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11307
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11308
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11309
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11310
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11311
- gi No. 4587236
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11312
- gi No. 4587236
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11313
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146

- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11314
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11315
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11316
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11317
- gi No. 4587236
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11318
- gi No. 4589760
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11319
- gi No. 463363
- % Identity 84.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11320
- gi No. 463365
- % Identity 90
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11321
- gi No. 463367
- % Identity 88.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11322
- gi No. 463369
- % Identity 91.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11323
- gi No. 463371
- % Identity 87.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11324
- gi No. 463373
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11325
- gi No. 463375
- % Identity 91.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11326
- gi No. 464989
- % Identity 78.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11327
- gi No. 464990
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11328
- gi No. 468272
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11329
- gi No. 4737
- % Identity 95.7
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1321: from 1 to 47

- Alignment No. 11330
- gi No. 477437
- % Identity 76
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1321: from 3 to 27

- Alignment No. 11331
- gi No. 477630
- % Identity 94.4
- Alignment Length 126
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11332
- gi No. 477815
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11333
- gi No. 478811
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11334
- gi No. 478811
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11335
- gi No. 478811
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11336
- gi No. 4809266
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11337
- gi No. 4809266
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11338
- gi No. 4809266
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11339
- gi No. 4809266
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11340
- gi No. 481477
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11341
- gi No. 481477
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11342
- gi No. 481477
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11343
- gi No. 481477
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11344

- gi No. 481477
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11345
- gi No. 485427
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11346
- gi No. 485518
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11347
- gi No. 49586
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11348
- gi No. 49586
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11349
- gi No. 510473
- % Identity 85.4
- Alignment Length 89
- Location of Alignment in SEQ ID NO 1321: from 1 to 13

- Alignment No. 11350
- gi No. 510473
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11351
- gi No. 510473
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11352
- gi No. 510473
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11353
- gi No. 510473
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11354
- gi No. 510473

- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11355
- gi No. 510473
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11356
- gi No. 510473
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11357
- gi No. 510473
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11358
- gi No. 510476
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11359
- gi No. 5107695
- % Identity 85.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11360
- gi No. 539404
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11361
- gi No. 539404
- % Identity 85.2
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1321: from 1 to 11

- Alignment No. 11362
- gi No. 539935
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11363
- gi No. 539935
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11364
- gi No. 539935
- % Identity 95.9

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11365
- gi No. 541546
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11366
- gi No. 541546
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11367
- gi No. 541546
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11368
- gi No. 541546
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11369
- gi No. 541953
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11370
- gi No. 541954
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11371
- gi No. 542395
- % Identity 97.9
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1321: from 23 to 70

- Alignment No. 11372
- gi No. 5441519
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11373
- gi No. 552237
- % Identity 97.1
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1321: from 36 to 70

- Alignment No. 11374
- gi No. 552237
- % Identity 94.8
- Alignment Length 77

- Location of Alignment in SEQ ID NO 1321: from 1 to 36
- Alignment No. 11375
- gi No. 5523967
- % Identity 96.6
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11376
- gi No. 5523969
- % Identity 95.1
- Alignment Length 82
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11377
- gi No. 5523969
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11378
- gi No. 5523971
- % Identity 95.5
- Alignment Length 89
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11379
- gi No. 5523973
- % Identity 87.6
- Alignment Length 121
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11380
- gi No. 5523975
- % Identity 95.9
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11381
- gi No. 5523977
- % Identity 95.6
- Alignment Length 114
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11382
- gi No. 5523979
- % Identity 72.2
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11383
- gi No. 5523979
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11384
- gi No. 5523981
- % Identity 89.7
- Alignment Length 97
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11385
- gi No. 5523983
- % Identity 94.1
- Alignment Length 68
- Location of Alignment in SEQ ID NO 1321: from 3 to 70

- Alignment No. 11386
- gi No. 5523985
- % Identity 94.9
- Alignment Length 118
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11387
- gi No. 5523987
- % Identity 96.6
- Alignment Length 118
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11388
- gi No. 5531273
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11389
- gi No. 5531273
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11390
- gi No. 5531273
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11391
- gi No. 5531273
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11392
- gi No. 5531278
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11393
- gi No. 5531278
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1321: from 1 to 11

- Alignment No. 11394
- gi No. 5531281
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11395
- gi No. 554564
- % Identity 93.2
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11396
- gi No. 567767
- % Identity 84
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11397
- gi No. 567767
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11398
- gi No. 571519
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11399
- gi No. 571519
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11400
- gi No. 571519
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11401
- gi No. 571519
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11402
- gi No. 571519
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11403
- gi No. 576773
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11404
- gi No. 576773
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11405

- gi No. 576773
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11406
- gi No. 576773
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11407
- gi No. 576775
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11408
- gi No. 576775
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1321: from 1 to 11

- Alignment No. 11409
- gi No. 578545
- % Identity 89
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11410
- gi No. 578545
- % Identity 84.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11411
- gi No. 578545
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11412
- gi No. 578545
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11413
- gi No. 578546
- % Identity 87
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11414
- gi No. 578546
- % Identity 83.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11415
- gi No. 578546

- % Identity 84.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11416
- gi No. 578546
- % Identity 87
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11417
- gi No. 578549
- % Identity 85.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11418
- gi No. 578549
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11419
- gi No. 578549
- % Identity 84.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11420
- gi No. 578551
- % Identity 86.8
- Alignment Length 144
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11421
- gi No. 578551
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11422
- gi No. 578551
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11423
- gi No. 578551
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11424
- gi No. 600539
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11425
- gi No. 602076
- % Identity 100

- Alignment Length 113
- Location of Alignment in SEQ ID NO 1321: from 1 to 37
- Alignment No. 11426
- gi No. 602076
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11427
- gi No. 602076
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11428
- gi No. 602076
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11429
- gi No. 625174
- % Identity 86.7
- Alignment Length 90
- Location of Alignment in SEQ ID NO 1321: from 1 to 13
- Alignment No. 11430
- gi No. 625174
- % Identity 95.3
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11431
- gi No. 625174
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11432
- gi No. 625509
- % Identity 100
- Alignment Length 90
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11433
- gi No. 625509
- % Identity 97.7
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1321: from 1 to 53
- Alignment No. 11434
- gi No. 625509
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11435
- gi No. 625509
- % Identity 98.6
- Alignment Length 146

- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11436
- gi No. 630455
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11437
- gi No. 630479
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11438
- gi No. 630479
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11439
- gi No. 630479
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11440
- gi No. 630479
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11441
- gi No. 630479
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11442
- gi No. 70636
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11443
- gi No. 70636
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11444
- gi No. 70637
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11445
- gi No. 70639
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11446
 - gi No. 70639
 - % Identity 97.3
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11447
 - gi No. 70639
 - % Identity 97.3
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11448
 - gi No. 70640
 - % Identity 97.1
 - Alignment Length 70
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11449
 - gi No. 70642
 - % Identity 100
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11450
 - gi No. 70642
 - % Identity 100
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11451
 - gi No. 70642
 - % Identity 100
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11452
 - gi No. 70642
 - % Identity 100
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11453
 - gi No. 70643
 - % Identity 100
 - Alignment Length 81
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11454
 - gi No. 70644
 - % Identity 100
 - Alignment Length 99
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11455
 - gi No. 70644
 - % Identity 100
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11456
- gi No. 70644
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11457
- gi No. 70644
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11458
- gi No. 70644
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11459
- gi No. 70645
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11460
- gi No. 70645
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11461
- gi No. 70645
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11462
- gi No. 70645
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11463
- gi No. 70646
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11464
- gi No. 70647
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11465
- gi No. 70647
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11466

- gi No. 70648
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11467
- gi No. 70650
- % Identity 74.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11468
- gi No. 70653
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11469
- gi No. 70654
- % Identity 98.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11470
- gi No. 70657
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11471
- gi No. 70658
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11472
- gi No. 70659
- % Identity 96.9
- Alignment Length 65
- Location of Alignment in SEQ ID NO 1321: from 6 to 70

- Alignment No. 11473
- gi No. 70660
- % Identity 92.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11474
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11475
- gi No. 726391
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11476
- gi No. 726391

- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11477
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11478
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11479
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11480
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11481
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11482
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11483
- gi No. 726391
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11484
- gi No. 82040
- % Identity 99.1
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11485
- gi No. 82040
- % Identity 100
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1321: from 1 to 36

- Alignment No. 11486
- gi No. 82040
- % Identity 100

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11487
- gi No. 82040
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11488
- gi No. 82284
- % Identity 100
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1321: from 1 to 56

- Alignment No. 11489
- gi No. 82286
- % Identity 100
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1321: from 57 to 70

- Alignment No. 11490
- gi No. 82287
- % Identity 100
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1321: from 1 to 48

- Alignment No. 11491
- gi No. 82288
- % Identity 100
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1321: from 37 to 70

- Alignment No. 11492
- gi No. 82426
- % Identity 100
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11493
- gi No. 82426
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11494
- gi No. 82512
- % Identity 100
- Alignment Length 106
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11495
- gi No. 82512
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11496
- gi No. 825728
- % Identity 96.8
- Alignment Length 31

- Location of Alignment in SEQ ID NO 1321: from 40 to 70
- Alignment No. 11497
- gi No. 82733
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11498
- gi No. 82734
- % Identity 100
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11499
- gi No. 82734
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11500
- gi No. 82734
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11501
- gi No. 829173
- % Identity 93.1
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1321: from 13 to 70
- Alignment No. 11502
- gi No. 83594
- % Identity 97.1
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11503
- gi No. 83594
- % Identity 87.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1321: from 1 to 11
- Alignment No. 11504
- gi No. 83596
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11505
- gi No. 83596
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11506
- gi No. 83596
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11507
- gi No. 83596
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11508
- gi No. 84151
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11509
- gi No. 84151
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11510
- gi No. 84152
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11511
- gi No. 84152
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11512
- gi No. 84152
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11513
- gi No. 84152
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11514
- gi No. 84336
- % Identity 94.2
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1321: from 19 to 70

- Alignment No. 11515
- gi No. 84337
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11516
- gi No. 84337
- % Identity 93.7
- Alignment Length 95
- Location of Alignment in SEQ ID NO 1321: from 1 to 19

- Alignment No. 11517
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11518
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11519
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11520
- gi No. 84478
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11521
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11522
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11523
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11524
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11525
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11526
- gi No. 84478
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11527

- gi No. 84834
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11528
- gi No. 84834
- % Identity 96.7
- Alignment Length 92
- Location of Alignment in SEQ ID NO 1321: from 1 to 16

- Alignment No. 11529
- gi No. 84834
- % Identity 89.2
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11530
- gi No. 85106
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11531
- gi No. 85106
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11532
- gi No. 86473
- % Identity 96.2
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1321: from 45 to 70

- Alignment No. 11533
- gi No. 870794
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11534
- gi No. 870794
- % Identity 75.5
- Alignment Length 149
- Location of Alignment in SEQ ID NO 1321: from 1 to 71

- Alignment No. 11535
- gi No. 870794
- % Identity 79.6
- Alignment Length 152
- Location of Alignment in SEQ ID NO 1321: from 1 to 69

- Alignment No. 11536
- gi No. 870794
- % Identity 70.5
- Alignment Length 167
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11537
- gi No. 89311

- % Identity 95.8
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11538
- gi No. 89311
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11539
- gi No. 89311
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11540
- gi No. 899115
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11541
- gi No. 899115
- % Identity 100
- Alignment Length 99
- Location of Alignment in SEQ ID NO 1321: from 1 to 23

- Alignment No. 11542
- gi No. 899608
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11543
- gi No. 899608
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11544
- gi No. 899608
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11545
- gi No. 899608
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11546
- gi No. 902525
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11547
- gi No. 902584
- % Identity 100

- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11548
- gi No. 902584
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11549
- gi No. 902584
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11550
- gi No. 902584
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11551
- gi No. 902584
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11552
- gi No. 902584
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11553
- gi No. 902586
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11554
- gi No. 902586
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11555
- gi No. 902586
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11556
- gi No. 902586
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11557
- gi No. 91870
- % Identity 96
- Alignment Length 75

- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11558
- gi No. 91870
- % Identity 93.9
- Alignment Length 98
- Location of Alignment in SEQ ID NO 1321: from 1 to 22
- Alignment No. 11559
- gi No. 91871
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11560
- gi No. 9295
- % Identity 85.7
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1321: from 8 to 70
- Alignment No. 11561
- gi No. 940395
- % Identity 88.9
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1321: from 1 to 32
- Alignment No. 11562
- gi No. 940395
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11563
- gi No. 940395
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11564
- gi No. 940395
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11565
- gi No. 940395
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11566
- gi No. 940395
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70
- Alignment No. 11567
- gi No. 940395
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11568
- gi No. 940395
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11569
- gi No. 967985
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11570
- gi No. 99469
- % Identity 100
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1321: from 38 to 70

- Alignment No. 11571
- gi No. 99771
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11572
- gi No. 99772
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

- Alignment No. 11573
- gi No. 99975
- % Identity 100
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1321: from 1 to 70

Maximum Length Sequence corresponding to clone ID 254904

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1322
- Ceres seq_id 1500057

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1323
- Ceres seq_id 1500058
- Location of start within SEQ ID NO 1322: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11574
- Ezrin/radixin/moesin family
- Location within SEQ ID NO 1323: from 144 to 304 aa.

- Alignment No. 11575
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 1323: from 129 to 346 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1324
- Ceres seq_id 1500059

- Location of start within SEQ ID NO 1322: at 118 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11576
- Ezrin/radixin/moesin family
- Location within SEQ ID NO 1324: from 105 to 265 aa.
- Alignment No. 11577
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 1324: from 90 to 307 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1325
- Ceres seq_id 1500060
- Location of start within SEQ ID NO 1322: at 142 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11578
- Ezrin/radixin/moesin family
- Location within SEQ ID NO 1325: from 97 to 257 aa.
- Alignment No. 11579
- Eukaryotic DNA topoisomerase I
- Location within SEQ ID NO 1325: from 82 to 299 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 255048

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1326
- Ceres seq_id 1500065

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1327
- Ceres seq_id 1500066
- Location of start within SEQ ID NO 1326: at 199 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11580
- gi No. 1041702
- % Identity 86.6
- Alignment Length 236
- Location of Alignment in SEQ ID NO 1327: from 19 to 118
- Alignment No. 11581
- gi No. 1778097
- % Identity 71.4
- Alignment Length 84
- Location of Alignment in SEQ ID NO 1327: from 4 to 87
- Alignment No. 11582
- gi No. 1778107
- % Identity 72.6
- Alignment Length 84
- Location of Alignment in SEQ ID NO 1327: from 1 to 82

- Alignment No. 11583
- gi No. 1778109
- % Identity 71.3
- Alignment Length 80
- Location of Alignment in SEQ ID NO 1327: from 1 to 77
- Alignment No. 11584
- gi No. 3461833
- % Identity 73.8
- Alignment Length 241
- Location of Alignment in SEQ ID NO 1327: from 14 to 118
- Alignment No. 11585
- gi No. 4027897
- % Identity 70.2
- Alignment Length 249
- Location of Alignment in SEQ ID NO 1327: from 1 to 118

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1328
- Ceres seq_id 1500067
- Location of start within SEQ ID NO 1326: at 241 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11586
- gi No. 1041702
- % Identity 86.6
- Alignment Length 236
- Location of Alignment in SEQ ID NO 1328: from 5 to 104
- Alignment No. 11587
- gi No. 1778097
- % Identity 71.4
- Alignment Length 84
- Location of Alignment in SEQ ID NO 1328: from 1 to 73
- Alignment No. 11588
- gi No. 1778107
- % Identity 72.6
- Alignment Length 84
- Location of Alignment in SEQ ID NO 1328: from 1 to 68
- Alignment No. 11589
- gi No. 1778109
- % Identity 71.3
- Alignment Length 80
- Location of Alignment in SEQ ID NO 1328: from 1 to 63
- Alignment No. 11590
- gi No. 3461833
- % Identity 73.8
- Alignment Length 241
- Location of Alignment in SEQ ID NO 1328: from 1 to 104
- Alignment No. 11591
- gi No. 4027897
- % Identity 70.2
- Alignment Length 249
- Location of Alignment in SEQ ID NO 1328: from 1 to 104

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1329
 - Ceres seq_id 1500068
 - Location of start within SEQ ID NO 1326: at 740 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 255050

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1330
 - Ceres seq_id 1500069
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1331
 - Ceres seq_id 1500070
 - Location of start within SEQ ID NO 1330: at 200 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11592
- TBC domain
- Location within SEQ ID NO 1331: from 113 to 327 aa.

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1332
 - Ceres seq_id 1500071
 - Location of start within SEQ ID NO 1330: at 233 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11593
- TBC domain
- Location within SEQ ID NO 1332: from 102 to 316 aa.

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1333
 - Ceres seq_id 1500072
 - Location of start within SEQ ID NO 1330: at 659 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11594
- TBC domain
- Location within SEQ ID NO 1333: from 1 to 174 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 255298

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1334
 - Ceres seq_id 1500073
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1335
 - Ceres seq_id 1500074
 - Location of start within SEQ ID NO 1334: at 363 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11595
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1335: from 78 to 348 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11596
- gi No. 1778440
- % Identity 72.3
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1335: from 215 to 261
- Alignment No. 11597
- gi No. 1778442
- % Identity 71.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1335: from 189 to 262
- Alignment No. 11598
- gi No. 1778444
- % Identity 78.4
- Alignment Length 51
- Location of Alignment in SEQ ID NO 1335: from 200 to 250

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1336
- Ceres seq_id 1500075
- Location of start within SEQ ID NO 1334: at 735 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11599
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1336: from 1 to 224 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11600
- gi No. 1778440
- % Identity 72.3
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1336: from 91 to 137
- Alignment No. 11601
- gi No. 1778442
- % Identity 71.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1336: from 65 to 138
- Alignment No. 11602
- gi No. 1778444
- % Identity 78.4
- Alignment Length 51
- Location of Alignment in SEQ ID NO 1336: from 76 to 126

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1337
- Ceres seq_id 1500076
- Location of start within SEQ ID NO 1334: at 822 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 11603
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1337: from 1 to 195 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11604
- gi No. 1778440
- % Identity 72.3
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1337: from 62 to 108
- Alignment No. 11605
- gi No. 1778442
- % Identity 71.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1337: from 36 to 109
- Alignment No. 11606
- gi No. 1778444
- % Identity 78.4
- Alignment Length 51
- Location of Alignment in SEQ ID NO 1337: from 47 to 97

Maximum Length Sequence corresponding to clone ID 255307

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1338
- Ceres seq_id 1500077

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1339
- Ceres seq_id 1500078
- Location of start within SEQ ID NO 1338: at 90 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 11607
- Polygalacturonase (pectinase)
- Location within SEQ ID NO 1339: from 97 to 436 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11608
- gi No. 1346702
- % Identity 100
- Alignment Length 444
- Location of Alignment in SEQ ID NO 1339: from 1 to 444
- Alignment No. 11609
- gi No. 3004442
- % Identity 97.5
- Alignment Length 445
- Location of Alignment in SEQ ID NO 1339: from 1 to 444
- Alignment No. 11610
- gi No. 421833
- % Identity 97.3
- Alignment Length 445
- Location of Alignment in SEQ ID NO 1339: from 1 to 444

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1340

- Ceres seq_id 1500079
- Location of start within SEQ ID NO 1338: at 141 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11611
- Polygalacturonase (pectinase)
- Location within SEQ ID NO 1340: from 80 to 419 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11612
- gi No. 1346702
- % Identity 100
- Alignment Length 444
- Location of Alignment in SEQ ID NO 1340: from 1 to 427

- Alignment No. 11613
- gi No. 3004442
- % Identity 97.5
- Alignment Length 445
- Location of Alignment in SEQ ID NO 1340: from 1 to 427

- Alignment No. 11614
- gi No. 421833
- % Identity 97.3
- Alignment Length 445
- Location of Alignment in SEQ ID NO 1340: from 1 to 427

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1341
- Ceres seq_id 1500080
- Location of start within SEQ ID NO 1338: at 420 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11615
- Polygalacturonase (pectinase)
- Location within SEQ ID NO 1341: from 1 to 326 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11616
- gi No. 1346702
- % Identity 100
- Alignment Length 444
- Location of Alignment in SEQ ID NO 1341: from 1 to 334

- Alignment No. 11617
- gi No. 3004442
- % Identity 97.5
- Alignment Length 445
- Location of Alignment in SEQ ID NO 1341: from 1 to 334

- Alignment No. 11618
- gi No. 421833
- % Identity 97.3
- Alignment Length 445
- Location of Alignment in SEQ ID NO 1341: from 1 to 334

Maximum Length Sequence corresponding to clone ID 255364

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1342

- Ceres seq_id 1500081
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1343
 - Ceres seq_id 1500082
 - Location of start within SEQ ID NO 1342: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 11619
 - gi No. 4768976
 - % Identity 71.7
 - Alignment Length 92
 - Location of Alignment in SEQ ID NO 1343: from 246 to 337

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1344
 - Ceres seq_id 1500083
 - Location of start within SEQ ID NO 1342: at 94 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 11620
 - gi No. 4768976
 - % Identity 71.7
 - Alignment Length 92
 - Location of Alignment in SEQ ID NO 1344: from 215 to 306

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1345
 - Ceres seq_id 1500084
 - Location of start within SEQ ID NO 1342: at 277 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 11621
 - gi No. 4768976
 - % Identity 71.7
 - Alignment Length 92
 - Location of Alignment in SEQ ID NO 1345: from 154 to 245

Maximum Length Sequence corresponding to clone ID 255477

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1346
 - Ceres seq_id 1500085

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1347
 - Ceres seq_id 1500086
 - Location of start within SEQ ID NO 1346: at 286 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 11622
 - gi No. 5430753
 - % Identity 81.9
 - Alignment Length 234
 - Location of Alignment in SEQ ID NO 1347: from 110 to 341

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1348
- Ceres seq_id 1500087
- Location of start within SEQ ID NO 1346: at 613 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11623
- gi No. 5430753
- % Identity 81.9
- Alignment Length 234
- Location of Alignment in SEQ ID NO 1348: from 1 to 232

Maximum Length Sequence corresponding to clone ID 255542

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1349
- Ceres seq_id 1500088

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1350
- Ceres seq_id 1500089
- Location of start within SEQ ID NO 1349: at 51 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11624
- gi No. 100214
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 329 to 346
- Alignment No. 11625
- gi No. 100214
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 329 to 346
- Alignment No. 11626
- gi No. 100216
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 329 to 346
- Alignment No. 11627
- gi No. 102424
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1350: from 279 to 293
- Alignment No. 11628
- gi No. 102427
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
- Alignment No. 11629
- gi No. 1061334
- % Identity 82.4
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1350: from 279 to 295

- Alignment No. 11630
- gi No. 1065941
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1350: from 282 to 294
- Alignment No. 11631
- gi No. 1065941
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
- Alignment No. 11632
- gi No. 1065941
- % Identity 72.2
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1350: from 329 to 345
- Alignment No. 11633
- gi No. 1076555
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 329 to 346
- Alignment No. 11634
- gi No. 108231
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
- Alignment No. 11635
- gi No. 113210
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
- Alignment No. 11636
- gi No. 1163054
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
- Alignment No. 11637
- gi No. 1163054
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
- Alignment No. 11638
- gi No. 1185397
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1350: from 329 to 339
- Alignment No. 11639
- gi No. 1185397
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1350: from 280 to 293

- Alignment No. 11640
- gi No. 1185397
- % Identity 81.3
- Alignment Length 16
- Location of Alignment in SEQ ID NO 1350: from 280 to 294
- Alignment No. 11641
- gi No. 119111
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
- Alignment No. 11642
- gi No. 119111
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
- Alignment No. 11643
- gi No. 1326381
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1350: from 323 to 337
- Alignment No. 11644
- gi No. 1345537
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 329 to 346
- Alignment No. 11645
- gi No. 134920
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1350: from 329 to 339
- Alignment No. 11646
- gi No. 134920
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1350: from 329 to 348
- Alignment No. 11647
- gi No. 1351865
- % Identity 84.6
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1350: from 281 to 293
- Alignment No. 11648
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
- Alignment No. 11649
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
- Alignment No. 11650

- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293

- Alignment No. 11651
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293

- Alignment No. 11652
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293

- Alignment No. 11653
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293

- Alignment No. 11654
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293

- Alignment No. 11655
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293

- Alignment No. 11656
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293

- Alignment No. 11657
- gi No. 1480413
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293

- Alignment No. 11658
- gi No. 1644457
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1350: from 329 to 339

- Alignment No. 11659
- gi No. 1644459
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1350: from 329 to 339

- Alignment No. 11660
- gi No. 1644461

- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1350: from 329 to 339
- Alignment No. 11661
- gi No. 1655699
- % Identity 100
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1350: from 329 to 339
- Alignment No. 11662
- gi No. 1655699
- % Identity 92.9
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
- Alignment No. 11663
- gi No. 1655699
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 329 to 346
- Alignment No. 11664
- gi No. 1655699
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 329 to 346
- Alignment No. 11665
- gi No. 169345
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 329 to 346
- Alignment No. 11666
- gi No. 1911629
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
- Alignment No. 11667
- gi No. 1911629
- % Identity 86.7
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1350: from 280 to 294
- Alignment No. 11668
- gi No. 1914851
- % Identity 92.9
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
- Alignment No. 11669
- gi No. 1914851
- % Identity 82.4
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1350: from 278 to 293
- Alignment No. 11670
- gi No. 1914851
- % Identity 77.8

- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 278 to 293

- Alignment No. 11671
- gi No. 1914851
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1350: from 278 to 293

- Alignment No. 11672
- gi No. 2108256
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 329 to 346

- Alignment No. 11673
- gi No. 2108256
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 329 to 346

- Alignment No. 11674
- gi No. 2129478
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1350: from 280 to 293

- Alignment No. 11675
- gi No. 2147342
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 323 to 336

- Alignment No. 11676
- gi No. 2147342
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 1350: from 323 to 338

- Alignment No. 11677
- gi No. 226743
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1350: from 329 to 348

- Alignment No. 11678
- gi No. 2494630
- % Identity 90.9
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1350: from 283 to 293

- Alignment No. 11679
- gi No. 2494630
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1350: from 329 to 340

- Alignment No. 11680
- gi No. 3204132
- % Identity 77.8
- Alignment Length 18

- Location of Alignment in SEQ ID NO 1350: from 329 to 346
- Alignment No. 11681
- gi No. 3204132
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1350: from 327 to 346
- Alignment No. 11682
- gi No. 322758
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
- Alignment No. 11683
- gi No. 322758
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1350: from 280 to 291
- Alignment No. 11684
- gi No. 347455
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1350: from 327 to 346
- Alignment No. 11685
- gi No. 3875441
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1350: from 324 to 334
- Alignment No. 11686
- gi No. 3875441
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1350: from 324 to 334
- Alignment No. 11687
- gi No. 4008584
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1350: from 329 to 340
- Alignment No. 11688
- gi No. 4033606
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 329 to 346
- Alignment No. 11689
- gi No. 4096360
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1350: from 329 to 339
- Alignment No. 11690
- gi No. 4096360
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1350: from 280 to 293

- Alignment No. 11691
- gi No. 4096360
- % Identity 81.3
- Alignment Length 16
- Location of Alignment in SEQ ID NO 1350: from 280 to 294
- Alignment No. 11692
- gi No. 4467884
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 329 to 346
- Alignment No. 11693
- gi No. 4522026
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1350: from 329 to 347
- Alignment No. 11694
- gi No. 4589678
- % Identity 91.7
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1350: from 329 to 340
- Alignment No. 11695
- gi No. 497413
- % Identity 90.9
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1350: from 283 to 293
- Alignment No. 11696
- gi No. 497413
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1350: from 329 to 340
- Alignment No. 11697
- gi No. 5302801
- % Identity 99.6
- Alignment Length 473
- Location of Alignment in SEQ ID NO 1350: from 1 to 473
- Alignment No. 11698
- gi No. 5441495
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1350: from 329 to 340
- Alignment No. 11699
- gi No. 5441495
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1350: from 331 to 343
- Alignment No. 11700
- gi No. 628112
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293

- Alignment No. 11701
- gi No. 628112
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
- Alignment No. 11702
- gi No. 628185
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
- Alignment No. 11703
- gi No. 628185
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
- Alignment No. 11704
- gi No. 628185
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
- Alignment No. 11705
- gi No. 628185
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1350: from 280 to 293
- Alignment No. 11706
- gi No. 628185
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1350: from 280 to 294
- Alignment No. 11707
- gi No. 81870
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1350: from 329 to 346

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1351
- Ceres seq_id 1500090
- Location of start within SEQ ID NO 1349: at 492 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11708
- gi No. 100214
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199
- Alignment No. 11709
- gi No. 100214
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199

- Alignment No. 11710
- gi No. 100216
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199

- Alignment No. 11711
- gi No. 102424
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1351: from 132 to 146

- Alignment No. 11712
- gi No. 102427
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11713
- gi No. 1061334
- % Identity 82.4
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1351: from 132 to 148

- Alignment No. 11714
- gi No. 1065941
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1351: from 135 to 147

- Alignment No. 11715
- gi No. 1065941
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11716
- gi No. 1065941
- % Identity 72.2
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1351: from 182 to 198

- Alignment No. 11717
- gi No. 1076555
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199

- Alignment No. 11718
- gi No. 108231
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11719
- gi No. 113210
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11720
- gi No. 1163054
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
- Alignment No. 11721
- gi No. 1163054
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
- Alignment No. 11722
- gi No. 1185397
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1351: from 182 to 192
- Alignment No. 11723
- gi No. 1185397
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
- Alignment No. 11724
- gi No. 1185397
- % Identity 81.3
- Alignment Length 16
- Location of Alignment in SEQ ID NO 1351: from 133 to 147
- Alignment No. 11725
- gi No. 119111
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
- Alignment No. 11726
- gi No. 119111
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
- Alignment No. 11727
- gi No. 1326381
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1351: from 176 to 190
- Alignment No. 11728
- gi No. 1345537
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199
- Alignment No. 11729
- gi No. 134920
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1351: from 182 to 192
- Alignment No. 11730

- gi No. 134920
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1351: from 182 to 201

- Alignment No. 11731
- gi No. 1351865
- % Identity 84.6
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1351: from 134 to 146

- Alignment No. 11732
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11733
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11734
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11735
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11736
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11737
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11738
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11739
- gi No. 141279
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11740
- gi No. 141279

- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11741
- gi No. 1480413
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11742
- gi No. 1644457
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1351: from 182 to 192

- Alignment No. 11743
- gi No. 1644459
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1351: from 182 to 192

- Alignment No. 11744
- gi No. 1644461
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1351: from 182 to 192

- Alignment No. 11745
- gi No. 1655699
- % Identity 100
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1351: from 182 to 192

- Alignment No. 11746
- gi No. 1655699
- % Identity 92.9
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11747
- gi No. 1655699
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199

- Alignment No. 11748
- gi No. 1655699
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199

- Alignment No. 11749
- gi No. 169345
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199

- Alignment No. 11750
- gi No. 1911629
- % Identity 78.6

- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11751
- gi No. 1911629
- % Identity 86.7
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1351: from 133 to 147

- Alignment No. 11752
- gi No. 1914851
- % Identity 92.9
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11753
- gi No. 1914851
- % Identity 82.4
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1351: from 131 to 146

- Alignment No. 11754
- gi No. 1914851
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 131 to 146

- Alignment No. 11755
- gi No. 1914851
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1351: from 131 to 146

- Alignment No. 11756
- gi No. 2108256
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199

- Alignment No. 11757
- gi No. 2108256
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199

- Alignment No. 11758
- gi No. 2129478
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1351: from 133 to 146

- Alignment No. 11759
- gi No. 2147342
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 176 to 189

- Alignment No. 11760
- gi No. 2147342
- % Identity 75
- Alignment Length 16

- Location of Alignment in SEQ ID NO 1351: from 176 to 191
- Alignment No. 11761
- gi No. 226743
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1351: from 182 to 201
- Alignment No. 11762
- gi No. 2494630
- % Identity 90.9
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1351: from 136 to 146
- Alignment No. 11763
- gi No. 2494630
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1351: from 182 to 193
- Alignment No. 11764
- gi No. 3204132
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199
- Alignment No. 11765
- gi No. 3204132
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1351: from 180 to 199
- Alignment No. 11766
- gi No. 322758
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
- Alignment No. 11767
- gi No. 322758
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1351: from 133 to 144
- Alignment No. 11768
- gi No. 347455
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1351: from 180 to 199
- Alignment No. 11769
- gi No. 3875441
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1351: from 177 to 187
- Alignment No. 11770
- gi No. 3875441
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1351: from 177 to 187

- Alignment No. 11771
- gi No. 4008584
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1351: from 182 to 193
- Alignment No. 11772
- gi No. 4033606
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199
- Alignment No. 11773
- gi No. 4096360
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1351: from 182 to 192
- Alignment No. 11774
- gi No. 4096360
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
- Alignment No. 11775
- gi No. 4096360
- % Identity 81.3
- Alignment Length 16
- Location of Alignment in SEQ ID NO 1351: from 133 to 147
- Alignment No. 11776
- gi No. 4467884
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199
- Alignment No. 11777
- gi No. 4522026
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1351: from 182 to 200
- Alignment No. 11778
- gi No. 4589678
- % Identity 91.7
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1351: from 182 to 193
- Alignment No. 11779
- gi No. 497413
- % Identity 90.9
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1351: from 136 to 146
- Alignment No. 11780
- gi No. 497413
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1351: from 182 to 193

- Alignment No. 11781
- gi No. 5302801
- % Identity 99.6
- Alignment Length 473
- Location of Alignment in SEQ ID NO 1351: from 1 to 326
- Alignment No. 11782
- gi No. 5441495
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1351: from 182 to 193
- Alignment No. 11783
- gi No. 5441495
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1351: from 184 to 196
- Alignment No. 11784
- gi No. 628112
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
- Alignment No. 11785
- gi No. 628112
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
- Alignment No. 11786
- gi No. 628185
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
- Alignment No. 11787
- gi No. 628185
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
- Alignment No. 11788
- gi No. 628185
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
- Alignment No. 11789
- gi No. 628185
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1351: from 133 to 146
- Alignment No. 11790
- gi No. 628185
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1351: from 133 to 147
- Alignment No. 11791

- gi No. 81870
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1351: from 182 to 199

Maximum Length Sequence corresponding to clone ID 255685

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1352
- Ceres seq_id 1500091

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1353
- Ceres seq_id 1500092
- Location of start within SEQ ID NO 1352: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11792
- Lipase/Acylhydrolase with GDSL-like motif
- Location within SEQ ID NO 1353: from 1 to 80 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1354
- Ceres seq_id 1500093
- Location of start within SEQ ID NO 1352: at 434 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 255876

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1355
- Ceres seq_id 1500097

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1356
- Ceres seq_id 1500098
- Location of start within SEQ ID NO 1355: at 52 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11793
- Lyase
- Location within SEQ ID NO 1356: from 63 to 473 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11794
- gi No. 2252472
- % Identity 100
- Alignment Length 474
- Location of Alignment in SEQ ID NO 1356: from 1 to 473

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1357
- Ceres seq_id 1500099
- Location of start within SEQ ID NO 1355: at 190 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11795

- Lyase
- Location within SEQ ID NO 1357: from 17 to 427 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11796
- gi No. 2252472
- % Identity 100
- Alignment Length 474
- Location of Alignment in SEQ ID NO 1357: from 1 to 427

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1358
- Ceres seq_id 1500100
- Location of start within SEQ ID NO 1355: at 325 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11797
- Lyase
- Location within SEQ ID NO 1358: from 1 to 382 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11798
- gi No. 2252472
- % Identity 100
- Alignment Length 474
- Location of Alignment in SEQ ID NO 1358: from 1 to 382

Maximum Length Sequence corresponding to clone ID 256052

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1359
- Ceres seq_id 1500101

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1360
- Ceres seq_id 1500102
- Location of start within SEQ ID NO 1359: at 129 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11799
- NifU-like domain
- Location within SEQ ID NO 1360: from 89 to 155 aa.

- Alignment No. 11800
- NifU-like domain
- Location within SEQ ID NO 1360: from 171 to 233 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11801
- gi No. 4538920
- % Identity 99.1
- Alignment Length 224
- Location of Alignment in SEQ ID NO 1360: from 13 to 236

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1361
- Ceres seq_id 1500103
- Location of start within SEQ ID NO 1359: at 165 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11802
- NifU-like domain
- Location within SEQ ID NO 1361: from 77 to 143 aa.

- Alignment No. 11803
- NifU-like domain
- Location within SEQ ID NO 1361: from 159 to 221 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11804
- gi No. 4538920
- % Identity 99.1
- Alignment Length 224
- Location of Alignment in SEQ ID NO 1361: from 1 to 224

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1362
- Ceres seq_id 1500104
- Location of start within SEQ ID NO 1359: at 372 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11805
- NifU-like domain
- Location within SEQ ID NO 1362: from 8 to 74 aa.
- Alignment No. 11806
- NifU-like domain
- Location within SEQ ID NO 1362: from 90 to 152 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11807
- gi No. 4538920
- % Identity 99.1
- Alignment Length 224
- Location of Alignment in SEQ ID NO 1362: from 1 to 155

Maximum Length Sequence corresponding to clone ID 256076

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1363
- Ceres seq_id 1500105

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1364
- Ceres seq_id 1500106
- Location of start within SEQ ID NO 1363: at 424 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11808
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1364: from 1 to 240 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11809
- gi No. 1076387
- % Identity 76.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
- Alignment No. 11810
- gi No. 1076641

- % Identity 82.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

- Alignment No. 11811
- gi No. 1076649
- % Identity 82.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

- Alignment No. 11812
- gi No. 1076651
- % Identity 79.6
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

- Alignment No. 11813
- gi No. 1170711
- % Identity 82.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

- Alignment No. 11814
- gi No. 1170714
- % Identity 83.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

- Alignment No. 11815
- gi No. 125373
- % Identity 70.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 244

- Alignment No. 11816
- gi No. 125374
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

- Alignment No. 11817
- gi No. 1431622
- % Identity 82.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

- Alignment No. 11818
- gi No. 1480078
- % Identity 91.2
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

- Alignment No. 11819
- gi No. 1504063
- % Identity 76.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

- Alignment No. 11820
- gi No. 1617200
- % Identity 81.1

- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
- Alignment No. 11821
- gi No. 1709127
- % Identity 82.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
- Alignment No. 11822
- gi No. 1709128
- % Identity 81.7
- Alignment Length 284
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
- Alignment No. 11823
- gi No. 1709129
- % Identity 82.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
- Alignment No. 11824
- gi No. 1730039
- % Identity 70.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 244
- Alignment No. 11825
- gi No. 1877393
- % Identity 83
- Alignment Length 171
- Location of Alignment in SEQ ID NO 1364: from 76 to 245
- Alignment No. 11826
- gi No. 1877397
- % Identity 93.4
- Alignment Length 226
- Location of Alignment in SEQ ID NO 1364: from 20 to 245
- Alignment No. 11827
- gi No. 1944518
- % Identity 79
- Alignment Length 290
- Location of Alignment in SEQ ID NO 1364: from 1 to 250
- Alignment No. 11828
- gi No. 2117783
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
- Alignment No. 11829
- gi No. 2117784
- % Identity 70.2
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
- Alignment No. 11830
- gi No. 2129738
- % Identity 90.5
- Alignment Length 285

- Location of Alignment in SEQ ID NO 1364: from 1 to 245
- Alignment No. 11831
- gi No. 2129739
- % Identity 96.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
- Alignment No. 11832
- gi No. 2160191
- % Identity 76.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
- Alignment No. 11833
- gi No. 2182029
- % Identity 89.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
- Alignment No. 11834
- gi No. 2191169
- % Identity 78.7
- Alignment Length 300
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
- Alignment No. 11835
- gi No. 2398519
- % Identity 82.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
- Alignment No. 11836
- gi No. 2569931
- % Identity 74.1
- Alignment Length 290
- Location of Alignment in SEQ ID NO 1364: from 1 to 250
- Alignment No. 11837
- gi No. 2569950
- % Identity 79.9
- Alignment Length 284
- Location of Alignment in SEQ ID NO 1364: from 1 to 244
- Alignment No. 11838
- gi No. 2598601
- % Identity 77.9
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
- Alignment No. 11839
- gi No. 2598603
- % Identity 78.6
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
- Alignment No. 11840
- gi No. 2641994
- % Identity 70.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 244

- Alignment No. 11841
- gi No. 2911533
- % Identity 79.6
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

- Alignment No. 11842
- gi No. 3201623
- % Identity 91.2
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

- Alignment No. 11843
- gi No. 3236115
- % Identity 81.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

- Alignment No. 11844
- gi No. 3236117
- % Identity 80
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

- Alignment No. 11845
- gi No. 3250738
- % Identity 73.7
- Alignment Length 293
- Location of Alignment in SEQ ID NO 1364: from 1 to 250

- Alignment No. 11846
- gi No. 3264607
- % Identity 81.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1364: from 176 to 245

- Alignment No. 11847
- gi No. 3702608
- % Identity 77.2
- Alignment Length 290
- Location of Alignment in SEQ ID NO 1364: from 1 to 250

- Alignment No. 11848
- gi No. 3928148
- % Identity 81.6
- Alignment Length 266
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

- Alignment No. 11849
- gi No. 402652
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

- Alignment No. 11850
- gi No. 4140287
- % Identity 71.6
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

- Alignment No. 11851
- gi No. 4504163
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
- Alignment No. 11852
- gi No. 4539390
- % Identity 100
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1364: from 1 to 245
- Alignment No. 11853
- gi No. 5070700
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1364: from 1 to 245

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1365
- Ceres seq_id 1500107
- Location of start within SEQ ID NO 1363: at 433 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11854
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1365: from 1 to 237 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11855
- gi No. 1076387
- % Identity 76.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
- Alignment No. 11856
- gi No. 1076641
- % Identity 82.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
- Alignment No. 11857
- gi No. 1076649
- % Identity 82.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
- Alignment No. 11858
- gi No. 1076651
- % Identity 79.6
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
- Alignment No. 11859
- gi No. 1170711
- % Identity 82.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
- Alignment No. 11860

- gi No. 1170714
- % Identity 83.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
- Alignment No. 11861
- gi No. 125373
- % Identity 70.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 241
- Alignment No. 11862
- gi No. 125374
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
- Alignment No. 11863
- gi No. 1431622
- % Identity 82.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
- Alignment No. 11864
- gi No. 1480078
- % Identity 91.2
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
- Alignment No. 11865
- gi No. 1504063
- % Identity 76.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
- Alignment No. 11866
- gi No. 1617200
- % Identity 81.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
- Alignment No. 11867
- gi No. 1709127
- % Identity 82.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
- Alignment No. 11868
- gi No. 1709128
- % Identity 81.7
- Alignment Length 284
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
- Alignment No. 11869
- gi No. 1709129
- % Identity 82.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
- Alignment No. 11870
- gi No. 1730039

- % Identity 70.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 241

- Alignment No. 11871
- gi No. 1877393
- % Identity 83
- Alignment Length 171
- Location of Alignment in SEQ ID NO 1365: from 73 to 242

- Alignment No. 11872
- gi No. 1877397
- % Identity 93.4
- Alignment Length 226
- Location of Alignment in SEQ ID NO 1365: from 17 to 242

- Alignment No. 11873
- gi No. 1944518
- % Identity 79
- Alignment Length 290
- Location of Alignment in SEQ ID NO 1365: from 1 to 247

- Alignment No. 11874
- gi No. 2117783
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1365: from 1 to 242

- Alignment No. 11875
- gi No. 2117784
- % Identity 70.2
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1365: from 1 to 242

- Alignment No. 11876
- gi No. 2129738
- % Identity 90.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242

- Alignment No. 11877
- gi No. 2129739
- % Identity 96.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242

- Alignment No. 11878
- gi No. 2160191
- % Identity 76.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242

- Alignment No. 11879
- gi No. 2182029
- % Identity 89.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242

- Alignment No. 11880
- gi No. 2191169
- % Identity 78.7

- Alignment Length 300
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
- Alignment No. 11881
- gi No. 2398519
- % Identity 82.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
- Alignment No. 11882
- gi No. 2569931
- % Identity 74.1
- Alignment Length 290
- Location of Alignment in SEQ ID NO 1365: from 1 to 247
- Alignment No. 11883
- gi No. 2569950
- % Identity 79.9
- Alignment Length 284
- Location of Alignment in SEQ ID NO 1365: from 1 to 241
- Alignment No. 11884
- gi No. 2598601
- % Identity 77.9
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
- Alignment No. 11885
- gi No. 2598603
- % Identity 78.6
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
- Alignment No. 11886
- gi No. 2641994
- % Identity 70.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 241
- Alignment No. 11887
- gi No. 2911533
- % Identity 79.6
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
- Alignment No. 11888
- gi No. 3201623
- % Identity 91.2
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
- Alignment No. 11889
- gi No. 3236115
- % Identity 81.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
- Alignment No. 11890
- gi No. 3236117
- % Identity 80
- Alignment Length 285

- Location of Alignment in SEQ ID NO 1365: from 1 to 242
- Alignment No. 11891
- gi No. 3250738
- % Identity 73.7
- Alignment Length 293
- Location of Alignment in SEQ ID NO 1365: from 1 to 247
- Alignment No. 11892
- gi No. 3264607
- % Identity 81.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1365: from 173 to 242
- Alignment No. 11893
- gi No. 3702608
- % Identity 77.2
- Alignment Length 290
- Location of Alignment in SEQ ID NO 1365: from 1 to 247
- Alignment No. 11894
- gi No. 3928148
- % Identity 81.6
- Alignment Length 266
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
- Alignment No. 11895
- gi No. 402652
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
- Alignment No. 11896
- gi No. 4140287
- % Identity 71.6
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
- Alignment No. 11897
- gi No. 4504163
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
- Alignment No. 11898
- gi No. 4539390
- % Identity 100
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1365: from 1 to 242
- Alignment No. 11899
- gi No. 5070700
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1365: from 1 to 242

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1366
- Ceres seq_id 1500108
- Location of start within SEQ ID NO 1363: at 514 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 11900
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1366: from 1 to 210 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11901
- gi No. 1076387
- % Identity 76.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
- Alignment No. 11902
- gi No. 1076641
- % Identity 82.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
- Alignment No. 11903
- gi No. 1076649
- % Identity 82.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
- Alignment No. 11904
- gi No. 1076651
- % Identity 79.6
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
- Alignment No. 11905
- gi No. 1170711
- % Identity 82.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
- Alignment No. 11906
- gi No. 1170714
- % Identity 83.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
- Alignment No. 11907
- gi No. 125373
- % Identity 70.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 214
- Alignment No. 11908
- gi No. 125374
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
- Alignment No. 11909
- gi No. 1431622
- % Identity 82.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215

- Alignment No. 11910
- gi No. 1480078
- % Identity 91.2
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215

- Alignment No. 11911
- gi No. 1504063
- % Identity 76.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215

- Alignment No. 11912
- gi No. 1617200
- % Identity 81.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215

- Alignment No. 11913
- gi No. 1709127
- % Identity 82.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215

- Alignment No. 11914
- gi No. 1709128
- % Identity 81.7
- Alignment Length 284
- Location of Alignment in SEQ ID NO 1366: from 1 to 215

- Alignment No. 11915
- gi No. 1709129
- % Identity 82.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215

- Alignment No. 11916
- gi No. 1730039
- % Identity 70.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 214

- Alignment No. 11917
- gi No. 1877393
- % Identity 83
- Alignment Length 171
- Location of Alignment in SEQ ID NO 1366: from 46 to 215

- Alignment No. 11918
- gi No. 1877397
- % Identity 93.4
- Alignment Length 226
- Location of Alignment in SEQ ID NO 1366: from 1 to 215

- Alignment No. 11919
- gi No. 1944518
- % Identity 79
- Alignment Length 290
- Location of Alignment in SEQ ID NO 1366: from 1 to 220

- Alignment No. 11920

- gi No. 2117783
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1366: from 1 to 215

- Alignment No. 11921
- gi No. 2117784
- % Identity 70.2
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1366: from 1 to 215

- Alignment No. 11922
- gi No. 2129738
- % Identity 90.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215

- Alignment No. 11923
- gi No. 2129739
- % Identity 96.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215

- Alignment No. 11924
- gi No. 2160191
- % Identity 76.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215

- Alignment No. 11925
- gi No. 2182029
- % Identity 89.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215

- Alignment No. 11926
- gi No. 2191169
- % Identity 78.7
- Alignment Length 300
- Location of Alignment in SEQ ID NO 1366: from 1 to 215

- Alignment No. 11927
- gi No. 2398519
- % Identity 82.5
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215

- Alignment No. 11928
- gi No. 2569931
- % Identity 74.1
- Alignment Length 290
- Location of Alignment in SEQ ID NO 1366: from 1 to 220

- Alignment No. 11929
- gi No. 2569950
- % Identity 79.9
- Alignment Length 284
- Location of Alignment in SEQ ID NO 1366: from 1 to 214

- Alignment No. 11930
- gi No. 2598601

- % Identity 77.9
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215

- Alignment No. 11931
- gi No. 2598603
- % Identity 78.6
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215

- Alignment No. 11932
- gi No. 2641994
- % Identity 70.8
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 214

- Alignment No. 11933
- gi No. 2911533
- % Identity 79.6
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215

- Alignment No. 11934
- gi No. 3201623
- % Identity 91.2
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215

- Alignment No. 11935
- gi No. 3236115
- % Identity 81.1
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215

- Alignment No. 11936
- gi No. 3236117
- % Identity 80
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215

- Alignment No. 11937
- gi No. 3250738
- % Identity 73.7
- Alignment Length 293
- Location of Alignment in SEQ ID NO 1366: from 1 to 220

- Alignment No. 11938
- gi No. 3264607
- % Identity 81.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1366: from 146 to 215

- Alignment No. 11939
- gi No. 3702608
- % Identity 77.2
- Alignment Length 290
- Location of Alignment in SEQ ID NO 1366: from 1 to 220

- Alignment No. 11940
- gi No. 3928148
- % Identity 81.6

- Alignment Length 266
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
- Alignment No. 11941
- gi No. 402652
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
- Alignment No. 11942
- gi No. 4140287
- % Identity 71.6
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
- Alignment No. 11943
- gi No. 4504163
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
- Alignment No. 11944
- gi No. 4539390
- % Identity 100
- Alignment Length 285
- Location of Alignment in SEQ ID NO 1366: from 1 to 215
- Alignment No. 11945
- gi No. 5070700
- % Identity 70.9
- Alignment Length 286
- Location of Alignment in SEQ ID NO 1366: from 1 to 215

Maximum Length Sequence corresponding to clone ID 256152

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1367
- Ceres seq_id 1500109

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1368
- Ceres seq_id 1500110
- Location of start within SEQ ID NO 1367: at 416 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11946
- gi No. 3386609
- % Identity 99.7
- Alignment Length 348
- Location of Alignment in SEQ ID NO 1368: from 1 to 348

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1369
- Ceres seq_id 1500111
- Location of start within SEQ ID NO 1367: at 434 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11947
- gi No. 3386609

- % Identity 99.7
- Alignment Length 348
- Location of Alignment in SEQ ID NO 1369: from 1 to 342

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1370
- Ceres seq_id 1500112
- Location of start within SEQ ID NO 1367: at 668 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11948
- gi No. 3386609
- % Identity 99.7
- Alignment Length 348
- Location of Alignment in SEQ ID NO 1370: from 1 to 264

Maximum Length Sequence corresponding to clone ID 256433

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1371
- Ceres seq_id 1500115

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1372
- Ceres seq_id 1500116
- Location of start within SEQ ID NO 1371: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11949
- Iron/Ascorbate oxidoreductase family
- Location within SEQ ID NO 1372: from 82 to 185 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11950
- gi No. 3335372
- % Identity 89.8
- Alignment Length 176
- Location of Alignment in SEQ ID NO 1372: from 29 to 185

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1373
- Ceres seq_id 1500117
- Location of start within SEQ ID NO 1371: at 85 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11951
- Iron/Ascorbate oxidoreductase family
- Location within SEQ ID NO 1373: from 54 to 157 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11952
- gi No. 3335372
- % Identity 89.8
- Alignment Length 176
- Location of Alignment in SEQ ID NO 1373: from 1 to 157

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1374
- Ceres seq_id 1500118

- Location of start within SEQ ID NO 1371: at 662 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11953
- Iron/Ascorbate oxidoreductase family
- Location within SEQ ID NO 1374: from 1 to 126 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11954
- gi No. 3335372
- % Identity 99.5
- Alignment Length 200
- Location of Alignment in SEQ ID NO 1374: from 1 to 161

Maximum Length Sequence corresponding to clone ID 256780

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1375
- Ceres seq_id 1500131

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1376
- Ceres seq_id 1500132
- Location of start within SEQ ID NO 1375: at 87 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11955
- gi No. 136739
- % Identity 83.3
- Alignment Length 468
- Location of Alignment in SEQ ID NO 1376: from 3 to 469
- Alignment No. 11956
- gi No. 1388021
- % Identity 82.1
- Alignment Length 476
- Location of Alignment in SEQ ID NO 1376: from 1 to 469
- Alignment No. 11957
- gi No. 2117937
- % Identity 81.6
- Alignment Length 467
- Location of Alignment in SEQ ID NO 1376: from 3 to 469
- Alignment No. 11958
- gi No. 3107931
- % Identity 81.7
- Alignment Length 469
- Location of Alignment in SEQ ID NO 1376: from 2 to 469
- Alignment No. 11959
- gi No. 322794
- % Identity 82.9
- Alignment Length 468
- Location of Alignment in SEQ ID NO 1376: from 3 to 469

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1377
- Ceres seq_id 1500133
- Location of start within SEQ ID NO 1375: at 147 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11960
- gi No. 136739
- % Identity 83.3
- Alignment Length 468
- Location of Alignment in SEQ ID NO 1377: from 1 to 449

- Alignment No. 11961
- gi No. 1388021
- % Identity 82.1
- Alignment Length 476
- Location of Alignment in SEQ ID NO 1377: from 1 to 449

- Alignment No. 11962
- gi No. 2117937
- % Identity 81.6
- Alignment Length 467
- Location of Alignment in SEQ ID NO 1377: from 1 to 449

- Alignment No. 11963
- gi No. 3107931
- % Identity 81.7
- Alignment Length 469
- Location of Alignment in SEQ ID NO 1377: from 1 to 449

- Alignment No. 11964
- gi No. 322794
- % Identity 82.9
- Alignment Length 468
- Location of Alignment in SEQ ID NO 1377: from 1 to 449

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1378
- Ceres seq_id 1500134
- Location of start within SEQ ID NO 1375: at 273 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11965
- gi No. 136739
- % Identity 83.3
- Alignment Length 468
- Location of Alignment in SEQ ID NO 1378: from 1 to 407

- Alignment No. 11966
- gi No. 1388021
- % Identity 82.1
- Alignment Length 476
- Location of Alignment in SEQ ID NO 1378: from 1 to 407

- Alignment No. 11967
- gi No. 2117937
- % Identity 81.6
- Alignment Length 467
- Location of Alignment in SEQ ID NO 1378: from 1 to 407

- Alignment No. 11968

- gi No. 3107931
- % Identity 81.7
- Alignment Length 469
- Location of Alignment in SEQ ID NO 1378: from 1 to 407

- Alignment No. 11969
- gi No. 322794
- % Identity 82.9
- Alignment Length 468
- Location of Alignment in SEQ ID NO 1378: from 1 to 407

Maximum Length Sequence corresponding to clone ID 257053

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1379
- Ceres seq_id 1500135

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1380
- Ceres seq_id 1500136
- Location of start within SEQ ID NO 1379: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11970
- Zinc finger, C3HC4 type (RING finger)
- Location within SEQ ID NO 1380: from 267 to 301 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1381
- Ceres seq_id 1500137
- Location of start within SEQ ID NO 1379: at 7 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11971
- Zinc finger, C3HC4 type (RING finger)
- Location within SEQ ID NO 1381: from 265 to 299 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1382
- Ceres seq_id 1500138
- Location of start within SEQ ID NO 1379: at 136 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 11972
- Zinc finger, C3HC4 type (RING finger)
- Location within SEQ ID NO 1382: from 222 to 256 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 257278

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1383
- Ceres seq_id 1500149

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1384
- Ceres seq_id 1500150

- Location of start within SEQ ID NO 1383: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1385
- Ceres seq_id 1500151
- Location of start within SEQ ID NO 1383: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1386
- Ceres seq_id 1500152
- Location of start within SEQ ID NO 1383: at 230 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 11973
- gi No. 3717946
- % Identity 72.6
- Alignment Length 84
- Location of Alignment in SEQ ID NO 1386: from 3 to 86
- Alignment No. 11974
- gi No. 3717987
- % Identity 76.2
- Alignment Length 84
- Location of Alignment in SEQ ID NO 1386: from 3 to 86
- Alignment No. 11975
- gi No. 3717989
- % Identity 72.6
- Alignment Length 84
- Location of Alignment in SEQ ID NO 1386: from 3 to 86

Maximum Length Sequence corresponding to clone ID 257311

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1387
- Ceres seq_id 1500153

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1388
- Ceres seq_id 1500154
- Location of start within SEQ ID NO 1387: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1389
- Ceres seq_id 1500155
- Location of start within SEQ ID NO 1387: at 272 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 11976
 - gi No. 3834307
 - % Identity 70
 - Alignment Length 40
 - Location of Alignment in SEQ ID NO 1389: from 18 to 57

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1390
 - Ceres seq_id 1500156
 - Location of start within SEQ ID NO 1387: at 323 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 11977
 - gi No. 3834307
 - % Identity 70
 - Alignment Length 40
 - Location of Alignment in SEQ ID NO 1390: from 1 to 40

Maximum Length Sequence corresponding to clone ID 257315

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1391
 - Ceres seq_id 1500157

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1392
 - Ceres seq_id 1500158
 - Location of start within SEQ ID NO 1391: at 264 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 11978
 - gi No. 3335359
 - % Identity 70.2
 - Alignment Length 131
 - Location of Alignment in SEQ ID NO 1392: from 1 to 85

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1393
 - Ceres seq_id 1500159
 - Location of start within SEQ ID NO 1391: at 291 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 11979
 - gi No. 3335359
 - % Identity 70.2
 - Alignment Length 131
 - Location of Alignment in SEQ ID NO 1393: from 1 to 76

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1394
 - Ceres seq_id 1500160
 - Location of start within SEQ ID NO 1391: at 351 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences

- Alignment No. 11980
- gi No. 3335359
- % Identity 70.2
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1394: from 1 to 56

Maximum Length Sequence corresponding to clone ID 257348
(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1395
- Ceres seq_id 1500165

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1396
- Ceres seq_id 1500166
- Location of start within SEQ ID NO 1395: at 285 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 11981
- Peptidyl-prolyl cis-trans isomerase
- Location within SEQ ID NO 1396: from 5 to 73 aa.

(D) Related Amino Acid Sequences

- Alignment No. 11982
- gi No. 1045518
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 1396: from 22 to 73

- Alignment No. 11983
- gi No. 1076366
- % Identity 77
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73

- Alignment No. 11984
- gi No. 1076367
- % Identity 78.4
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73

- Alignment No. 11985
- gi No. 1076510
- % Identity 81.1
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73

- Alignment No. 11986
- gi No. 1084454
- % Identity 77.8
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1396: from 3 to 73

- Alignment No. 11987
- gi No. 1084455
- % Identity 93.2
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73

- Alignment No. 11988
- gi No. 118099
- % Identity 73.2

- Alignment Length 71
- Location of Alignment in SEQ ID NO 1396: from 4 to 73

- Alignment No. 11989
- gi No. 118103
- % Identity 86.5
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73

- Alignment No. 11990
- gi No. 118104
- % Identity 100
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73

- Alignment No. 11991
- gi No. 1279366
- % Identity 80
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1396: from 50 to 73

- Alignment No. 11992
- gi No. 1345921
- % Identity 82.4
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73

- Alignment No. 11993
- gi No. 1480461
- % Identity 74.3
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73

- Alignment No. 11994
- gi No. 1480463
- % Identity 74.3
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73

- Alignment No. 11995
- gi No. 1480465
- % Identity 82.4
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73

- Alignment No. 11996
- gi No. 1561575
- % Identity 83.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73

- Alignment No. 11997
- gi No. 1563719
- % Identity 86.5
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73

- Alignment No. 11998
- gi No. 1652923
- % Identity 75.7
- Alignment Length 70

- Location of Alignment in SEQ ID NO 1396: from 5 to 73
- Alignment No. 11999
- gi No. 167138
- % Identity 83.1
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1396: from 4 to 73
- Alignment No. 12000
- gi No. 1703696
- % Identity 71.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
- Alignment No. 12001
- gi No. 1706247
- % Identity 73
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
- Alignment No. 12002
- gi No. 1706248
- % Identity 73
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
- Alignment No. 12003
- gi No. 1706253
- % Identity 81.1
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
- Alignment No. 12004
- gi No. 1706258
- % Identity 73
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
- Alignment No. 12005
- gi No. 1928939
- % Identity 87.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
- Alignment No. 12006
- gi No. 2129568
- % Identity 71.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
- Alignment No. 12007
- gi No. 2129569
- % Identity 81.9
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1396: from 3 to 73
- Alignment No. 12008
- gi No. 227879
- % Identity 80.5
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1396: from 1 to 73

- Alignment No. 12009
- gi No. 2443755
- % Identity 72.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1396: from 5 to 73

- Alignment No. 12010
- gi No. 2443757
- % Identity 82.2
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1396: from 2 to 73

- Alignment No. 12011
- gi No. 2655157
- % Identity 73.2
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1396: from 4 to 73

- Alignment No. 12012
- gi No. 2655159
- % Identity 73.2
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1396: from 4 to 73

- Alignment No. 12013
- gi No. 2760537
- % Identity 83.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73

- Alignment No. 12014
- gi No. 2959712
- % Identity 83.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73

- Alignment No. 12015
- gi No. 3063396
- % Identity 79.7
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73

- Alignment No. 12016
- gi No. 3334157
- % Identity 82.4
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73

- Alignment No. 12017
- gi No. 3420055
- % Identity 72.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1396: from 5 to 73

- Alignment No. 12018
- gi No. 348725
- % Identity 72.5
- Alignment Length 51
- Location of Alignment in SEQ ID NO 1396: from 25 to 73

- Alignment No. 12019
- gi No. 3550686
- % Identity 70.1
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
- Alignment No. 12020
- gi No. 3881310
- % Identity 81.1
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
- Alignment No. 12021
- gi No. 3881755
- % Identity 75.7
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
- Alignment No. 12022
- gi No. 4097889
- % Identity 70.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1396: from 5 to 73
- Alignment No. 12023
- gi No. 4559302
- % Identity 87.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
- Alignment No. 12024
- gi No. 4589980
- % Identity 81.9
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1396: from 3 to 73
- Alignment No. 12025
- gi No. 461902
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 1396: from 22 to 73
- Alignment No. 12026
- gi No. 461903
- % Identity 78.4
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73
- Alignment No. 12027
- gi No. 4803930
- % Identity 82.2
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1396: from 2 to 73
- Alignment No. 12028
- gi No. 544125
- % Identity 76.5
- Alignment Length 68
- Location of Alignment in SEQ ID NO 1396: from 7 to 73
- Alignment No. 12029

- gi No. 600769
- % Identity 93.2
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73

- Alignment No. 12030
- gi No. 630464
- % Identity 73.3
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1396: from 1 to 73

- Alignment No. 12031
- gi No. 68406
- % Identity 87.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73

- Alignment No. 12032
- gi No. 68407
- % Identity 83.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73

- Alignment No. 12033
- gi No. 939726
- % Identity 71.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1396: from 1 to 73

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1397
- Ceres seq_id 1500167
- Location of start within SEQ ID NO 1395: at 312 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12034
- Peptidyl-prolyl cis-trans isomerase
- Location within SEQ ID NO 1397: from 1 to 64 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12035
- gi No. 1045518
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 1397: from 13 to 64

- Alignment No. 12036
- gi No. 1076366
- % Identity 77
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64

- Alignment No. 12037
- gi No. 1076367
- % Identity 78.4
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64

- Alignment No. 12038
- gi No. 1076510

- % Identity 81.1
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64

- Alignment No. 12039
- gi No. 1084454
- % Identity 77.8
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1397: from 1 to 64

- Alignment No. 12040
- gi No. 1084455
- % Identity 93.2
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64

- Alignment No. 12041
- gi No. 118099
- % Identity 73.2
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1397: from 1 to 64

- Alignment No. 12042
- gi No. 118103
- % Identity 86.5
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64

- Alignment No. 12043
- gi No. 118104
- % Identity 100
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64

- Alignment No. 12044
- gi No. 1279366
- % Identity 80
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1397: from 41 to 64

- Alignment No. 12045
- gi No. 1345921
- % Identity 82.4
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64

- Alignment No. 12046
- gi No. 1480461
- % Identity 74.3
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64

- Alignment No. 12047
- gi No. 1480463
- % Identity 74.3
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64

- Alignment No. 12048
- gi No. 1480465
- % Identity 82.4

- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64

- Alignment No. 12049
- gi No. 1561575
- % Identity 83.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64

- Alignment No. 12050
- gi No. 1563719
- % Identity 86.5
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64

- Alignment No. 12051
- gi No. 1652923
- % Identity 75.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1397: from 1 to 64

- Alignment No. 12052
- gi No. 167138
- % Identity 83.1
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1397: from 1 to 64

- Alignment No. 12053
- gi No. 1703696
- % Identity 71.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64

- Alignment No. 12054
- gi No. 1706247
- % Identity 73
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64

- Alignment No. 12055
- gi No. 1706248
- % Identity 73
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64

- Alignment No. 12056
- gi No. 1706253
- % Identity 81.1
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64

- Alignment No. 12057
- gi No. 1706258
- % Identity 73
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64

- Alignment No. 12058
- gi No. 1928939
- % Identity 87.8
- Alignment Length 74

- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12059
- gi No. 2129568
- % Identity 71.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12060
- gi No. 2129569
- % Identity 81.9
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12061
- gi No. 227879
- % Identity 80.5
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12062
- gi No. 2443755
- % Identity 72.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12063
- gi No. 2443757
- % Identity 82.2
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12064
- gi No. 2655157
- % Identity 73.2
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12065
- gi No. 2655159
- % Identity 73.2
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12066
- gi No. 2760537
- % Identity 83.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12067
- gi No. 2959712
- % Identity 83.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12068
- gi No. 3063396
- % Identity 79.7
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64

- Alignment No. 12069
- gi No. 3334157
- % Identity 82.4
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12070
- gi No. 3420055
- % Identity 72.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12071
- gi No. 348725
- % Identity 72.5
- Alignment Length 51
- Location of Alignment in SEQ ID NO 1397: from 16 to 64
- Alignment No. 12072
- gi No. 3550686
- % Identity 70.1
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12073
- gi No. 3881310
- % Identity 81.1
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12074
- gi No. 3881755
- % Identity 75.7
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12075
- gi No. 4097889
- % Identity 70.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12076
- gi No. 4559302
- % Identity 87.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12077
- gi No. 4589980
- % Identity 81.9
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1397: from 1 to 64
- Alignment No. 12078
- gi No. 461902
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 1397: from 13 to 64

- Alignment No. 12079
- gi No. 461903
- % Identity 78.4
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64

- Alignment No. 12080
- gi No. 4803930
- % Identity 82.2
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1397: from 1 to 64

- Alignment No. 12081
- gi No. 544125
- % Identity 76.5
- Alignment Length 68
- Location of Alignment in SEQ ID NO 1397: from 1 to 64

- Alignment No. 12082
- gi No. 600769
- % Identity 93.2
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64

- Alignment No. 12083
- gi No. 630464
- % Identity 73.3
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1397: from 1 to 64

- Alignment No. 12084
- gi No. 68406
- % Identity 87.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64

- Alignment No. 12085
- gi No. 68407
- % Identity 83.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64

- Alignment No. 12086
- gi No. 939726
- % Identity 71.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1397: from 1 to 64

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1398
- Ceres seq_id 1500168
- Location of start within SEQ ID NO 1395: at 348 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12087
- Peptidyl-prolyl cis-trans isomerase
- Location within SEQ ID NO 1398: from 1 to 52 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12088

- gi No. 1045518
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12089
- gi No. 1076366
- % Identity 77
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12090
- gi No. 1076367
- % Identity 78.4
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12091
- gi No. 1076510
- % Identity 81.1
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12092
- gi No. 1084454
- % Identity 77.8
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12093
- gi No. 1084455
- % Identity 93.2
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12094
- gi No. 118099
- % Identity 73.2
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12095
- gi No. 118103
- % Identity 86.5
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12096
- gi No. 118104
- % Identity 100
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12097
- gi No. 1279366
- % Identity 80
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1398: from 29 to 52
- Alignment No. 12098
- gi No. 1345921

- % Identity 82.4
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52

- Alignment No. 12099
- gi No. 1480461
- % Identity 74.3
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52

- Alignment No. 12100
- gi No. 1480463
- % Identity 74.3
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52

- Alignment No. 12101
- gi No. 1480465
- % Identity 82.4
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52

- Alignment No. 12102
- gi No. 1561575
- % Identity 83.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52

- Alignment No. 12103
- gi No. 1563719
- % Identity 86.5
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52

- Alignment No. 12104
- gi No. 1652923
- % Identity 75.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1398: from 1 to 52

- Alignment No. 12105
- gi No. 167138
- % Identity 83.1
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1398: from 1 to 52

- Alignment No. 12106
- gi No. 1703696
- % Identity 71.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52

- Alignment No. 12107
- gi No. 1706247
- % Identity 73
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52

- Alignment No. 12108
- gi No. 1706248
- % Identity 73

- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52

- Alignment No. 12109
- gi No. 1706253
- % Identity 81.1
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52

- Alignment No. 12110
- gi No. 1706258
- % Identity 73
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52

- Alignment No. 12111
- gi No. 1928939
- % Identity 87.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52

- Alignment No. 12112
- gi No. 2129568
- % Identity 71.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52

- Alignment No. 12113
- gi No. 2129569
- % Identity 81.9
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1398: from 1 to 52

- Alignment No. 12114
- gi No. 227879
- % Identity 80.5
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1398: from 1 to 52

- Alignment No. 12115
- gi No. 2443755
- % Identity 72.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1398: from 1 to 52

- Alignment No. 12116
- gi No. 2443757
- % Identity 82.2
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1398: from 1 to 52

- Alignment No. 12117
- gi No. 2655157
- % Identity 73.2
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1398: from 1 to 52

- Alignment No. 12118
- gi No. 2655159
- % Identity 73.2
- Alignment Length 71

- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12119
- gi No. 2760537
- % Identity 83.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12120
- gi No. 2959712
- % Identity 83.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12121
- gi No. 3063396
- % Identity 79.7
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12122
- gi No. 3334157
- % Identity 82.4
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12123
- gi No. 3420055
- % Identity 72.9
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12124
- gi No. 348725
- % Identity 72.5
- Alignment Length 51
- Location of Alignment in SEQ ID NO 1398: from 4 to 52
- Alignment No. 12125
- gi No. 3550686
- % Identity 70.1
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12126
- gi No. 3881310
- % Identity 81.1
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12127
- gi No. 3881755
- % Identity 75.7
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52
- Alignment No. 12128
- gi No. 4097889
- % Identity 70.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1398: from 1 to 52

- Alignment No. 12129
- gi No. 4559302
- % Identity 87.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52

- Alignment No. 12130
- gi No. 4589980
- % Identity 81.9
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1398: from 1 to 52

- Alignment No. 12131
- gi No. 461902
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 1398: from 1 to 52

- Alignment No. 12132
- gi No. 461903
- % Identity 78.4
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52

- Alignment No. 12133
- gi No. 4803930
- % Identity 82.2
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1398: from 1 to 52

- Alignment No. 12134
- gi No. 544125
- % Identity 76.5
- Alignment Length 68
- Location of Alignment in SEQ ID NO 1398: from 1 to 52

- Alignment No. 12135
- gi No. 600769
- % Identity 93.2
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52

- Alignment No. 12136
- gi No. 630464
- % Identity 73.3
- Alignment Length 75
- Location of Alignment in SEQ ID NO 1398: from 1 to 52

- Alignment No. 12137
- gi No. 68406
- % Identity 87.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52

- Alignment No. 12138
- gi No. 68407
- % Identity 83.8
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52

- Alignment No. 12139
- gi No. 939726
- % Identity 71.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1398: from 1 to 52

Maximum Length Sequence corresponding to clone ID 257355

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1399
- Ceres seq_id 1500169

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1400
- Ceres seq_id 1500170
- Location of start within SEQ ID NO 1399: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12140
- ATPases associated with various cellular activities (AAA)
- Location within SEQ ID NO 1400: from 117 to 168 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 257369

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1401
- Ceres seq_id 1500179

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1402
- Ceres seq_id 1500180
- Location of start within SEQ ID NO 1401: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1403
- Ceres seq_id 1500181
- Location of start within SEQ ID NO 1401: at 67 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12141
- gi No. 2642158
- % Identity 70.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1403: from 11 to 155

- Alignment No. 12142
- gi No. 81286
- % Identity 71.4
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1403: from 4 to 17

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1404
- Ceres seq_id 1500182
- Location of start within SEQ ID NO 1401: at 181 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 12143
 - gi No. 2642158
 - % Identity 70.5
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 1404: from 1 to 117

Maximum Length Sequence corresponding to clone ID 257391

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1405
- Ceres seq_id 1500186

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1406
- Ceres seq_id 1500187
- Location of start within SEQ ID NO 1405: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12144
- Syntaxin
- Location within SEQ ID NO 1406: from 51 to 178 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1407
- Ceres seq_id 1500188
- Location of start within SEQ ID NO 1405: at 92 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12145
- Syntaxin
- Location within SEQ ID NO 1407: from 21 to 148 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1408
- Ceres seq_id 1500189
- Location of start within SEQ ID NO 1405: at 161 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12146
- Syntaxin
- Location within SEQ ID NO 1408: from 1 to 125 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 257556

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1409
- Ceres seq_id 1500190

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1410
- Ceres seq_id 1500191
- Location of start within SEQ ID NO 1409: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 12147
- CTF/NF-I family
- Location within SEQ ID NO 1410: from 32 to 107 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12148
- gi No. 1914853
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1410: from 166 to 176
- Alignment No. 12149
- gi No. 3650031
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1410: from 163 to 173
- Alignment No. 12150
- gi No. 5420387
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1410: from 290 to 300

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1411
- Ceres seq_id 1500192
- Location of start within SEQ ID NO 1409: at 21 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 12151
- CTF/NF-I family
- Location within SEQ ID NO 1411: from 26 to 101 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12152
- gi No. 1914853
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1411: from 160 to 170
- Alignment No. 12153
- gi No. 3650031
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1411: from 157 to 167
- Alignment No. 12154
- gi No. 5420387
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1411: from 284 to 294

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1412
- Ceres seq_id 1500193
- Location of start within SEQ ID NO 1409: at 612 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 12155
 - gi No. 5420387
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 1412: from 87 to 97

Maximum Length Sequence corresponding to clone ID 257654

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1413
- Ceres seq_id 1500198

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1414
- Ceres seq_id 1500199
- Location of start within SEQ ID NO 1413: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1415
- Ceres seq_id 1500200
- Location of start within SEQ ID NO 1413: at 245 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 12156
- SRF-type transcription factor (DNA-binding and dimerisation

domain)

- Location within SEQ ID NO 1415: from 1 to 59 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12157
- gi No. 1001935
- % Identity 74.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1415: from 1 to 70

- Alignment No. 12158
- gi No. 1049022
- % Identity 74.1
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1415: from 1 to 85

- Alignment No. 12159
- gi No. 1076646
- % Identity 73.9
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1415: from 1 to 85

- Alignment No. 12160
- gi No. 1076827
- % Identity 72.9
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1415: from 1 to 58

- Alignment No. 12161
- gi No. 1206003

- % Identity 71.8
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1415: from 1 to 70

- Alignment No. 12162
- gi No. 1208800
- % Identity 76
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1415: from 17 to 41

- Alignment No. 12163
- gi No. 1208802
- % Identity 84
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1415: from 17 to 41

- Alignment No. 12164
- gi No. 1208804
- % Identity 82.6
- Alignment Length 23
- Location of Alignment in SEQ ID NO 1415: from 19 to 41

- Alignment No. 12165
- gi No. 1239961
- % Identity 71.8
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1415: from 1 to 70

- Alignment No. 12166
- gi No. 1345965
- % Identity 70.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1415: from 1 to 70

- Alignment No. 12167
- gi No. 1362195
- % Identity 75.4
- Alignment Length 57
- Location of Alignment in SEQ ID NO 1415: from 3 to 59

- Alignment No. 12168
- gi No. 1362196
- % Identity 78.9
- Alignment Length 57
- Location of Alignment in SEQ ID NO 1415: from 3 to 59

- Alignment No. 12169
- gi No. 1362197
- % Identity 75.4
- Alignment Length 57
- Location of Alignment in SEQ ID NO 1415: from 3 to 59

- Alignment No. 12170
- gi No. 1362198
- % Identity 77.2
- Alignment Length 57
- Location of Alignment in SEQ ID NO 1415: from 3 to 59

- Alignment No. 12171
- gi No. 1362199
- % Identity 76.3

- Alignment Length 59
- Location of Alignment in SEQ ID NO 1415: from 1 to 59

- Alignment No. 12172
- gi No. 1362200
- % Identity 78
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1415: from 1 to 59

- Alignment No. 12173
- gi No. 1362201
- % Identity 84.4
- Alignment Length 45
- Location of Alignment in SEQ ID NO 1415: from 15 to 59

- Alignment No. 12174
- gi No. 1362202
- % Identity 77.3
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1415: from 16 to 59

- Alignment No. 12175
- gi No. 1362203
- % Identity 71.2
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1415: from 1 to 59

- Alignment No. 12176
- gi No. 1362204
- % Identity 81.8
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1415: from 16 to 59

- Alignment No. 12177
- gi No. 1362205
- % Identity 82.2
- Alignment Length 45
- Location of Alignment in SEQ ID NO 1415: from 16 to 60

- Alignment No. 12178
- gi No. 1362206
- % Identity 77.3
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1415: from 16 to 59

- Alignment No. 12179
- gi No. 1362209
- % Identity 73.3
- Alignment Length 60
- Location of Alignment in SEQ ID NO 1415: from 1 to 59

- Alignment No. 12180
- gi No. 2160701
- % Identity 75.4
- Alignment Length 69
- Location of Alignment in SEQ ID NO 1415: from 1 to 69

- Alignment No. 12181
- gi No. 2286109
- % Identity 71.4
- Alignment Length 70

- Location of Alignment in SEQ ID NO 1415: from 1 to 70
- Alignment No. 12182
- gi No. 2459835
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1415: from 1 to 56
- Alignment No. 12183
- gi No. 2463333
- % Identity 70.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1415: from 1 to 70
- Alignment No. 12184
- gi No. 2979566
- % Identity 75.3
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1415: from 1 to 85
- Alignment No. 12185
- gi No. 3023536
- % Identity 71.8
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1415: from 1 to 70
- Alignment No. 12186
- gi No. 3114588
- % Identity 71.8
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1415: from 1 to 70
- Alignment No. 12187
- gi No. 320596
- % Identity 70.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1415: from 1 to 70
- Alignment No. 12188
- gi No. 322801
- % Identity 70.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1415: from 3 to 79
- Alignment No. 12189
- gi No. 3292820
- % Identity 71.8
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1415: from 1 to 85
- Alignment No. 12190
- gi No. 3493647
- % Identity 80.2
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1415: from 1 to 81
- Alignment No. 12191
- gi No. 3646322
- % Identity 75
- Alignment Length 68
- Location of Alignment in SEQ ID NO 1415: from 4 to 70

- Alignment No. 12192
- gi No. 3646340
- % Identity 71.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1415: from 1 to 70

- Alignment No. 12193
- gi No. 3688591
- % Identity 71.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1415: from 1 to 70

- Alignment No. 12194
- gi No. 3851331
- % Identity 71.9
- Alignment Length 57
- Location of Alignment in SEQ ID NO 1415: from 16 to 71

- Alignment No. 12195
- gi No. 3851333
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 1415: from 16 to 69

- Alignment No. 12196
- gi No. 4033710
- % Identity 71.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1415: from 1 to 76

- Alignment No. 12197
- gi No. 4033721
- % Identity 71.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1415: from 1 to 76

- Alignment No. 12198
- gi No. 4033725
- % Identity 70.8
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1415: from 5 to 76

- Alignment No. 12199
- gi No. 4101710
- % Identity 71.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1415: from 1 to 76

- Alignment No. 12200
- gi No. 4103486
- % Identity 71.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1415: from 1 to 76

- Alignment No. 12201
- gi No. 4322475
- % Identity 77.1
- Alignment Length 83
- Location of Alignment in SEQ ID NO 1415: from 1 to 83

- Alignment No. 12202
- gi No. 497145
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1415: from 10 to 35
- Alignment No. 12203
- gi No. 497147
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1415: from 10 to 35
- Alignment No. 12204
- gi No. 497149
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1415: from 10 to 35
- Alignment No. 12205
- gi No. 5002523
- % Identity 76.3
- Alignment Length 80
- Location of Alignment in SEQ ID NO 1415: from 1 to 79
- Alignment No. 12206
- gi No. 5019431
- % Identity 72.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1415: from 1 to 76
- Alignment No. 12207
- gi No. 5031217
- % Identity 70.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1415: from 1 to 70
- Alignment No. 12208
- gi No. 5051933
- % Identity 81.6
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1415: from 1 to 85
- Alignment No. 12209
- gi No. 5051935
- % Identity 75
- Alignment Length 60
- Location of Alignment in SEQ ID NO 1415: from 12 to 70
- Alignment No. 12210
- gi No. 5070138
- % Identity 70.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1415: from 1 to 70
- Alignment No. 12211
- gi No. 5295990
- % Identity 90.7
- Alignment Length 86
- Location of Alignment in SEQ ID NO 1415: from 1 to 85
- Alignment No. 12212

- gi No. 542034
- % Identity 76.6
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1415: from 1 to 77

- Alignment No. 12213
- gi No. 542192
- % Identity 75
- Alignment Length 60
- Location of Alignment in SEQ ID NO 1415: from 11 to 70

- Alignment No. 12214
- gi No. 5566279
- % Identity 82.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1415: from 12 to 51

- Alignment No. 12215
- gi No. 5712746
- % Identity 78
- Alignment Length 50
- Location of Alignment in SEQ ID NO 1415: from 7 to 56

- Alignment No. 12216
- gi No. 5712748
- % Identity 78
- Alignment Length 50
- Location of Alignment in SEQ ID NO 1415: from 7 to 56

- Alignment No. 12217
- gi No. 695686
- % Identity 75.4
- Alignment Length 69
- Location of Alignment in SEQ ID NO 1415: from 1 to 69

- Alignment No. 12218
- gi No. 695688
- % Identity 71.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1415: from 1 to 76

- Alignment No. 12219
- gi No. 695690
- % Identity 73
- Alignment Length 89
- Location of Alignment in SEQ ID NO 1415: from 1 to 85

- Alignment No. 12220
- gi No. 793906
- % Identity 73.3
- Alignment Length 60
- Location of Alignment in SEQ ID NO 1415: from 1 to 59

- Alignment No. 12221
- gi No. 81611
- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 1415: from 3 to 57

- Alignment No. 12222
- gi No. 862644

- % Identity 74.3
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1415: from 7 to 79

- Alignment No. 12223
- gi No. 939779
- % Identity 71.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1415: from 1 to 70

- Alignment No. 12224
- gi No. 939783
- % Identity 75.9
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1415: from 1 to 57

- Alignment No. 12225
- gi No. 951172
- % Identity 71.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1415: from 1 to 70

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1416
- Ceres seq_id 1500201
- Location of start within SEQ ID NO 1413: at 266 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12226
- SRF-type transcription factor (DNA-binding and dimerisation domain)
- Location within SEQ ID NO 1416: from 1 to 52 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12227
- gi No. 1001935
- % Identity 74.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1416: from 1 to 63

- Alignment No. 12228
- gi No. 1049022
- % Identity 74.1
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1416: from 1 to 78

- Alignment No. 12229
- gi No. 1076646
- % Identity 73.9
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1416: from 1 to 78

- Alignment No. 12230
- gi No. 1076827
- % Identity 72.9
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1416: from 1 to 51

- Alignment No. 12231
- gi No. 1206003

- % Identity 71.8
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1416: from 1 to 63

- Alignment No. 12232
- gi No. 1208800
- % Identity 76
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1416: from 10 to 34

- Alignment No. 12233
- gi No. 1208802
- % Identity 84
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1416: from 10 to 34

- Alignment No. 12234
- gi No. 1208804
- % Identity 82.6
- Alignment Length 23
- Location of Alignment in SEQ ID NO 1416: from 12 to 34

- Alignment No. 12235
- gi No. 1239961
- % Identity 71.8
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1416: from 1 to 63

- Alignment No. 12236
- gi No. 1345965
- % Identity 70.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1416: from 1 to 63

- Alignment No. 12237
- gi No. 1362195
- % Identity 75.4
- Alignment Length 57
- Location of Alignment in SEQ ID NO 1416: from 1 to 52

- Alignment No. 12238
- gi No. 1362196
- % Identity 78.9
- Alignment Length 57
- Location of Alignment in SEQ ID NO 1416: from 1 to 52

- Alignment No. 12239
- gi No. 1362197
- % Identity 75.4
- Alignment Length 57
- Location of Alignment in SEQ ID NO 1416: from 1 to 52

- Alignment No. 12240
- gi No. 1362198
- % Identity 77.2
- Alignment Length 57
- Location of Alignment in SEQ ID NO 1416: from 1 to 52

- Alignment No. 12241
- gi No. 1362199
- % Identity 76.3

- Alignment Length 59
- Location of Alignment in SEQ ID NO 1416: from 1 to 52

- Alignment No. 12242
- gi No. 1362200
- % Identity 78
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1416: from 1 to 52

- Alignment No. 12243
- gi No. 1362201
- % Identity 84.4
- Alignment Length 45
- Location of Alignment in SEQ ID NO 1416: from 8 to 52

- Alignment No. 12244
- gi No. 1362202
- % Identity 77.3
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1416: from 9 to 52

- Alignment No. 12245
- gi No. 1362203
- % Identity 71.2
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1416: from 1 to 52

- Alignment No. 12246
- gi No. 1362204
- % Identity 81.8
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1416: from 9 to 52

- Alignment No. 12247
- gi No. 1362205
- % Identity 82.2
- Alignment Length 45
- Location of Alignment in SEQ ID NO 1416: from 9 to 53

- Alignment No. 12248
- gi No. 1362206
- % Identity 77.3
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1416: from 9 to 52

- Alignment No. 12249
- gi No. 1362209
- % Identity 73.3
- Alignment Length 60
- Location of Alignment in SEQ ID NO 1416: from 1 to 52

- Alignment No. 12250
- gi No. 2160701
- % Identity 75.4
- Alignment Length 69
- Location of Alignment in SEQ ID NO 1416: from 1 to 62

- Alignment No. 12251
- gi No. 2286109
- % Identity 71.4
- Alignment Length 70

- Location of Alignment in SEQ ID NO 1416: from 1 to 63
- Alignment No. 12252
- gi No. 2459835
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1416: from 1 to 49
- Alignment No. 12253
- gi No. 2463333
- % Identity 70.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1416: from 1 to 63
- Alignment No. 12254
- gi No. 2979566
- % Identity 75.3
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1416: from 1 to 78
- Alignment No. 12255
- gi No. 3023536
- % Identity 71.8
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1416: from 1 to 63
- Alignment No. 12256
- gi No. 3114588
- % Identity 71.8
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1416: from 1 to 63
- Alignment No. 12257
- gi No. 320596
- % Identity 70.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1416: from 1 to 63
- Alignment No. 12258
- gi No. 322801
- % Identity 70.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1416: from 1 to 72
- Alignment No. 12259
- gi No. 3292820
- % Identity 71.8
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1416: from 1 to 78
- Alignment No. 12260
- gi No. 3493647
- % Identity 80.2
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1416: from 1 to 74
- Alignment No. 12261
- gi No. 3646322
- % Identity 75
- Alignment Length 68
- Location of Alignment in SEQ ID NO 1416: from 1 to 63

- Alignment No. 12262
- gi No. 3646340
- % Identity 71.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1416: from 1 to 63
- Alignment No. 12263
- gi No. 3688591
- % Identity 71.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1416: from 1 to 63
- Alignment No. 12264
- gi No. 3851331
- % Identity 71.9
- Alignment Length 57
- Location of Alignment in SEQ ID NO 1416: from 9 to 64
- Alignment No. 12265
- gi No. 3851333
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 1416: from 9 to 62
- Alignment No. 12266
- gi No. 4033710
- % Identity 71.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1416: from 1 to 69
- Alignment No. 12267
- gi No. 4033721
- % Identity 71.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1416: from 1 to 69
- Alignment No. 12268
- gi No. 4033725
- % Identity 70.8
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1416: from 1 to 69
- Alignment No. 12269
- gi No. 4101710
- % Identity 71.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1416: from 1 to 69
- Alignment No. 12270
- gi No. 4103486
- % Identity 71.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1416: from 1 to 69
- Alignment No. 12271
- gi No. 4322475
- % Identity 77.1
- Alignment Length 83
- Location of Alignment in SEQ ID NO 1416: from 1 to 76

- Alignment No. 12272
- gi No. 497145
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1416: from 3 to 28
- Alignment No. 12273
- gi No. 497147
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1416: from 3 to 28
- Alignment No. 12274
- gi No. 497149
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1416: from 3 to 28
- Alignment No. 12275
- gi No. 5002523
- % Identity 76.3
- Alignment Length 80
- Location of Alignment in SEQ ID NO 1416: from 1 to 72
- Alignment No. 12276
- gi No. 5019431
- % Identity 72.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1416: from 1 to 69
- Alignment No. 12277
- gi No. 5031217
- % Identity 70.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1416: from 1 to 63
- Alignment No. 12278
- gi No. 5051933
- % Identity 81.6
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1416: from 1 to 78
- Alignment No. 12279
- gi No. 5051935
- % Identity 75
- Alignment Length 60
- Location of Alignment in SEQ ID NO 1416: from 5 to 63
- Alignment No. 12280
- gi No. 5070138
- % Identity 70.4
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1416: from 1 to 63
- Alignment No. 12281
- gi No. 5295990
- % Identity 90.7
- Alignment Length 86
- Location of Alignment in SEQ ID NO 1416: from 1 to 78
- Alignment No. 12282

- gi No. 542034
- % Identity 76.6
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1416: from 1 to 70

- Alignment No. 12283
- gi No. 542192
- % Identity 75
- Alignment Length 60
- Location of Alignment in SEQ ID NO 1416: from 4 to 63

- Alignment No. 12284
- gi No. 5566279
- % Identity 82.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1416: from 5 to 44

- Alignment No. 12285
- gi No. 5712746
- % Identity 78
- Alignment Length 50
- Location of Alignment in SEQ ID NO 1416: from 1 to 49

- Alignment No. 12286
- gi No. 5712748
- % Identity 78
- Alignment Length 50
- Location of Alignment in SEQ ID NO 1416: from 1 to 49

- Alignment No. 12287
- gi No. 695686
- % Identity 75.4
- Alignment Length 69
- Location of Alignment in SEQ ID NO 1416: from 1 to 62

- Alignment No. 12288
- gi No. 695688
- % Identity 71.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1416: from 1 to 69

- Alignment No. 12289
- gi No. 695690
- % Identity 73
- Alignment Length 89
- Location of Alignment in SEQ ID NO 1416: from 1 to 78

- Alignment No. 12290
- gi No. 793906
- % Identity 73.3
- Alignment Length 60
- Location of Alignment in SEQ ID NO 1416: from 1 to 52

- Alignment No. 12291
- gi No. 81611
- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 1416: from 1 to 50

- Alignment No. 12292
- gi No. 862644

- % Identity 74.3
- Alignment Length 74
- Location of Alignment in SEQ ID NO 1416: from 1 to 72
- Alignment No. 12293
- gi No. 939779
- % Identity 71.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1416: from 1 to 63
- Alignment No. 12294
- gi No. 939783
- % Identity 75.9
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1416: from 1 to 50
- Alignment No. 12295
- gi No. 951172
- % Identity 71.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1416: from 1 to 63

Maximum Length Sequence corresponding to clone ID 257713

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1417
- Ceres seq_id 1500202

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1418
- Ceres seq_id 1500203
- Location of start within SEQ ID NO 1417: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1419
- Ceres seq_id 1500204
- Location of start within SEQ ID NO 1417: at 469 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12296
- gi No. 4680201
- % Identity 90.9
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1419: from 20 to 63
- Alignment No. 12297
- gi No. 4680489
- % Identity 73
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1419: from 1 to 63

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1420
- Ceres seq_id 1500205
- Location of start within SEQ ID NO 1417: at 499 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12298
- gi No. 4680201
- % Identity 90.9
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1420: from 10 to 53

- Alignment No. 12299
- gi No. 4680489
- % Identity 73
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1420: from 1 to 53

Maximum Length Sequence corresponding to clone ID 257780

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1421
- Ceres seq_id 1500212

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1422
- Ceres seq_id 1500213
- Location of start within SEQ ID NO 1421: at 351 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12300
- Ribosomal protein S17
- Location within SEQ ID NO 1422: from 1 to 57 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12301
- gi No. 1173221
- % Identity 85
- Alignment Length 133
- Location of Alignment in SEQ ID NO 1422: from 1 to 57

- Alignment No. 12302
- gi No. 1173223
- % Identity 88
- Alignment Length 133
- Location of Alignment in SEQ ID NO 1422: from 1 to 57

- Alignment No. 12303
- gi No. 133866
- % Identity 86.5
- Alignment Length 133
- Location of Alignment in SEQ ID NO 1422: from 1 to 57

- Alignment No. 12304
- gi No. 133867
- % Identity 92.5
- Alignment Length 133
- Location of Alignment in SEQ ID NO 1422: from 1 to 57

- Alignment No. 12305
- gi No. 166867
- % Identity 86.5
- Alignment Length 133
- Location of Alignment in SEQ ID NO 1422: from 1 to 57

- Alignment No. 12306
- gi No. 5708091
- % Identity 85.7
- Alignment Length 133
- Location of Alignment in SEQ ID NO 1422: from 1 to 57
- Alignment No. 12307
- gi No. 81811
- % Identity 88.2
- Alignment Length 119
- Location of Alignment in SEQ ID NO 1422: from 1 to 57

Maximum Length Sequence corresponding to clone ID 257928

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1423
- Ceres seq_id 1500234

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1424
- Ceres seq_id 1500235
- Location of start within SEQ ID NO 1423: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1425
- Ceres seq_id 1500236
- Location of start within SEQ ID NO 1423: at 62 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1426
- Ceres seq_id 1500237
- Location of start within SEQ ID NO 1423: at 201 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12308
- gi No. 2258365
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 1426: from 46 to 92
- Alignment No. 12309
- gi No. 3342734
- % Identity 71.4
- Alignment Length 49
- Location of Alignment in SEQ ID NO 1426: from 44 to 92
- Alignment No. 12310
- gi No. 3860916
- % Identity 70.5
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1426: from 49 to 92

Maximum Length Sequence corresponding to clone ID 257979

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1427
- Ceres seq_id 1500246

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1428
- Ceres seq_id 1500247
- Location of start within SEQ ID NO 1427: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12311
- recA bacterial DNA recombination proteins
- Location within SEQ ID NO 1428: from 104 to 154 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12312
- gi No. 1172887
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1428: from 137 to 154
- Alignment No. 12313
- gi No. 403968
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1428: from 136 to 153
- Alignment No. 12314
- gi No. 464598
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1428: from 135 to 154
- Alignment No. 12315
- gi No. 543677
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1428: from 135 to 154

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1429
- Ceres seq_id 1500248
- Location of start within SEQ ID NO 1427: at 60 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12316
- recA bacterial DNA recombination proteins
- Location within SEQ ID NO 1429: from 85 to 135 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12317
- gi No. 1172887
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1429: from 118 to 135
- Alignment No. 12318
- gi No. 403968
- % Identity 77.8
- Alignment Length 18

- Location of Alignment in SEQ ID NO 1429: from 117 to 134
- Alignment No. 12319
- gi No. 464598
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1429: from 116 to 135
- Alignment No. 12320
- gi No. 543677
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1429: from 116 to 135

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1430
- Ceres seq_id 1500249
- Location of start within SEQ ID NO 1427: at 249 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12321
- recA bacterial DNA recombination proteins
- Location within SEQ ID NO 1430: from 22 to 72 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12322
- gi No. 1172887
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1430: from 55 to 72
- Alignment No. 12323
- gi No. 403968
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1430: from 54 to 71
- Alignment No. 12324
- gi No. 464598
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1430: from 53 to 72
- Alignment No. 12325
- gi No. 543677
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1430: from 53 to 72

Maximum Length Sequence corresponding to clone ID 257985

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1431
- Ceres seq_id 1500250

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1432
- Ceres seq_id 1500251
- Location of start within SEQ ID NO 1431: at 160 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12326
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 1432: from 64 to 135 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12327
- gi No. 140346
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1432: from 45 to 57

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1433
- Ceres seq_id 1500252
- Location of start within SEQ ID NO 1431: at 272 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 258340

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1434
- Ceres seq_id 1500263

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1435
- Ceres seq_id 1500264
- Location of start within SEQ ID NO 1434: at 209 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12328
- Syntaxin
- Location within SEQ ID NO 1435: from 5 to 306 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1436
- Ceres seq_id 1500265
- Location of start within SEQ ID NO 1434: at 305 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12329
- Syntaxin
- Location within SEQ ID NO 1436: from 1 to 274 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1437
- Ceres seq_id 1500266
- Location of start within SEQ ID NO 1434: at 401 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12330
- Syntaxin
- Location within SEQ ID NO 1437: from 1 to 242 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 258706

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1438
- Ceres seq_id 1500283

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1439
- Ceres seq_id 1500284
- Location of start within SEQ ID NO 1438: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1440
- Ceres seq_id 1500285
- Location of start within SEQ ID NO 1438: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12331
- gi No. 5042457
- % Identity 95.5
- Alignment Length 66
- Location of Alignment in SEQ ID NO 1440: from 42 to 107

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1441
- Ceres seq_id 1500286
- Location of start within SEQ ID NO 1438: at 125 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12332
- gi No. 5042457
- % Identity 95.5
- Alignment Length 66
- Location of Alignment in SEQ ID NO 1441: from 1 to 66

Maximum Length Sequence corresponding to clone ID 259439

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1442
- Ceres seq_id 1500298

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1443
- Ceres seq_id 1500299
- Location of start within SEQ ID NO 1442: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12333
- Zinc finger C-x8-C-x5-C-x3-H type (and similar).
- Location within SEQ ID NO 1443: from 30 to 55 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1444
- Ceres seq_id 1500300
- Location of start within SEQ ID NO 1442: at 7 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12334
- Zinc finger C-x8-C-x5-C-x3-H type (and similar).
- Location within SEQ ID NO 1444: from 28 to 53 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1445
- Ceres seq_id 1500301
- Location of start within SEQ ID NO 1442: at 106 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 259532

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1446
- Ceres seq_id 1500305

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1447
- Ceres seq_id 1500306
- Location of start within SEQ ID NO 1446: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12335
- DEAD/DEAH box helicase
- Location within SEQ ID NO 1447: from 95 to 166 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12336
- gi No. 1749748
- % Identity 80
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1447: from 127 to 166
- Alignment No. 12337
- gi No. 2500530
- % Identity 73
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1447: from 41 to 166
- Alignment No. 12338
- gi No. 2500531
- % Identity 74
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1447: from 41 to 166
- Alignment No. 12339
- gi No. 3132829
- % Identity 73.8
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1447: from 41 to 166

- Alignment No. 12340
- gi No. 3776005
- % Identity 72.9
- Alignment Length 156
- Location of Alignment in SEQ ID NO 1447: from 15 to 166

- Alignment No. 12341
- gi No. 3805815
- % Identity 73.2
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1447: from 41 to 166

- Alignment No. 12342
- gi No. 4235116
- % Identity 74
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1447: from 41 to 166

- Alignment No. 12343
- gi No. 4758112
- % Identity 73.2
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1447: from 41 to 166

- Alignment No. 12344
- gi No. 5031659
- % Identity 70.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1447: from 41 to 166

- Alignment No. 12345
- gi No. 539961
- % Identity 74
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1447: from 41 to 166

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1448
- Ceres seq_id 1500307
- Location of start within SEQ ID NO 1446: at 103 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12346
- DEAD/DEAH box helicase
- Location within SEQ ID NO 1448: from 61 to 132 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12347
- gi No. 1749748
- % Identity 80
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1448: from 93 to 132

- Alignment No. 12348
- gi No. 2500530
- % Identity 73
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1448: from 7 to 132

- Alignment No. 12349

- gi No. 2500531
- % Identity 74
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1448: from 7 to 132

- Alignment No. 12350
- gi No. 3132829
- % Identity 73.8
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1448: from 7 to 132

- Alignment No. 12351
- gi No. 3776005
- % Identity 72.9
- Alignment Length 156
- Location of Alignment in SEQ ID NO 1448: from 1 to 132

- Alignment No. 12352
- gi No. 3805815
- % Identity 73.2
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1448: from 7 to 132

- Alignment No. 12353
- gi No. 4235116
- % Identity 74
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1448: from 7 to 132

- Alignment No. 12354
- gi No. 4758112
- % Identity 73.2
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1448: from 7 to 132

- Alignment No. 12355
- gi No. 5031659
- % Identity 70.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1448: from 7 to 132

- Alignment No. 12356
- gi No. 539961
- % Identity 74
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1448: from 7 to 132

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1449
- Ceres seq_id 1500308
- Location of start within SEQ ID NO 1446: at 106 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12357
- DEAD/DEAH box helicase
- Location within SEQ ID NO 1449: from 60 to 131 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12358
- gi No. 1749748

- % Identity 80
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1449: from 92 to 131
- Alignment No. 12359
- gi No. 2500530
- % Identity 73
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1449: from 6 to 131
- Alignment No. 12360
- gi No. 2500531
- % Identity 74
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1449: from 6 to 131
- Alignment No. 12361
- gi No. 3132829
- % Identity 73.8
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1449: from 6 to 131
- Alignment No. 12362
- gi No. 3776005
- % Identity 72.9
- Alignment Length 156
- Location of Alignment in SEQ ID NO 1449: from 1 to 131
- Alignment No. 12363
- gi No. 3805815
- % Identity 73.2
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1449: from 6 to 131
- Alignment No. 12364
- gi No. 4235116
- % Identity 74
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1449: from 6 to 131
- Alignment No. 12365
- gi No. 4758112
- % Identity 73.2
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1449: from 6 to 131
- Alignment No. 12366
- gi No. 5031659
- % Identity 70.6
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1449: from 6 to 131
- Alignment No. 12367
- gi No. 539961
- % Identity 74
- Alignment Length 129
- Location of Alignment in SEQ ID NO 1449: from 6 to 131

Maximum Length Sequence corresponding to clone ID 259555

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1450

- Ceres seq_id 1500313
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1451
 - Ceres seq_id 1500314
 - Location of start within SEQ ID NO 1450: at 481 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 12368
 - gi No. 1708463
 - % Identity 77.8
 - Alignment Length 262
 - Location of Alignment in SEQ ID NO 1451: from 1 to 203

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1452
 - Ceres seq_id 1500315
 - Location of start within SEQ ID NO 1450: at 514 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 12369
 - gi No. 1708463
 - % Identity 77.8
 - Alignment Length 262
 - Location of Alignment in SEQ ID NO 1452: from 1 to 192

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1453
 - Ceres seq_id 1500316
 - Location of start within SEQ ID NO 1450: at 622 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 12370
 - gi No. 1708463
 - % Identity 77.8
 - Alignment Length 262
 - Location of Alignment in SEQ ID NO 1453: from 1 to 156

Maximum Length Sequence corresponding to clone ID 259571

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1454
 - Ceres seq_id 1500321

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1455
 - Ceres seq_id 1500322
 - Location of start within SEQ ID NO 1454: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1456
 - Ceres seq_id 1500323
 - Location of start within SEQ ID NO 1454: at 158 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12371
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1456: from 38 to 90 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1457
- Ceres seq_id 1500324
- Location of start within SEQ ID NO 1454: at 245 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12372
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1457: from 9 to 61 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 260361

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1458
- Ceres seq_id 1500367

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1459
- Ceres seq_id 1500368
- Location of start within SEQ ID NO 1458: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12373
- Nuclear transition protein 2
- Location within SEQ ID NO 1459: from 17 to 102 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12374
- gi No. 553165
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1459: from 74 to 86

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1460
- Ceres seq_id 1500369
- Location of start within SEQ ID NO 1458: at 44 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12375
- gi No. 347455
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1460: from 27 to 37

Maximum Length Sequence corresponding to clone ID 260368

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1461
- Ceres seq_id 1500370

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1462
- Ceres seq_id 1500371
- Location of start within SEQ ID NO 1461: at 96 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12376
- Zinc finger, C2H2 type
- Location within SEQ ID NO 1462: from 25 to 47 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12377
- gi No. 1361986
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1462: from 15 to 51

- Alignment No. 12378
- gi No. 1362015
- % Identity 76.7
- Alignment Length 30
- Location of Alignment in SEQ ID NO 1462: from 22 to 51

- Alignment No. 12379
- gi No. 1362017
- % Identity 81.5
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1462: from 25 to 51

- Alignment No. 12380
- gi No. 1362018
- % Identity 72
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1462: from 27 to 51

- Alignment No. 12381
- gi No. 1362020
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1462: from 25 to 51

- Alignment No. 12382
- gi No. 1871188
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1462: from 25 to 51

- Alignment No. 12383
- gi No. 790687
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1462: from 25 to 51

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1463
- Ceres seq_id 1500372
- Location of start within SEQ ID NO 1461: at 347 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1464
- Ceres seq_id 1500373
- Location of start within SEQ ID NO 1461: at 460 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 260388

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1465
- Ceres seq_id 1500374

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1466
- Ceres seq_id 1500375
- Location of start within SEQ ID NO 1465: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1467
- Ceres seq_id 1500376
- Location of start within SEQ ID NO 1465: at 100 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12384
- Ubiquitin family
- Location within SEQ ID NO 1467: from 1 to 38 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12385
- gi No. 100525
- % Identity 71
- Alignment Length 31
- Location of Alignment in SEQ ID NO 1467: from 1 to 31

- Alignment No. 12386
- gi No. 1050930
- % Identity 79.2
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1467: from 1 to 24

- Alignment No. 12387
- gi No. 208891
- % Identity 73.9
- Alignment Length 23
- Location of Alignment in SEQ ID NO 1467: from 1 to 23

- Alignment No. 12388
- gi No. 456779
- % Identity 79.2
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1467: from 1 to 24

- Alignment No. 12389

- gi No. 899115
- % Identity 75
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1467: from 1 to 24

- Alignment No. 12390
- gi No. 91870
- % Identity 73.9
- Alignment Length 23
- Location of Alignment in SEQ ID NO 1467: from 1 to 23

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1468
- Ceres seq_id 1500377
- Location of start within SEQ ID NO 1465: at 282 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 260615

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1469
- Ceres seq_id 1500387

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1470
- Ceres seq_id 1500388
- Location of start within SEQ ID NO 1469: at 144 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12391
- Mitochondrial carrier proteins
- Location within SEQ ID NO 1470: from 23 to 223 aa.

- Alignment No. 12392
- Mitochondrial carrier proteins
- Location within SEQ ID NO 1470: from 37 to 322 aa.

- Alignment No. 12393
- Mitochondrial carrier proteins
- Location within SEQ ID NO 1470: from 146 to 327 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1471
- Ceres seq_id 1500389
- Location of start within SEQ ID NO 1469: at 150 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12394
- Mitochondrial carrier proteins
- Location within SEQ ID NO 1471: from 21 to 221 aa.

- Alignment No. 12395
- Mitochondrial carrier proteins
- Location within SEQ ID NO 1471: from 35 to 320 aa.

- Alignment No. 12396

- Mitochondrial carrier proteins
- Location within SEQ ID NO 1471: from 144 to 325 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1472
- Ceres seq_id 1500390
- Location of start within SEQ ID NO 1469: at 342 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12397
- Mitochondrial carrier proteins
- Location within SEQ ID NO 1472: from 1 to 157 aa.

- Alignment No. 12398
- Mitochondrial carrier proteins
- Location within SEQ ID NO 1472: from 1 to 256 aa.

- Alignment No. 12399
- Mitochondrial carrier proteins
- Location within SEQ ID NO 1472: from 80 to 261 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 260891

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1473
- Ceres seq_id 1500391

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1474
- Ceres seq_id 1500392
- Location of start within SEQ ID NO 1473: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12400
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1474: from 5 to 108 aa.

- Alignment No. 12401
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1474: from 10 to 108 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1475
- Ceres seq_id 1500393
- Location of start within SEQ ID NO 1473: at 27 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12402
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1475: from 1 to 100 aa.

- Alignment No. 12403
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1475: from 2 to 100 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1476
- Ceres seq_id 1500394
- Location of start within SEQ ID NO 1473: at 120 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12404
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1476: from 1 to 69 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 260925

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1477
- Ceres seq_id 1500395

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1478
- Ceres seq_id 1500396
- Location of start within SEQ ID NO 1477: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1479
- Ceres seq_id 1500397
- Location of start within SEQ ID NO 1477: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12405
- Sperm histone P2
- Location within SEQ ID NO 1479: from 15 to 73 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1480
- Ceres seq_id 1500398
- Location of start within SEQ ID NO 1477: at 68 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 261148

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1481
- Ceres seq_id 1500407

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1482
- Ceres seq_id 1500408
- Location of start within SEQ ID NO 1481: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1483
- Ceres seq_id 1500409
- Location of start within SEQ ID NO 1481: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 12406
- GTP cyclohydrolase I
- Location within SEQ ID NO 1483: from 80 to 131 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1484
- Ceres seq_id 1500410
- Location of start within SEQ ID NO 1481: at 128 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 12407
- GTP cyclohydrolase I
- Location within SEQ ID NO 1484: from 38 to 89 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 261372

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1485
- Ceres seq_id 1500422

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1486
- Ceres seq_id 1500423
- Location of start within SEQ ID NO 1485: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 12408
- Ribosomal protein L21e
- Location within SEQ ID NO 1486: from 28 to 108 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12409
- gi No. 2851508
- % Identity 87.8
- Alignment Length 82
- Location of Alignment in SEQ ID NO 1486: from 27 to 108
- Alignment No. 12410
- gi No. 3885884
- % Identity 92.7
- Alignment Length 82
- Location of Alignment in SEQ ID NO 1486: from 27 to 108

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1487
- Ceres seq_id 1500424

- Location of start within SEQ ID NO 1485: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1488
- Ceres seq_id 1500425
- Location of start within SEQ ID NO 1485: at 80 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12411
- Ribosomal protein L21e
- Location within SEQ ID NO 1488: from 2 to 82 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12412
- gi No. 2851508
- % Identity 87.8
- Alignment Length 82
- Location of Alignment in SEQ ID NO 1488: from 1 to 82
- Alignment No. 12413
- gi No. 3885884
- % Identity 92.7
- Alignment Length 82
- Location of Alignment in SEQ ID NO 1488: from 1 to 82

Maximum Length Sequence corresponding to clone ID 261674

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1489
- Ceres seq_id 1500464

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1490
- Ceres seq_id 1500465
- Location of start within SEQ ID NO 1489: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12414
- gi No. 2145062
- % Identity 90.9
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1490: from 82 to 92

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1491
- Ceres seq_id 1500466
- Location of start within SEQ ID NO 1489: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12415
- Collagen triple helix repeat (20 copies)
- Location within SEQ ID NO 1491: from 11 to 59 aa.

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1492
 - Ceres seq_id 1500467
 - Location of start within SEQ ID NO 1489: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 12416
 - gi No. 3875441
 - % Identity 70.6
 - Alignment Length 17
 - Location of Alignment in SEQ ID NO 1492: from 81 to 97

Maximum Length Sequence corresponding to clone ID 261748

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1493
 - Ceres seq_id 1500468

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1494
 - Ceres seq_id 1500469
 - Location of start within SEQ ID NO 1493: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12417
- Sm protein
- Location within SEQ ID NO 1494: from 94 to 155 aa.

- (D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1495
 - Ceres seq_id 1500470
 - Location of start within SEQ ID NO 1493: at 179 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12418
- Sm protein
- Location within SEQ ID NO 1495: from 35 to 96 aa.

- (D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 261790

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1496
 - Ceres seq_id 1500474

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1497
 - Ceres seq_id 1500475
 - Location of start within SEQ ID NO 1496: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1498
 - Ceres seq_id 1500476
 - Location of start within SEQ ID NO 1496: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12419
- Cytochrome P450
- Location within SEQ ID NO 1498: from 59 to 127 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1499
- Ceres seq_id 1500477
- Location of start within SEQ ID NO 1496: at 72 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12420
- Cytochrome P450
- Location within SEQ ID NO 1499: from 36 to 104 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 261801

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1500
- Ceres seq_id 1500478

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1501
- Ceres seq_id 1500479
- Location of start within SEQ ID NO 1500: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12421
- Collagen triple helix repeat (20 copies)
- Location within SEQ ID NO 1501: from 49 to 108 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1502
- Ceres seq_id 1500480
- Location of start within SEQ ID NO 1500: at 161 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 261825

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1503
- Ceres seq_id 1500481

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1504
- Ceres seq_id 1500482
- Location of start within SEQ ID NO 1503: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12422
- Metallo-beta-lactamase superfamily

- Location within SEQ ID NO 1504: from 56 to 160 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1505
- Ceres seq_id 1500483
- Location of start within SEQ ID NO 1503: at 68 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12423
- Metallo-beta-lactamase superfamily
- Location within SEQ ID NO 1505: from 34 to 138 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 261831

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1506
- Ceres seq_id 1500487

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1507
- Ceres seq_id 1500488
- Location of start within SEQ ID NO 1506: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1508
- Ceres seq_id 1500489
- Location of start within SEQ ID NO 1506: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12424
- gi No. 132933
- % Identity 77.8
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1508: from 26 to 52

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1509
- Ceres seq_id 1500490
- Location of start within SEQ ID NO 1506: at 221 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 261853

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1510
- Ceres seq_id 1500491

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1511
- Ceres seq_id 1500492
- Location of start within SEQ ID NO 1510: at 201 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12425
- gi No. 3834316
- % Identity 96.9
- Alignment Length 224
- Location of Alignment in SEQ ID NO 1511: from 1 to 173

Maximum Length Sequence corresponding to clone ID 261966

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1512
- Ceres seq_id 1500495

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1513
- Ceres seq_id 1500496
- Location of start within SEQ ID NO 1512: at 78 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12426
- gi No. 131176
- % Identity 71.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1513: from 1 to 135

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1514
- Ceres seq_id 1500497
- Location of start within SEQ ID NO 1512: at 93 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12427
- gi No. 131176
- % Identity 71.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1514: from 1 to 130

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1515
- Ceres seq_id 1500498
- Location of start within SEQ ID NO 1512: at 117 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12428
- gi No. 131176
- % Identity 71.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 1515: from 1 to 122

Maximum Length Sequence corresponding to clone ID 261978

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1516
- Ceres seq_id 1500501

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1517
- Ceres seq_id 1500502
- Location of start within SEQ ID NO 1516: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12429
- gi No. 1321924
- % Identity 73.9
- Alignment Length 23
- Location of Alignment in SEQ ID NO 1517: from 100 to 122

- Alignment No. 12430
- gi No. 1944132
- % Identity 81.8
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1517: from 101 to 122

- Alignment No. 12431
- gi No. 2894607
- % Identity 72
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1517: from 101 to 125

- Alignment No. 12432
- gi No. 4218537
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1517: from 96 to 122

- Alignment No. 12433
- gi No. 5091624
- % Identity 80
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1517: from 103 to 122

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1518
- Ceres seq_id 1500503
- Location of start within SEQ ID NO 1516: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 261997

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1519
- Ceres seq_id 1500504

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1520
- Ceres seq_id 1500505
- Location of start within SEQ ID NO 1519: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12434
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1520: from 64 to 161 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12435
- gi No. 1168470
- % Identity 72.4
- Alignment Length 134
- Location of Alignment in SEQ ID NO 1520: from 28 to 161

- Alignment No. 12436
- gi No. 1168471
- % Identity 83.3
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1520: from 138 to 161

- Alignment No. 12437
- gi No. 4432889
- % Identity 83.3
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1520: from 138 to 161

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1521
- Ceres seq_id 1500506
- Location of start within SEQ ID NO 1519: at 44 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12438
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1521: from 50 to 147 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12439
- gi No. 1168470
- % Identity 72.4
- Alignment Length 134
- Location of Alignment in SEQ ID NO 1521: from 14 to 147

- Alignment No. 12440
- gi No. 1168471
- % Identity 83.3
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1521: from 124 to 147

- Alignment No. 12441
- gi No. 4432889
- % Identity 83.3
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1521: from 124 to 147

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1522
- Ceres seq_id 1500507
- Location of start within SEQ ID NO 1519: at 173 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12442
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1522: from 7 to 104 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12443
- gi No. 1168470
- % Identity 72.4
- Alignment Length 134
- Location of Alignment in SEQ ID NO 1522: from 1 to 104

- Alignment No. 12444
- gi No. 1168471
- % Identity 83.3
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1522: from 81 to 104

- Alignment No. 12445
- gi No. 4432889
- % Identity 83.3
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1522: from 81 to 104

Maximum Length Sequence corresponding to clone ID 262057

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1523
- Ceres seq_id 1500516

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1524
- Ceres seq_id 1500517
- Location of start within SEQ ID NO 1523: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1525
- Ceres seq_id 1500518
- Location of start within SEQ ID NO 1523: at 303 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12446
- gi No. 4966357
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1525: from 32 to 52

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1526
- Ceres seq_id 1500519
- Location of start within SEQ ID NO 1523: at 346 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 262215

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1527
- Ceres seq_id 1500539

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1528
- Ceres seq_id 1500540

- Location of start within SEQ ID NO 1527: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 12447
 - gi No. 2342684
 - % Identity 75
 - Alignment Length 16
 - Location of Alignment in SEQ ID NO 1528: from 1 to 16
-
- Alignment No. 12448
 - gi No. 3540195
 - % Identity 75
 - Alignment Length 28
 - Location of Alignment in SEQ ID NO 1528: from 3 to 30

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1529
- Ceres seq_id 1500541
- Location of start within SEQ ID NO 1527: at 99 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1530
- Ceres seq_id 1500542
- Location of start within SEQ ID NO 1527: at 114 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 262351

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1531
- Ceres seq_id 1500554

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1532
- Ceres seq_id 1500555
- Location of start within SEQ ID NO 1531: at 189 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12449
 - gi No. 4468993
 - % Identity 99.7
 - Alignment Length 363
 - Location of Alignment in SEQ ID NO 1532: from 1 to 363
-
- Alignment No. 12450
 - gi No. 4539337
 - % Identity 92.2
 - Alignment Length 51
 - Location of Alignment in SEQ ID NO 1532: from 313 to 363
-
- Alignment No. 12451
 - gi No. 4539340

- % Identity 98.1
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1532: from 1 to 363

- Alignment No. 12452
- gi No. 4895222
- % Identity 98.6
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1532: from 293 to 363

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1533
- Ceres seq_id 1500556
- Location of start within SEQ ID NO 1531: at 246 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12453
- gi No. 4468993
- % Identity 99.7
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1533: from 1 to 344

- Alignment No. 12454
- gi No. 4539337
- % Identity 92.2
- Alignment Length 51
- Location of Alignment in SEQ ID NO 1533: from 294 to 344

- Alignment No. 12455
- gi No. 4539340
- % Identity 98.1
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1533: from 1 to 344

- Alignment No. 12456
- gi No. 4895222
- % Identity 98.6
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1533: from 274 to 344

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1534
- Ceres seq_id 1500557
- Location of start within SEQ ID NO 1531: at 585 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12457
- gi No. 4468993
- % Identity 99.7
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1534: from 1 to 231

- Alignment No. 12458
- gi No. 4539337
- % Identity 92.2
- Alignment Length 51
- Location of Alignment in SEQ ID NO 1534: from 181 to 231

- Alignment No. 12459
- gi No. 4539340
- % Identity 98.1
- Alignment Length 363
- Location of Alignment in SEQ ID NO 1534: from 1 to 231

- Alignment No. 12460
- gi No. 4895222
- % Identity 98.6
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1534: from 161 to 231

Maximum Length Sequence corresponding to clone ID 262550

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1535
- Ceres seq_id 1500558

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1536
- Ceres seq_id 1500559
- Location of start within SEQ ID NO 1535: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12461
- gi No. 4982480
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1536: from 123 to 178

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1537
- Ceres seq_id 1500560
- Location of start within SEQ ID NO 1535: at 14 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12462
- gi No. 4982480
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1537: from 119 to 174

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1538
- Ceres seq_id 1500561
- Location of start within SEQ ID NO 1535: at 104 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12463
- gi No. 4982480
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1538: from 89 to 144

Maximum Length Sequence corresponding to clone ID 262802

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1539
- Ceres seq_id 1500562

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1540
- Ceres seq_id 1500563
- Location of start within SEQ ID NO 1539: at 843 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12464
- Cytochrome P450
- Location within SEQ ID NO 1540: from 1 to 226 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1541
- Ceres seq_id 1500564
- Location of start within SEQ ID NO 1539: at 960 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12465
- Cytochrome P450
- Location within SEQ ID NO 1541: from 1 to 187 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1542
- Ceres seq_id 1500565
- Location of start within SEQ ID NO 1539: at 1095 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12466
- Cytochrome P450
- Location within SEQ ID NO 1542: from 1 to 142 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 263816

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1543
- Ceres seq_id 1500614

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1544
- Ceres seq_id 1500615
- Location of start within SEQ ID NO 1543: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12467
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1544: from 51 to 308 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12468
- gi No. 3450842
- % Identity 76.9
- Alignment Length 277

- Location of Alignment in SEQ ID NO 1544: from 37 to 313

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1545
- Ceres seq_id 1500616
- Location of start within SEQ ID NO 1543: at 84 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12469
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1545: from 24 to 281 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12470
- gi No. 3450842
- % Identity 76.9
- Alignment Length 277
- Location of Alignment in SEQ ID NO 1545: from 10 to 286

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1546
- Ceres seq_id 1500617
- Location of start within SEQ ID NO 1543: at 339 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12471
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1546: from 1 to 196 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12472
- gi No. 3450842
- % Identity 76.9
- Alignment Length 277
- Location of Alignment in SEQ ID NO 1546: from 1 to 201

Maximum Length Sequence corresponding to clone ID 264799

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1547
- Ceres seq_id 1500618

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1548
- Ceres seq_id 1500619
- Location of start within SEQ ID NO 1547: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12473
- Jacalin-like lectin domain
- Location within SEQ ID NO 1548: from 107 to 244 aa.
- Alignment No. 12474
- Jacalin-like lectin domain
- Location within SEQ ID NO 1548: from 264 to 391 aa.
- Alignment No. 12475
- von Willebrand factor type A domain
- Location within SEQ ID NO 1548: from 104 to 212 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12476
- gi No. 3402674
- % Identity 99.4
- Alignment Length 311
- Location of Alignment in SEQ ID NO 1548: from 92 to 402

- Alignment No. 12477
- gi No. 3402676
- % Identity 78.3
- Alignment Length 315
- Location of Alignment in SEQ ID NO 1548: from 92 to 404

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1549
- Ceres seq_id 1500620
- Location of start within SEQ ID NO 1547: at 133 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12478
- Jacalin-like lectin domain
- Location within SEQ ID NO 1549: from 63 to 200 aa.

- Alignment No. 12479
- Jacalin-like lectin domain
- Location within SEQ ID NO 1549: from 220 to 347 aa.

- Alignment No. 12480
- von Willebrand factor type A domain
- Location within SEQ ID NO 1549: from 60 to 168 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12481
- gi No. 3402674
- % Identity 99.4
- Alignment Length 311
- Location of Alignment in SEQ ID NO 1549: from 48 to 358

- Alignment No. 12482
- gi No. 3402676
- % Identity 78.3
- Alignment Length 315
- Location of Alignment in SEQ ID NO 1549: from 48 to 360

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1550
- Ceres seq_id 1500621
- Location of start within SEQ ID NO 1547: at 274 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12483
- Jacalin-like lectin domain
- Location within SEQ ID NO 1550: from 16 to 153 aa.

- Alignment No. 12484
- Jacalin-like lectin domain
- Location within SEQ ID NO 1550: from 173 to 300 aa.

- Alignment No. 12485

- von Willebrand factor type A domain
- Location within SEQ ID NO 1550: from 13 to 121 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12486
- gi No. 3402674
- % Identity 99.4
- Alignment Length 311
- Location of Alignment in SEQ ID NO 1550: from 1 to 311

- Alignment No. 12487
- gi No. 3402676
- % Identity 78.3
- Alignment Length 315
- Location of Alignment in SEQ ID NO 1550: from 1 to 313

Maximum Length Sequence corresponding to clone ID 264837

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1551
- Ceres seq_id 1500622

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1552
- Ceres seq_id 1500623
- Location Of start within SEQ ID NO 1551: at 23 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12488
- gi No. 4586265
- % Identity 70.6
- Alignment Length 143
- Location of Alignment in SEQ ID NO 1552: from 1 to 136

- Alignment No. 12489
- gi No. 5123937
- % Identity 100
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1552: from 1 to 136

Maximum Length Sequence corresponding to clone ID 265926

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1553
- Ceres seq_id 1500633

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1554
- Ceres seq_id 1500634
- Location Of start within SEQ ID NO 1553: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12490
- gi No. 1171429
- % Identity 80
- Alignment Length 30
- Location of Alignment in SEQ ID NO 1554: from 7 to 36

- Alignment No. 12491
- gi No. 2129537
- % Identity 80

- Alignment Length 30
- Location of Alignment in SEQ ID NO 1554: from 7 to 36

- Alignment No. 12492
- gi No. 2652938
- % Identity 80.6
- Alignment Length 31
- Location of Alignment in SEQ ID NO 1554: from 6 to 36

- Alignment No. 12493
- gi No. 4836931
- % Identity 77.4
- Alignment Length 31
- Location of Alignment in SEQ ID NO 1554: from 6 to 36

Maximum Length Sequence corresponding to clone ID 266518

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1555
- Ceres seq_id 1500645

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1556
- Ceres seq_id 1500646
- Location of start within SEQ ID NO 1555: at 84 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12494
- short chain dehydrogenase
- Location within SEQ ID NO 1556: from 72 to 264 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12495
- gi No. 348718
- % Identity 72.2
- Alignment Length 306
- Location of Alignment in SEQ ID NO 1556: from 50 to 353

- Alignment No. 12496
- gi No. 348720
- % Identity 71.1
- Alignment Length 329
- Location of Alignment in SEQ ID NO 1556: from 50 to 376

- Alignment No. 12497
- gi No. 4469027
- % Identity 100
- Alignment Length 232
- Location of Alignment in SEQ ID NO 1556: from 1 to 232

- Alignment No. 12498
- gi No. 4972108
- % Identity 100
- Alignment Length 176
- Location of Alignment in SEQ ID NO 1556: from 201 to 376

- Alignment No. 12499
- gi No. 957251
- % Identity 100
- Alignment Length 305
- Location of Alignment in SEQ ID NO 1556: from 72 to 376

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1557
- Ceres seq_id 1500647
- Location of start within SEQ ID NO 1555: at 150 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12500
- short chain dehydrogenase
- Location within SEQ ID NO 1557: from 50 to 242 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12501
- gi No. 348718
- % Identity 72.2
- Alignment Length 306
- Location of Alignment in SEQ ID NO 1557: from 28 to 331

- Alignment No. 12502
- gi No. 348720
- % Identity 71.1
- Alignment Length 329
- Location of Alignment in SEQ ID NO 1557: from 28 to 354

- Alignment No. 12503
- gi No. 4469027
- % Identity 100
- Alignment Length 232
- Location of Alignment in SEQ ID NO 1557: from 1 to 210

- Alignment No. 12504
- gi No. 4972108
- % Identity 100
- Alignment Length 176
- Location of Alignment in SEQ ID NO 1557: from 179 to 354

- Alignment No. 12505
- gi No. 957251
- % Identity 100
- Alignment Length 305
- Location of Alignment in SEQ ID NO 1557: from 50 to 354

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1558
- Ceres seq_id 1500648
- Location of start within SEQ ID NO 1555: at 159 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12506
- short chain dehydrogenase
- Location within SEQ ID NO 1558: from 47 to 239 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12507
- gi No. 348718
- % Identity 72.2
- Alignment Length 306
- Location of Alignment in SEQ ID NO 1558: from 25 to 328

- Alignment No. 12508

- gi No. 348720
- % Identity 71.1
- Alignment Length 329
- Location of Alignment in SEQ ID NO 1558: from 25 to 351

- Alignment No. 12509
- gi No. 4469027
- % Identity 100
- Alignment Length 232
- Location of Alignment in SEQ ID NO 1558: from 1 to 207

- Alignment No. 12510
- gi No. 4972108
- % Identity 100
- Alignment Length 176
- Location of Alignment in SEQ ID NO 1558: from 176 to 351

- Alignment No. 12511
- gi No. 957251
- % Identity 100
- Alignment Length 305
- Location of Alignment in SEQ ID NO 1558: from 47 to 351

Maximum Length Sequence corresponding to clone ID 266520

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1559
- Ceres seq_id 1500649

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1560
- Ceres seq_id 1500650
- Location of start within SEQ ID NO 1559: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12512
- gi No. 3426051
- % Identity 94.4
- Alignment Length 319
- Location of Alignment in SEQ ID NO 1560: from 14 to 332

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1561
- Ceres seq_id 1500651
- Location of start within SEQ ID NO 1559: at 258 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12513
- gi No. 3426051
- % Identity 94.4
- Alignment Length 319
- Location of Alignment in SEQ ID NO 1561: from 1 to 247

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1562
- Ceres seq_id 1500652
- Location of start within SEQ ID NO 1559: at 267 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 12514
 - gi No. 3426051
 - % Identity 94.4
 - Alignment Length 319
 - Location of Alignment in SEQ ID NO 1562: from 1 to 244

Maximum Length Sequence corresponding to clone ID 266544

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1563
- Ceres seq_id 1500653

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1564
- Ceres seq_id 1500654
- Location of start within SEQ ID NO 1563: at 118 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12515
- Regulator of chromosome condensation (RCC1)
- Location within SEQ ID NO 1564: from 34 to 92 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1565
- Ceres seq_id 1500655
- Location of start within SEQ ID NO 1563: at 218 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1566
- Ceres seq_id 1500656
- Location of start within SEQ ID NO 1563: at 247 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12516
- Regulator of chromosome condensation (RCC1)
- Location within SEQ ID NO 1566: from 1 to 49 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 266710

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1567
- Ceres seq_id 1500661

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1568
- Ceres seq_id 1500662
- Location of start within SEQ ID NO 1567: at 27 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12517

- gi No. 2980782
- % Identity 84.3
- Alignment Length 168
- Location of Alignment in SEQ ID NO 1568: from 1 to 157

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1569
- Ceres seq_id 1500663
- Location of start within SEQ ID NO 1567: at 33 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12518
- gi No. 2980782
- % Identity 84.3
- Alignment Length 168
- Location of Alignment in SEQ ID NO 1569: from 1 to 155

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1570
- Ceres seq_id 1500664
- Location of start within SEQ ID NO 1567: at 36 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12519
- gi No. 2980782
- % Identity 84.3
- Alignment Length 168
- Location of Alignment in SEQ ID NO 1570: from 1 to 154

Maximum Length Sequence corresponding to clone ID 266712

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1571
- Ceres seq_id 1500665

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1572
- Ceres seq_id 1500666
- Location of start within SEQ ID NO 1571: at 48 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12520
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 1572: from 8 to 79 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12521
- gi No. 1076672
- % Identity 71.6
- Alignment Length 102
- Location of Alignment in SEQ ID NO 1572: from 1 to 100
- Alignment No. 12522
- gi No. 1076731
- % Identity 73.8
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1572: from 1 to 100

- Alignment No. 12523
 - gi No. 1076731
 - % Identity 72.4
 - Alignment Length 105
 - Location of Alignment in SEQ ID NO 1572: from 1 to 101
- Alignment No. 12524
 - gi No. 1229138
 - % Identity 72.3
 - Alignment Length 101
 - Location of Alignment in SEQ ID NO 1572: from 1 to 101
- Alignment No. 12525
 - gi No. 1346180
 - % Identity 78.4
 - Alignment Length 97
 - Location of Alignment in SEQ ID NO 1572: from 3 to 99
- Alignment No. 12526
 - gi No. 1346181
 - % Identity 76.3
 - Alignment Length 97
 - Location of Alignment in SEQ ID NO 1572: from 3 to 99
- Alignment No. 12527
 - gi No. 1710625
 - % Identity 71.4
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 1572: from 86 to 99
- Alignment No. 12528
 - gi No. 1710626
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 1572: from 86 to 96
- Alignment No. 12529
 - gi No. 1710626
 - % Identity 71.4
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 1572: from 86 to 99
- Alignment No. 12530
 - gi No. 1710626
 - % Identity 73.3
 - Alignment Length 15
 - Location of Alignment in SEQ ID NO 1572: from 86 to 100
- Alignment No. 12531
 - gi No. 1710627
 - % Identity 76.9
 - Alignment Length 13
 - Location of Alignment in SEQ ID NO 1572: from 88 to 100
- Alignment No. 12532
 - gi No. 1934994
 - % Identity 73.7
 - Alignment Length 99
 - Location of Alignment in SEQ ID NO 1572: from 2 to 100
- Alignment No. 12533

- gi No. 2119042
- % Identity 77.9
- Alignment Length 104
- Location of Alignment in SEQ ID NO 1572: from 1 to 101

- Alignment No. 12534
- gi No. 2119042
- % Identity 71.9
- Alignment Length 114
- Location of Alignment in SEQ ID NO 1572: from 1 to 101

- Alignment No. 12535
- gi No. 2119043
- % Identity 74.3
- Alignment Length 101
- Location of Alignment in SEQ ID NO 1572: from 1 to 101

- Alignment No. 12536
- gi No. 2119044
- % Identity 75.7
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1572: from 1 to 100

- Alignment No. 12537
- gi No. 2129944
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1572: from 88 to 100

- Alignment No. 12538
- gi No. 2143460
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1572: from 87 to 98

- Alignment No. 12539
- gi No. 2226370
- % Identity 76.2
- Alignment Length 105
- Location of Alignment in SEQ ID NO 1572: from 1 to 101

- Alignment No. 12540
- gi No. 2267567
- % Identity 73.3
- Alignment Length 101
- Location of Alignment in SEQ ID NO 1572: from 2 to 101

- Alignment No. 12541
- gi No. 2267593
- % Identity 70.6
- Alignment Length 102
- Location of Alignment in SEQ ID NO 1572: from 3 to 101

- Alignment No. 12542
- gi No. 2293480
- % Identity 71.6
- Alignment Length 102
- Location of Alignment in SEQ ID NO 1572: from 3 to 101

- Alignment No. 12543
- gi No. 2293480

- % Identity 70.4
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1572: from 3 to 100

- Alignment No. 12544
- gi No. 2331131
- % Identity 72.7
- Alignment Length 99
- Location of Alignment in SEQ ID NO 1572: from 3 to 101

- Alignment No. 12545
- gi No. 2331133
- % Identity 71.6
- Alignment Length 102
- Location of Alignment in SEQ ID NO 1572: from 3 to 101

- Alignment No. 12546
- gi No. 2624326
- % Identity 74.5
- Alignment Length 102
- Location of Alignment in SEQ ID NO 1572: from 3 to 101

- Alignment No. 12547
- gi No. 2668742
- % Identity 71.2
- Alignment Length 104
- Location of Alignment in SEQ ID NO 1572: from 2 to 101

- Alignment No. 12548
- gi No. 2674201
- % Identity 71.2
- Alignment Length 104
- Location of Alignment in SEQ ID NO 1572: from 2 to 101

- Alignment No. 12549
- gi No. 283664
- % Identity 70.6
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1572: from 84 to 100

- Alignment No. 12550
- gi No. 3914466
- % Identity 85
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1572: from 59 to 78

- Alignment No. 12551
- gi No. 423560
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1572: from 87 to 98

- Alignment No. 12552
- gi No. 4567236
- % Identity 82.5
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1572: from 39 to 101

- Alignment No. 12553
- gi No. 4567236
- % Identity 73.2

- Alignment Length 71
- Location of Alignment in SEQ ID NO 1572: from 39 to 101
- Alignment No. 12554
- gi No. 4587684
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1572: from 49 to 65
- Alignment No. 12555
- gi No. 469072
- % Identity 76.2
- Alignment Length 101
- Location of Alignment in SEQ ID NO 1572: from 1 to 101
- Alignment No. 12556
- gi No. 4938296
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1572: from 86 to 100
- Alignment No. 12557
- gi No. 4938296
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1572: from 86 to 100
- Alignment No. 12558
- gi No. 5031693
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1572: from 88 to 100
- Alignment No. 12559
- gi No. 542649
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1572: from 86 to 99
- Alignment No. 12560
- gi No. 544416
- % Identity 84
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1572: from 1 to 100
- Alignment No. 12561
- gi No. 544416
- % Identity 76.1
- Alignment Length 113
- Location of Alignment in SEQ ID NO 1572: from 1 to 101
- Alignment No. 12562
- gi No. 544421
- % Identity 70.4
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1572: from 22 to 100
- Alignment No. 12563
- gi No. 544423
- % Identity 74
- Alignment Length 100

- Location of Alignment in SEQ ID NO 1572: from 2 to 101
- Alignment No. 12564
- gi No. 544424
- % Identity 79.8
- Alignment Length 99
- Location of Alignment in SEQ ID NO 1572: from 3 to 101
- Alignment No. 12565
- gi No. 544424
- % Identity 73.8
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1572: from 3 to 101
- Alignment No. 12566
- gi No. 544425
- % Identity 92.9
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1572: from 88 to 101
- Alignment No. 12567
- gi No. 544425
- % Identity 94.1
- Alignment Length 101
- Location of Alignment in SEQ ID NO 1572: from 1 to 101
- Alignment No. 12568
- gi No. 544425
- % Identity 82.9
- Alignment Length 117
- Location of Alignment in SEQ ID NO 1572: from 1 to 101
- Alignment No. 12569
- gi No. 544426
- % Identity 82.2
- Alignment Length 101
- Location of Alignment in SEQ ID NO 1572: from 1 to 101
- Alignment No. 12570
- gi No. 544426
- % Identity 79.2
- Alignment Length 106
- Location of Alignment in SEQ ID NO 1572: from 1 to 99
- Alignment No. 12571
- gi No. 5726567
- % Identity 70
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1572: from 2 to 101
- Alignment No. 12572
- gi No. 82696
- % Identity 71
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1572: from 2 to 100
- Alignment No. 12573
- gi No. 974605
- % Identity 74.3
- Alignment Length 101
- Location of Alignment in SEQ ID NO 1572: from 1 to 101

- Alignment No. 12574
- gi No. 974605
- % Identity 73.3
- Alignment Length 105
- Location of Alignment in SEQ ID NO 1572: from 1 to 100

Maximum Length Sequence corresponding to clone ID 266730

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1573
- Ceres seq_id 1500667

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1574
- Ceres seq_id 1500668
- Location of start within SEQ ID NO 1573: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1575
- Ceres seq_id 1500669
- Location of start within SEQ ID NO 1573: at 90 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1576
- Ceres seq_id 1500670
- Location of start within SEQ ID NO 1573: at 277 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12575
- gi No. 1513292
- % Identity 71.4
- Alignment Length 42
- Location of Alignment in SEQ ID NO 1576: from 9 to 49
- Alignment No. 12576
- gi No. 4539026
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1576: from 12 to 45

Maximum Length Sequence corresponding to clone ID 266771

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1577
- Ceres seq_id 1500675

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1578
- Ceres seq_id 1500676
- Location of start within SEQ ID NO 1577: at 450 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12577

- Zinc finger, C2H2 type
- Location within SEQ ID NO 1578: from 57 to 79 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12578
- gi No. 3551247
- % Identity 93
- Alignment Length 200
- Location of Alignment in SEQ ID NO 1578: from 3 to 202

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1579
- Ceres seq_id 1500677
- Location of start within SEQ ID NO 1577: at 645 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12579
- gi No. 3551247
- % Identity 93
- Alignment Length 200
- Location of Alignment in SEQ ID NO 1579: from 1 to 137

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1580
- Ceres seq_id 1500678
- Location of start within SEQ ID NO 1577: at 675 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12580
- gi No. 3551247
- % Identity 93
- Alignment Length 200
- Location of Alignment in SEQ ID NO 1580: from 1 to 127

Maximum Length Sequence corresponding to clone ID 266884

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1581
- Ceres seq_id 1500679

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1582
- Ceres seq_id 1500680
- Location of start within SEQ ID NO 1581: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12581
- Helix-loop-helix DNA-binding domain
- Location within SEQ ID NO 1582: from 69 to 114 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12582
- gi No. 4914417
- % Identity 72.2
- Alignment Length 116
- Location of Alignment in SEQ ID NO 1582: from 15 to 129

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1583
- Ceres seq_id 1500681
- Location of start within SEQ ID NO 1581: at 44 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12583
- Helix-loop-helix DNA-binding domain
- Location within SEQ ID NO 1583: from 55 to 100 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12584
- gi No. 4914417
- % Identity 72.2
- Alignment Length 116
- Location of Alignment in SEQ ID NO 1583: from 1 to 115

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1584
- Ceres seq_id 1500682
- Location of start within SEQ ID NO 1581: at 345 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 266907

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1585
- Ceres seq_id 1500683

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1586
- Ceres seq_id 1500684
- Location of start within SEQ ID NO 1585: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12585
- gi No. 5080769
- % Identity 100
- Alignment Length 155
- Location of Alignment in SEQ ID NO 1586: from 17 to 171

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1587
- Ceres seq_id 1500685
- Location of start within SEQ ID NO 1585: at 49 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12586
- gi No. 5080769
- % Identity 100
- Alignment Length 155
- Location of Alignment in SEQ ID NO 1587: from 1 to 155

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1588
- Ceres seq_id 1500686

- Location of start within SEQ ID NO 1585: at 169 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12587
- gi No. 5080769
- % Identity 100
- Alignment Length 155
- Location of Alignment in SEQ ID NO 1588: from 1 to 115

Maximum Length Sequence corresponding to clone ID 267121

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1589
- Ceres seq_id 1500687

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1590
- Ceres seq_id 1500688
- Location of start within SEQ ID NO 1589: at 149 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12588
- Myb-like DNA-binding domain
- Location within SEQ ID NO 1590: from 5 to 51 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12589
- gi No. 2832480
- % Identity 100
- Alignment Length 45
- Location of Alignment in SEQ ID NO 1590: from 45 to 89
- Alignment No. 12590
- gi No. 2832554
- % Identity 73.3
- Alignment Length 45
- Location of Alignment in SEQ ID NO 1590: from 45 to 89
- Alignment No. 12591
- gi No. 3063725
- % Identity 93.3
- Alignment Length 45
- Location of Alignment in SEQ ID NO 1590: from 45 to 89
- Alignment No. 12592
- gi No. 3941468
- % Identity 98.4
- Alignment Length 249
- Location of Alignment in SEQ ID NO 1590: from 1 to 249
- Alignment No. 12593
- gi No. 3941496
- % Identity 81.4
- Alignment Length 43
- Location of Alignment in SEQ ID NO 1590: from 66 to 108
- Alignment No. 12594
- gi No. 4490312
- % Identity 77.1
- Alignment Length 109

- Location of Alignment in SEQ ID NO 1590: from 1 to 108

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1591
- Ceres seq_id 1500689
- Location of start within SEQ ID NO 1589: at 152 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12595
- Myb-like DNA-binding domain
- Location within SEQ ID NO 1591: from 4 to 50 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12596
- gi No. 2832480
- % Identity 100
- Alignment Length 45
- Location of Alignment in SEQ ID NO 1591: from 44 to 88
- Alignment No. 12597
- gi No. 2832554
- % Identity 73.3
- Alignment Length 45
- Location of Alignment in SEQ ID NO 1591: from 44 to 88
- Alignment No. 12598
- gi No. 3063725
- % Identity 93.3
- Alignment Length 45
- Location of Alignment in SEQ ID NO 1591: from 44 to 88
- Alignment No. 12599
- gi No. 3941468
- % Identity 98.4
- Alignment Length 249
- Location of Alignment in SEQ ID NO 1591: from 1 to 248
- Alignment No. 12600
- gi No. 3941496
- % Identity 81.4
- Alignment Length 43
- Location of Alignment in SEQ ID NO 1591: from 65 to 107
- Alignment No. 12601
- gi No. 4490312
- % Identity 77.1
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1591: from 1 to 107

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1592
- Ceres seq_id 1500690
- Location of start within SEQ ID NO 1589: at 452 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12602
- gi No. 3941468
- % Identity 98.4

- Alignment Length 249
- Location of Alignment in SEQ ID NO 1592: from 1 to 148

Maximum Length Sequence corresponding to clone ID 267357

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1593
- Ceres seq_id 1500693

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1594
- Ceres seq_id 1500694
- Location of start within SEQ ID NO 1593: at 68 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12603
- Ribosomal protein L36e
- Location within SEQ ID NO 1594: from 6 to 93 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12604
- gi No. 3236242
- % Identity 83.9
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1594: from 1 to 102

Maximum Length Sequence corresponding to clone ID 267559

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1595
- Ceres seq_id 1500695

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1596
- Ceres seq_id 1500696
- Location of start within SEQ ID NO 1595: at 228 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12605
- gi No. 4680201
- % Identity 70.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1596: from 11 to 98

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1597
- Ceres seq_id 1500697
- Location of start within SEQ ID NO 1595: at 252 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12606
- gi No. 4680201
- % Identity 70.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1597: from 3 to 90

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1598
- Ceres seq_id 1500698
- Location of start within SEQ ID NO 1595: at 255 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12607
- gi No. 4680201
- % Identity 70.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1598: from 2 to 89

Maximum Length Sequence corresponding to clone ID 268117

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1599
- Ceres seq_id 1500703

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1600
- Ceres seq_id 1500704
- Location of start within SEQ ID NO 1599: at 338 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12608
- gi No. 2924518
- % Identity 71.5
- Alignment Length 258
- Location of Alignment in SEQ ID NO 1600: from 13 to 264

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1601
- Ceres seq_id 1500705
- Location of start within SEQ ID NO 1599: at 569 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12609
- gi No. 2924518
- % Identity 71.5
- Alignment Length 258
- Location of Alignment in SEQ ID NO 1601: from 1 to 187

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1602
- Ceres seq_id 1500706
- Location of start within SEQ ID NO 1599: at 659 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12610
- gi No. 2924518
- % Identity 71.5
- Alignment Length 258
- Location of Alignment in SEQ ID NO 1602: from 1 to 157

Maximum Length Sequence corresponding to clone ID 268199

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1603
- Ceres seq_id 1500707

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1604
- Ceres seq_id 1500708
- Location of start within SEQ ID NO 1603: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12611
- Asparaginase
- Location within SEQ ID NO 1604: from 20 to 182 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1605
- Ceres seq_id 1500709
- Location of start within SEQ ID NO 1603: at 55 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12612
- Asparaginase
- Location within SEQ ID NO 1605: from 2 to 164 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1606
- Ceres seq_id 1500710
- Location of start within SEQ ID NO 1603: at 292 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12613
- Asparaginase
- Location within SEQ ID NO 1606: from 1 to 85 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 268536

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1607
- Ceres seq_id 1500719

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1608
- Ceres seq_id 1500720
- Location of start within SEQ ID NO 1607: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12614
- Hsp20/alpha crystallin family
- Location within SEQ ID NO 1608: from 117 to 222 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1609
- Ceres seq_id 1500721
- Location of start within SEQ ID NO 1607: at 39 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12615
- Hsp20/alpha crystallin family
- Location within SEQ ID NO 1609: from 105 to 210 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1610
- Ceres seq_id 1500722
- Location of start within SEQ ID NO 1607: at 285 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12616
- Hsp20/alpha crystallin family
- Location within SEQ ID NO 1610: from 23 to 128 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 268621

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1611
- Ceres seq_id 1500734

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1612
- Ceres seq_id 1500735
- Location of start within SEQ ID NO 1611: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12617
- gi No. 4337197
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1612: from 23 to 78

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1613
- Ceres seq_id 1500736
- Location of start within SEQ ID NO 1611: at 69 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12618
- gi No. 4337197
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1613: from 1 to 56

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1614
- Ceres seq_id 1500737
- Location of start within SEQ ID NO 1611: at 87 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12619
- gi No. 4337197
- % Identity 96.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1614: from 1 to 50

Maximum Length Sequence corresponding to clone ID 268835

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1615
- Ceres seq_id 1500742

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1616
- Ceres seq_id 1500743
- Location of start within SEQ ID NO 1615: at 77 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12620
- gi No. 3510256
- % Identity 98.9
- Alignment Length 174
- Location of Alignment in SEQ ID NO 1616: from 1 to 174

Maximum Length Sequence corresponding to clone ID 268982

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1617
- Ceres seq_id 1500748

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1618
- Ceres seq_id 1500749
- Location of start within SEQ ID NO 1617: at 92 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12621
- Core histone H2A/H2B/H3/H4
- Location within SEQ ID NO 1618: from 17 to 135 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12622
- gi No. 10253
- % Identity 89
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136

- Alignment No. 12623
- gi No. 103198
- % Identity 91.2
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136

- Alignment No. 12624
- gi No. 104698
- % Identity 92
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1618: from 2 to 26

- Alignment No. 12625
- gi No. 1053045
- % Identity 95.3

- Alignment Length 127
- Location of Alignment in SEQ ID NO 1618: from 1 to 127

- Alignment No. 12626
- gi No. 1053047
- % Identity 95.3
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1618: from 1 to 127

- Alignment No. 12627
- gi No. 1053053
- % Identity 91.3
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1618: from 1 to 127

- Alignment No. 12628
- gi No. 1053055
- % Identity 86.2
- Alignment Length 29
- Location of Alignment in SEQ ID NO 1618: from 1 to 29

- Alignment No. 12629
- gi No. 1053057
- % Identity 95.3
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1618: from 1 to 127

- Alignment No. 12630
- gi No. 1053059
- % Identity 93.7
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1618: from 1 to 127

- Alignment No. 12631
- gi No. 1076583
- % Identity 95
- Alignment Length 60
- Location of Alignment in SEQ ID NO 1618: from 1 to 60

- Alignment No. 12632
- gi No. 1079199
- % Identity 90.4
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136

- Alignment No. 12633
- gi No. 1085857
- % Identity 91.6
- Alignment Length 83
- Location of Alignment in SEQ ID NO 1618: from 34 to 116

- Alignment No. 12634
- gi No. 1085858
- % Identity 91.6
- Alignment Length 83
- Location of Alignment in SEQ ID NO 1618: from 34 to 116

- Alignment No. 12635
- gi No. 108593
- % Identity 76.2
- Alignment Length 21

- Location of Alignment in SEQ ID NO 1618: from 112 to 132
- Alignment No. 12636
 - gi No. 109977
 - % Identity 91.4
 - Alignment Length 35
 - Location of Alignment in SEQ ID NO 1618: from 2 to 36
- Alignment No. 12637
 - gi No. 1166436
 - % Identity 81.4
 - Alignment Length 59
 - Location of Alignment in SEQ ID NO 1618: from 36 to 94
- Alignment No. 12638
 - gi No. 1197519
 - % Identity 85.5
 - Alignment Length 124
 - Location of Alignment in SEQ ID NO 1618: from 13 to 136
- Alignment No. 12639
 - gi No. 1208642
 - % Identity 94.6
 - Alignment Length 56
 - Location of Alignment in SEQ ID NO 1618: from 25 to 80
- Alignment No. 12640
 - gi No. 1208644
 - % Identity 94.6
 - Alignment Length 56
 - Location of Alignment in SEQ ID NO 1618: from 25 to 80
- Alignment No. 12641
 - gi No. 1208646
 - % Identity 96.4
 - Alignment Length 56
 - Location of Alignment in SEQ ID NO 1618: from 25 to 80
- Alignment No. 12642
 - gi No. 1208656
 - % Identity 94.6
 - Alignment Length 56
 - Location of Alignment in SEQ ID NO 1618: from 25 to 80
- Alignment No. 12643
 - gi No. 1208658
 - % Identity 94.6
 - Alignment Length 56
 - Location of Alignment in SEQ ID NO 1618: from 25 to 80
- Alignment No. 12644
 - gi No. 1208664
 - % Identity 94.6
 - Alignment Length 56
 - Location of Alignment in SEQ ID NO 1618: from 25 to 80
- Alignment No. 12645
 - gi No. 1208668
 - % Identity 92.9
 - Alignment Length 56
 - Location of Alignment in SEQ ID NO 1618: from 25 to 80

- Alignment No. 12646
- gi No. 1208699
- % Identity 94.6
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80

- Alignment No. 12647
- gi No. 1208701
- % Identity 94.6
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80

- Alignment No. 12648
- gi No. 1208707
- % Identity 94.6
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80

- Alignment No. 12649
- gi No. 1208715
- % Identity 94.6
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80

- Alignment No. 12650
- gi No. 1208725
- % Identity 94.6
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80

- Alignment No. 12651
- gi No. 1208727
- % Identity 94.6
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80

- Alignment No. 12652
- gi No. 1213291
- % Identity 94.6
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80

- Alignment No. 12653
- gi No. 1213307
- % Identity 94.6
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80

- Alignment No. 12654
- gi No. 1213313
- % Identity 94.6
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80

- Alignment No. 12655
- gi No. 1213315
- % Identity 89.3
- Alignment Length 56
- Location of Alignment in SEQ ID NO 1618: from 25 to 80

- Alignment No. 12656
- gi No. 122065
- % Identity 86
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
- Alignment No. 12657
- gi No. 122066
- % Identity 84.4
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 1 to 135
- Alignment No. 12658
- gi No. 122068
- % Identity 91.9
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
- Alignment No. 12659
- gi No. 122070
- % Identity 92.6
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
- Alignment No. 12660
- gi No. 122071
- % Identity 85.4
- Alignment Length 41
- Location of Alignment in SEQ ID NO 1618: from 1 to 41
- Alignment No. 12661
- gi No. 122072
- % Identity 80.5
- Alignment Length 41
- Location of Alignment in SEQ ID NO 1618: from 1 to 41
- Alignment No. 12662
- gi No. 122074
- % Identity 88.2
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
- Alignment No. 12663
- gi No. 122076
- % Identity 85.3
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
- Alignment No. 12664
- gi No. 122077
- % Identity 84.6
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
- Alignment No. 12665
- gi No. 122078
- % Identity 77.9
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
- Alignment No. 12666

- gi No. 122079
- % Identity 91.9
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136

- Alignment No. 12667
- gi No. 122080
- % Identity 83.8
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136

- Alignment No. 12668
- gi No. 122081
- % Identity 90.4
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136

- Alignment No. 12669
- gi No. 122082
- % Identity 90.4
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136

- Alignment No. 12670
- gi No. 122083
- % Identity 93.3
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 2 to 136

- Alignment No. 12671
- gi No. 122084
- % Identity 96.3
- Alignment Length 80
- Location of Alignment in SEQ ID NO 1618: from 57 to 136

- Alignment No. 12672
- gi No. 122085
- % Identity 94.1
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136

- Alignment No. 12673
- gi No. 122086
- % Identity 83.7
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 1 to 135

- Alignment No. 12674
- gi No. 122087
- % Identity 94.1
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136

- Alignment No. 12675
- gi No. 122088
- % Identity 91.2
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136

- Alignment No. 12676
- gi No. 122089

- % Identity 90.4
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136

- Alignment No. 12677
- gi No. 122090
- % Identity 92.6
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136

- Alignment No. 12678
- gi No. 122091
- % Identity 83.1
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136

- Alignment No. 12679
- gi No. 1360625
- % Identity 79.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 1618: from 1 to 135

- Alignment No. 12680
- gi No. 1360627
- % Identity 77.6
- Alignment Length 98
- Location of Alignment in SEQ ID NO 1618: from 1 to 96

- Alignment No. 12681
- gi No. 1362108
- % Identity 93.4
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136

- Alignment No. 12682
- gi No. 1362171
- % Identity 90.6
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1618: from 105 to 136

- Alignment No. 12683
- gi No. 159967
- % Identity 89.7
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136

- Alignment No. 12684
- gi No. 161319
- % Identity 90.4
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136

- Alignment No. 12685
- gi No. 166384
- % Identity 93.4
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136

- Alignment No. 12686
- gi No. 1708108
- % Identity 91.9

- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136

- Alignment No. 12687
- gi No. 1708109
- % Identity 91.2
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136

- Alignment No. 12688
- gi No. 171637
- % Identity 87.9
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1618: from 3 to 35

- Alignment No. 12689
- gi No. 1723293
- % Identity 91.2
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1618: from 46 to 136

- Alignment No. 12690
- gi No. 1731925
- % Identity 91.3
- Alignment Length 115
- Location of Alignment in SEQ ID NO 1618: from 3 to 117

- Alignment No. 12691
- gi No. 1762791
- % Identity 71.4
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1618: from 4 to 136

- Alignment No. 12692
- gi No. 1763308
- % Identity 83.8
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136

- Alignment No. 12693
- gi No. 1870700
- % Identity 91.9
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1618: from 1 to 111

- Alignment No. 12694
- gi No. 1881589
- % Identity 89.6
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1618: from 89 to 136

- Alignment No. 12695
- gi No. 1881594
- % Identity 91
- Alignment Length 89
- Location of Alignment in SEQ ID NO 1618: from 1 to 87

- Alignment No. 12696
- gi No. 1881601
- % Identity 93.1
- Alignment Length 87

- Location of Alignment in SEQ ID NO 1618: from 1 to 87
- Alignment No. 12697
 - gi No. 19611
 - % Identity 94.3
 - Alignment Length 123
 - Location of Alignment in SEQ ID NO 1618: from 14 to 136
- Alignment No. 12698
 - gi No. 19614
 - % Identity 93.1
 - Alignment Length 58
 - Location of Alignment in SEQ ID NO 1618: from 79 to 136
- Alignment No. 12699
 - gi No. 208461
 - % Identity 84.2
 - Alignment Length 19
 - Location of Alignment in SEQ ID NO 1618: from 17 to 35
- Alignment No. 12700
 - gi No. 208463
 - % Identity 87.9
 - Alignment Length 33
 - Location of Alignment in SEQ ID NO 1618: from 3 to 35
- Alignment No. 12701
 - gi No. 2116601
 - % Identity 90.4
 - Alignment Length 136
 - Location of Alignment in SEQ ID NO 1618: from 1 to 136
- Alignment No. 12702
 - gi No. 211855
 - % Identity 91.2
 - Alignment Length 136
 - Location of Alignment in SEQ ID NO 1618: from 1 to 136
- Alignment No. 12703
 - gi No. 2119011
 - % Identity 91.2
 - Alignment Length 136
 - Location of Alignment in SEQ ID NO 1618: from 1 to 136
- Alignment No. 12704
 - gi No. 2119012
 - % Identity 90.4
 - Alignment Length 136
 - Location of Alignment in SEQ ID NO 1618: from 1 to 136
- Alignment No. 12705
 - gi No. 2119013
 - % Identity 91.9
 - Alignment Length 136
 - Location of Alignment in SEQ ID NO 1618: from 1 to 136
- Alignment No. 12706
 - gi No. 2119014
 - % Identity 92.1
 - Alignment Length 76
 - Location of Alignment in SEQ ID NO 1618: from 61 to 136

- Alignment No. 12707
- gi No. 2119018
- % Identity 91.9
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136

- Alignment No. 12708
- gi No. 2135356
- % Identity 92.6
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1618: from 1 to 27

- Alignment No. 12709
- gi No. 2136686
- % Identity 93.1
- Alignment Length 29
- Location of Alignment in SEQ ID NO 1618: from 2 to 30

- Alignment No. 12710
- gi No. 2147399
- % Identity 92.3
- Alignment Length 39
- Location of Alignment in SEQ ID NO 1618: from 1 to 39

- Alignment No. 12711
- gi No. 2252516
- % Identity 92.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1618: from 1 to 38

- Alignment No. 12712
- gi No. 2253166
- % Identity 87.1
- Alignment Length 62
- Location of Alignment in SEQ ID NO 1618: from 1 to 62

- Alignment No. 12713
- gi No. 2253615
- % Identity 79.1
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1618: from 1 to 136

- Alignment No. 12714
- gi No. 2909431
- % Identity 82.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1618: from 13 to 122

- Alignment No. 12715
- gi No. 2995213
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1618: from 1 to 36

- Alignment No. 12716
- gi No. 2995216
- % Identity 80.6
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1618: from 1 to 36

- Alignment No. 12717
- gi No. 2995219
- % Identity 77.8
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1618: from 1 to 36
- Alignment No. 12718
- gi No. 2995225
- % Identity 86.1
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1618: from 1 to 36
- Alignment No. 12719
- gi No. 2995264
- % Identity 83.3
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1618: from 1 to 36
- Alignment No. 12720
- gi No. 3002595
- % Identity 91.2
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1618: from 15 to 105
- Alignment No. 12721
- gi No. 3002597
- % Identity 90.1
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1618: from 15 to 105
- Alignment No. 12722
- gi No. 3002603
- % Identity 88
- Alignment Length 92
- Location of Alignment in SEQ ID NO 1618: from 15 to 105
- Alignment No. 12723
- gi No. 3002613
- % Identity 89
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1618: from 15 to 105
- Alignment No. 12724
- gi No. 3002621
- % Identity 87.9
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1618: from 15 to 105
- Alignment No. 12725
- gi No. 3002633
- % Identity 90.1
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1618: from 15 to 105
- Alignment No. 12726
- gi No. 3002635
- % Identity 90.1
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1618: from 15 to 105
- Alignment No. 12727

- gi No. 3002637
- % Identity 90
- Alignment Length 90
- Location of Alignment in SEQ ID NO 1618: from 16 to 105

- Alignment No. 12728
- gi No. 3002643
- % Identity 90.1
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1618: from 15 to 105

- Alignment No. 12729
- gi No. 3002647
- % Identity 91.1
- Alignment Length 90
- Location of Alignment in SEQ ID NO 1618: from 15 to 104

- Alignment No. 12730
- gi No. 3002649
- % Identity 88.8
- Alignment Length 89
- Location of Alignment in SEQ ID NO 1618: from 15 to 103

- Alignment No. 12731
- gi No. 3002657
- % Identity 90.1
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1618: from 15 to 105

- Alignment No. 12732
- gi No. 3002663
- % Identity 89
- Alignment Length 91
- Location of Alignment in SEQ ID NO 1618: from 15 to 105

- Alignment No. 12733
- gi No. 3219788
- % Identity 84.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1618: from 13 to 122

- Alignment No. 12734
- gi No. 3219789
- % Identity 83.9
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1618: from 13 to 122

- Alignment No. 12735
- gi No. 3219790
- % Identity 85.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1618: from 13 to 122

- Alignment No. 12736
- gi No. 3219791
- % Identity 84.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1618: from 13 to 122

- Alignment No. 12737
- gi No. 3219792

- % Identity 83.9
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1618: from 13 to 122

- Alignment No. 12738
- gi No. 3219803
- % Identity 83
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1618: from 13 to 122

- Alignment No. 12739
- gi No. 3219805
- % Identity 81.1
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1618: from 13 to 122

- Alignment No. 12740
- gi No. 352175
- % Identity 84.3
- Alignment Length 134
- Location of Alignment in SEQ ID NO 1618: from 2 to 135

- Alignment No. 12741
- gi No. 3745758
- % Identity 91.4
- Alignment Length 116
- Location of Alignment in SEQ ID NO 1618: from 21 to 136

- Alignment No. 12742
- gi No. 386772
- % Identity 91.8
- Alignment Length 134
- Location of Alignment in SEQ ID NO 1618: from 1 to 134

- Alignment No. 12743
- gi No. 3875420
- % Identity 84.6
- Alignment Length 123
- Location of Alignment in SEQ ID NO 1618: from 13 to 135

- Alignment No. 12744
- gi No. 3875421
- % Identity 75.6
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1618: from 1 to 127

- Alignment No. 12745
- gi No. 3880527
- % Identity 88.2
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136

- Alignment No. 12746
- gi No. 3880606
- % Identity 85
- Alignment Length 80
- Location of Alignment in SEQ ID NO 1618: from 57 to 136

- Alignment No. 12747
- gi No. 3979986
- % Identity 91.9

- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136

- Alignment No. 12748
- gi No. 404466
- % Identity 90.4
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136

- Alignment No. 12749
- gi No. 4139869
- % Identity 91.4
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1618: from 44 to 136

- Alignment No. 12750
- gi No. 417103
- % Identity 95.6
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136

- Alignment No. 12751
- gi No. 422605
- % Identity 88.2
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136

- Alignment No. 12752
- gi No. 422606
- % Identity 91.2
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136

- Alignment No. 12753
- gi No. 4388695
- % Identity 90.8
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1618: from 61 to 136

- Alignment No. 12754
- gi No. 4504279
- % Identity 91.2
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136

- Alignment No. 12755
- gi No. 4504281
- % Identity 91.9
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136

- Alignment No. 12756
- gi No. 4504283
- % Identity 91.2
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136

- Alignment No. 12757
- gi No. 4504299
- % Identity 89
- Alignment Length 136

- Location of Alignment in SEQ ID NO 1618: from 1 to 136
- Alignment No. 12758
- gi No. 4574208
- % Identity 96.5
- Alignment Length 115
- Location of Alignment in SEQ ID NO 1618: from 22 to 136
- Alignment No. 12759
- gi No. 4761212
- % Identity 91.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 1618: from 8 to 119
- Alignment No. 12760
- gi No. 484441
- % Identity 91.2
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
- Alignment No. 12761
- gi No. 484530
- % Identity 89.6
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 2 to 136
- Alignment No. 12762
- gi No. 484531
- % Identity 88.9
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 2 to 136
- Alignment No. 12763
- gi No. 4883733
- % Identity 90.6
- Alignment Length 106
- Location of Alignment in SEQ ID NO 1618: from 11 to 116
- Alignment No. 12764
- gi No. 4883734
- % Identity 91.6
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1618: from 10 to 116
- Alignment No. 12765
- gi No. 4883735
- % Identity 91.7
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1618: from 9 to 117
- Alignment No. 12766
- gi No. 4883736
- % Identity 90.5
- Alignment Length 105
- Location of Alignment in SEQ ID NO 1618: from 11 to 115
- Alignment No. 12767
- gi No. 4883737
- % Identity 91.3
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1618: from 13 to 115

- Alignment No. 12768
- gi No. 4883738
- % Identity 87.1
- Alignment Length 93
- Location of Alignment in SEQ ID NO 1618: from 17 to 109

- Alignment No. 12769
- gi No. 4883739
- % Identity 91.3
- Alignment Length 104
- Location of Alignment in SEQ ID NO 1618: from 13 to 116

- Alignment No. 12770
- gi No. 4883740
- % Identity 90.3
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1618: from 13 to 115

- Alignment No. 12771
- gi No. 4883741
- % Identity 91.7
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1618: from 9 to 116

- Alignment No. 12772
- gi No. 4883743
- % Identity 89
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1618: from 9 to 117

- Alignment No. 12773
- gi No. 4883744
- % Identity 90.8
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1618: from 9 to 117

- Alignment No. 12774
- gi No. 4883745
- % Identity 91.7
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1618: from 9 to 116

- Alignment No. 12775
- gi No. 4883746
- % Identity 89.8
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1618: from 9 to 116

- Alignment No. 12776
- gi No. 4883747
- % Identity 90.8
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1618: from 9 to 117

- Alignment No. 12777
- gi No. 4883748
- % Identity 90.8
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1618: from 9 to 117

- Alignment No. 12778
- gi No. 4883749
- % Identity 92.4
- Alignment Length 105
- Location of Alignment in SEQ ID NO 1618: from 13 to 117

- Alignment No. 12779
- gi No. 4883751
- % Identity 90.7
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1618: from 9 to 116

- Alignment No. 12780
- gi No. 4883752
- % Identity 90.7
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1618: from 10 to 117

- Alignment No. 12781
- gi No. 4883753
- % Identity 90.8
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1618: from 9 to 117

- Alignment No. 12782
- gi No. 4883754
- % Identity 89.7
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1618: from 9 to 115

- Alignment No. 12783
- gi No. 4883755
- % Identity 92.2
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1618: from 13 to 115

- Alignment No. 12784
- gi No. 4883756
- % Identity 90.8
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1618: from 9 to 117

- Alignment No. 12785
- gi No. 4883758
- % Identity 92.2
- Alignment Length 102
- Location of Alignment in SEQ ID NO 1618: from 13 to 114

- Alignment No. 12786
- gi No. 4883759
- % Identity 89.9
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1618: from 9 to 117

- Alignment No. 12787
- gi No. 4883760
- % Identity 89
- Alignment Length 109
- Location of Alignment in SEQ ID NO 1618: from 9 to 117

- Alignment No. 12788

- gi No. 4883762
- % Identity 89.8
- Alignment Length 108
- Location of Alignment in SEQ ID NO 1618: from 9 to 116

- Alignment No. 12789
- gi No. 488571
- % Identity 95.3
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1618: from 10 to 136

- Alignment No. 12790
- gi No. 488573
- % Identity 96
- Alignment Length 124
- Location of Alignment in SEQ ID NO 1618: from 13 to 136

- Alignment No. 12791
- gi No. 529954
- % Identity 81.4
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1618: from 1 to 136

- Alignment No. 12792
- gi No. 539427
- % Identity 91.7
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1618: from 2 to 49

- Alignment No. 12793
- gi No. 556612
- % Identity 83.1
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136

- Alignment No. 12794
- gi No. 559807
- % Identity 87.5
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136

- Alignment No. 12795
- gi No. 578470
- % Identity 90.3
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1618: from 61 to 132

- Alignment No. 12796
- gi No. 630475
- % Identity 86.8
- Alignment Length 76
- Location of Alignment in SEQ ID NO 1618: from 1 to 76

- Alignment No. 12797
- gi No. 630476
- % Identity 88.7
- Alignment Length 62
- Location of Alignment in SEQ ID NO 1618: from 1 to 62

- Alignment No. 12798
- gi No. 631693

- % Identity 91.4
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1618: from 79 to 136

- Alignment No. 12799
- gi No. 70743
- % Identity 91.9
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 2 to 136

- Alignment No. 12800
- gi No. 70747
- % Identity 91.1
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 2 to 136

- Alignment No. 12801
- gi No. 70748
- % Identity 90.4
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 2 to 136

- Alignment No. 12802
- gi No. 70749
- % Identity 91.9
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 2 to 136

- Alignment No. 12803
- gi No. 70753
- % Identity 94.1
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 2 to 136

- Alignment No. 12804
- gi No. 70755
- % Identity 88.1
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 2 to 136

- Alignment No. 12805
- gi No. 70760
- % Identity 77.8
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 2 to 136

- Alignment No. 12806
- gi No. 729676
- % Identity 86.7
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 1 to 135

- Alignment No. 12807
- gi No. 729677
- % Identity 83.7
- Alignment Length 135
- Location of Alignment in SEQ ID NO 1618: from 1 to 135

- Alignment No. 12808
- gi No. 81850
- % Identity 96.6

- Alignment Length 118
- Location of Alignment in SEQ ID NO 1618: from 19 to 136
- Alignment No. 12809
- gi No. 84300
- % Identity 82.9
- Alignment Length 41
- Location of Alignment in SEQ ID NO 1618: from 1 to 41
- Alignment No. 12810
- gi No. 84329
- % Identity 86.6
- Alignment Length 134
- Location of Alignment in SEQ ID NO 1618: from 2 to 135
- Alignment No. 12811
- gi No. 85000
- % Identity 92.2
- Alignment Length 115
- Location of Alignment in SEQ ID NO 1618: from 2 to 116
- Alignment No. 12812
- gi No. 85001
- % Identity 89.7
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
- Alignment No. 12813
- gi No. 90622
- % Identity 91.2
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1618: from 1 to 136
- Alignment No. 12814
- gi No. 995959
- % Identity 85
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1618: from 1 to 40
- Alignment No. 12815
- gi No. 99980
- % Identity 93.8
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1618: from 85 to 116
- Alignment No. 12816
- gi No. 99980
- % Identity 93.2
- Alignment Length 44
- Location of Alignment in SEQ ID NO 1618: from 2 to 45
- Alignment No. 12817
- gi No. 99981
- % Identity 94.1
- Alignment Length 51
- Location of Alignment in SEQ ID NO 1618: from 2 to 52

Maximum Length Sequence corresponding to clone ID 269337

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 1619
 - Ceres seq_id 1500758

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1620
 - Ceres seq_id 1500759
 - Location of start within SEQ ID NO 1619: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12818
- Dihydroorotase-like
- Location within SEQ ID NO 1620: from 103 to 493 aa.

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1621
 - Ceres seq_id 1500760
 - Location of start within SEQ ID NO 1619: at 19 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12819
- Dihydroorotase-like
- Location within SEQ ID NO 1621: from 97 to 487 aa.

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1622
 - Ceres seq_id 1500761
 - Location of start within SEQ ID NO 1619: at 310 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12820
- Dihydroorotase-like
- Location within SEQ ID NO 1622: from 1 to 390 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 269402

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1623
- Ceres seq_id 1500766

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1624
- Ceres seq_id 1500767
- Location of start within SEQ ID NO 1623: at 519 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12821
- Fatty acid desaturase
- Location within SEQ ID NO 1624: from 1 to 111 aa.

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1625
 - Ceres seq_id 1500768
 - Location of start within SEQ ID NO 1623: at 558 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 12822
- Fatty acid desaturase
- Location within SEQ ID NO 1625: from 1 to 98 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1626
- Ceres seq_id 1500769
- Location of start within SEQ ID NO 1623: at 582 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 12823
- Fatty acid desaturase
- Location within SEQ ID NO 1626: from 1 to 90 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 269483

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1627
- Ceres seq_id 1500778

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1628
- Ceres seq_id 1500779
- Location of start within SEQ ID NO 1627: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 12824
- Peroxidase
- Location within SEQ ID NO 1628: from 59 to 221 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12825
- gi No. 2342726
- % Identity 99.5
- Alignment Length 215
- Location of Alignment in SEQ ID NO 1628: from 7 to 221
- Alignment No. 12826
- gi No. 3643121
- % Identity 72.5
- Alignment Length 138
- Location of Alignment in SEQ ID NO 1628: from 84 to 221
- Alignment No. 12827
- gi No. 538502
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1628: from 210 to 221

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1629
- Ceres seq_id 1500780
- Location of start within SEQ ID NO 1627: at 19 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12828
- Peroxidase
- Location within SEQ ID NO 1629: from 53 to 215 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12829
- gi No. 2342726
- % Identity 99.5
- Alignment Length 215
- Location of Alignment in SEQ ID NO 1629: from 1 to 215
- Alignment No. 12830
- gi No. 3643121
- % Identity 72.5
- Alignment Length 138
- Location of Alignment in SEQ ID NO 1629: from 78 to 215
- Alignment No. 12831
- gi No. 538502
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1629: from 204 to 215

Maximum Length Sequence corresponding to clone ID 269542

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1630
- Ceres seq_id 1500785

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1631
- Ceres seq_id 1500786
- Location of start within SEQ ID NO 1630: at 412 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12832
- gi No. 2827535
- % Identity 94.7
- Alignment Length 281
- Location of Alignment in SEQ ID NO 1631: from 1 to 172

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1632
- Ceres seq_id 1500787
- Location of start within SEQ ID NO 1630: at 490 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12833
- gi No. 2827535
- % Identity 94.7
- Alignment Length 281
- Location of Alignment in SEQ ID NO 1632: from 1 to 146

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1633
- Ceres seq_id 1500788
- Location of start within SEQ ID NO 1630: at 547 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 12834
 - gi No. 2827535
 - % Identity 94.7
 - Alignment Length 281
 - Location of Alignment in SEQ ID NO 1633: from 1 to 127

Maximum Length Sequence corresponding to clone ID 269578

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1634
- Ceres seq_id 1500793

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1635
- Ceres seq_id 1500794
- Location of start within SEQ ID NO 1634: at 52 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 12835
 - gi No. 4220523
 - % Identity 91.4
 - Alignment Length 454
 - Location of Alignment in SEQ ID NO 1635: from 1 to 254

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1636
- Ceres seq_id 1500795
- Location of start within SEQ ID NO 1634: at 88 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 12836
 - gi No. 4220523
 - % Identity 91.4
 - Alignment Length 454
 - Location of Alignment in SEQ ID NO 1636: from 1 to 242

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1637
- Ceres seq_id 1500796
- Location of start within SEQ ID NO 1634: at 835 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 12837
 - gi No. 4220523
 - % Identity 91.4
 - Alignment Length 454
 - Location of Alignment in SEQ ID NO 1637: from 1 to 179

Maximum Length Sequence corresponding to clone ID 269582

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1638
- Ceres seq_id 1500797

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1639
- Ceres seq_id 1500798
- Location of start within SEQ ID NO 1638: at 87 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12838
- Iron/Ascorbate oxidoreductase family
- Location within SEQ ID NO 1639: from 11 to 272 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1640
- Ceres seq_id 1500799
- Location of start within SEQ ID NO 1638: at 420 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12839
- Iron/Ascorbate oxidoreductase family
- Location within SEQ ID NO 1640: from 1 to 161 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1641
- Ceres seq_id 1500800
- Location of start within SEQ ID NO 1638: at 462 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12840
- Iron/Ascorbate oxidoreductase family
- Location within SEQ ID NO 1641: from 1 to 147 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 269610

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1642
- Ceres seq_id 1500801

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1643
- Ceres seq_id 1500802
- Location of start within SEQ ID NO 1642: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12841
- Polyphenyl synthetases
- Location within SEQ ID NO 1643: from 1 to 205 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12842
- gi No. 4836881
- % Identity 99.5
- Alignment Length 206
- Location of Alignment in SEQ ID NO 1643: from 1 to 205

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1644
- Ceres seq_id 1500803
- Location of start within SEQ ID NO 1642: at 29 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12843
- Polyprenyl synthetases
- Location within SEQ ID NO 1644: from 1 to 196 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12844
- gi No. 4836881
- % Identity 99.5
- Alignment Length 206
- Location of Alignment in SEQ ID NO 1644: from 1 to 196

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1645
- Ceres seq_id 1500804
- Location of start within SEQ ID NO 1642: at 80 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12845
- Polyprenyl synthetases
- Location within SEQ ID NO 1645: from 1 to 179 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12846
- gi No. 4836881
- % Identity 99.5
- Alignment Length 206
- Location of Alignment in SEQ ID NO 1645: from 1 to 179

Maximum Length Sequence corresponding to clone ID 269714

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1646
- Ceres seq_id 1500805

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1647
- Ceres seq_id 1500806
- Location of start within SEQ ID NO 1646: at 412 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12847
- gi No. 2832658
- % Identity 70
- Alignment Length 51
- Location of Alignment in SEQ ID NO 1647: from 81 to 129

- Alignment No. 12848
- gi No. 2832658
- % Identity 96.4
- Alignment Length 196
- Location of Alignment in SEQ ID NO 1647: from 198 to 389

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1648

- Ceres seq_id 1500807
- Location of start within SEQ ID NO 1646: at 427 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12849
- gi No. 2832658
- % Identity 70
- Alignment Length 51
- Location of Alignment in SEQ ID NO 1648: from 76 to 124
- Alignment No. 12850
- gi No. 2832658
- % Identity 96.4
- Alignment Length 196
- Location of Alignment in SEQ ID NO 1648: from 193 to 384

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1649
- Ceres seq_id 1500808
- Location of start within SEQ ID NO 1646: at 556 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12851
- gi No. 2832658
- % Identity 70
- Alignment Length 51
- Location of Alignment in SEQ ID NO 1649: from 33 to 81
- Alignment No. 12852
- gi No. 2832658
- % Identity 96.4
- Alignment Length 196
- Location of Alignment in SEQ ID NO 1649: from 150 to 341

Maximum Length Sequence corresponding to clone ID 269772

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1650
- Ceres seq_id 1500809

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1651
- Ceres seq_id 1500810
- Location of start within SEQ ID NO 1650: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12853
- Glycosyl hydrolases family 17
- Location within SEQ ID NO 1651: from 59 to 179 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1652
- Ceres seq_id 1500811
- Location of start within SEQ ID NO 1650: at 92 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12854
- Glycosyl hydrolases family 17
- Location within SEQ ID NO 1652: from 29 to 149 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 269883

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1653
- Ceres seq_id 1500820

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1654
- Ceres seq_id 1500821
- Location of start within SEQ ID NO 1653: at 87 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12855
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1654: from 20 to 192 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12856
- gi No. 2129698
- % Identity 84.5
- Alignment Length 187
- Location of Alignment in SEQ ID NO 1654: from 7 to 192

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1655
- Ceres seq_id 1500822
- Location of start within SEQ ID NO 1653: at 111 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12857
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1655: from 12 to 184 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12858
- gi No. 2129698
- % Identity 84.5
- Alignment Length 187
- Location of Alignment in SEQ ID NO 1655: from 1 to 184

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1656
- Ceres seq_id 1500823
- Location of start within SEQ ID NO 1653: at 297 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12859
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1656: from 1 to 122 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12860

- gi No. 2129698
- % Identity 84.5
- Alignment Length 187
- Location of Alignment in SEQ ID NO 1656: from 1 to 122

Maximum Length Sequence corresponding to clone ID 270032

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1657
- Ceres seq_id 1500828

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1658
- Ceres seq_id 1500829
- Location of start within SEQ ID NO 1657: at 309 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12861
- EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase)
- Location within SEQ ID NO 1658: from 27 to 458 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12862
- gi No. 114165
- % Identity 77.1
- Alignment Length 493
- Location of Alignment in SEQ ID NO 1658: from 1 to 464

- Alignment No. 12863
- gi No. 114167
- % Identity 84.9
- Alignment Length 338
- Location of Alignment in SEQ ID NO 1658: from 127 to 464

- Alignment No. 12864
- gi No. 114171
- % Identity 91.3
- Alignment Length 508
- Location of Alignment in SEQ ID NO 1658: from 1 to 464

- Alignment No. 12865
- gi No. 114174
- % Identity 77.9
- Alignment Length 493
- Location of Alignment in SEQ ID NO 1658: from 1 to 464

- Alignment No. 12866
- gi No. 114176
- % Identity 79.3
- Alignment Length 483
- Location of Alignment in SEQ ID NO 1658: from 1 to 464

- Alignment No. 12867
- gi No. 1351978
- % Identity 90.7
- Alignment Length 508
- Location of Alignment in SEQ ID NO 1658: from 1 to 464

- Alignment No. 12868
- gi No. 1524383
- % Identity 82.6
- Alignment Length 443

- Location of Alignment in SEQ ID NO 1658: from 22 to 464
- Alignment No. 12869
- gi No. 2583124
- % Identity 91.1
- Alignment Length 508
- Location of Alignment in SEQ ID NO 1658: from 1 to 464
- Alignment No. 12870
- gi No. 3410961
- % Identity 81.1
- Alignment Length 391
- Location of Alignment in SEQ ID NO 1658: from 74 to 464
- Alignment No. 12871
- gi No. 66618
- % Identity 90.9
- Alignment Length 508
- Location of Alignment in SEQ ID NO 1658: from 1 to 464
- Alignment No. 12872
- gi No. 66619
- % Identity 78.1
- Alignment Length 493
- Location of Alignment in SEQ ID NO 1658: from 1 to 464

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1659
- Ceres seq_id 1500830
- Location of start within SEQ ID NO 1657: at 528 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12873
- EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase)
- Location within SEQ ID NO 1659: from 1 to 385 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12874
- gi No. 114165
- % Identity 77.1
- Alignment Length 493
- Location of Alignment in SEQ ID NO 1659: from 1 to 391
- Alignment No. 12875
- gi No. 114167
- % Identity 84.9
- Alignment Length 338
- Location of Alignment in SEQ ID NO 1659: from 54 to 391
- Alignment No. 12876
- gi No. 114171
- % Identity 91.3
- Alignment Length 508
- Location of Alignment in SEQ ID NO 1659: from 1 to 391
- Alignment No. 12877
- gi No. 114174
- % Identity 77.9
- Alignment Length 493
- Location of Alignment in SEQ ID NO 1659: from 1 to 391

- Alignment No. 12878
- gi No. 114176
- % Identity 79.3
- Alignment Length 483
- Location of Alignment in SEQ ID NO 1659: from 1 to 391

- Alignment No. 12879
- gi No. 1351978
- % Identity 90.7
- Alignment Length 508
- Location of Alignment in SEQ ID NO 1659: from 1 to 391

- Alignment No. 12880
- gi No. 1524383
- % Identity 82.6
- Alignment Length 443
- Location of Alignment in SEQ ID NO 1659: from 1 to 391

- Alignment No. 12881
- gi No. 2583124
- % Identity 91.1
- Alignment Length 508
- Location of Alignment in SEQ ID NO 1659: from 1 to 391

- Alignment No. 12882
- gi No. 3410961
- % Identity 81.1
- Alignment Length 391
- Location of Alignment in SEQ ID NO 1659: from 1 to 391

- Alignment No. 12883
- gi No. 66618
- % Identity 90.9
- Alignment Length 508
- Location of Alignment in SEQ ID NO 1659: from 1 to 391

- Alignment No. 12884
- gi No. 66619
- % Identity 78.1
- Alignment Length 493
- Location of Alignment in SEQ ID NO 1659: from 1 to 391

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1660
- Ceres seq_id 1500831
- Location of start within SEQ ID NO 1657: at 678 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12885
- EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase)
- Location within SEQ ID NO 1660: from 1 to 335 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12886
- gi No. 114165
- % Identity 77.1
- Alignment Length 493
- Location of Alignment in SEQ ID NO 1660: from 1 to 341

- Alignment No. 12887
- gi No. 114167
- % Identity 84.9
- Alignment Length 338
- Location of Alignment in SEQ ID NO 1660: from 4 to 341
- Alignment No. 12888
- gi No. 114171
- % Identity 91.3
- Alignment Length 508
- Location of Alignment in SEQ ID NO 1660: from 1 to 341
- Alignment No. 12889
- gi No. 114174
- % Identity 77.9
- Alignment Length 493
- Location of Alignment in SEQ ID NO 1660: from 1 to 341
- Alignment No. 12890
- gi No. 114176
- % Identity 79.3
- Alignment Length 483
- Location of Alignment in SEQ ID NO 1660: from 1 to 341
- Alignment No. 12891
- gi No. 1351978
- % Identity 90.7
- Alignment Length 508
- Location of Alignment in SEQ ID NO 1660: from 1 to 341
- Alignment No. 12892
- gi No. 1524383
- % Identity 82.6
- Alignment Length 443
- Location of Alignment in SEQ ID NO 1660: from 1 to 341
- Alignment No. 12893
- gi No. 2583124
- % Identity 91.1
- Alignment Length 508
- Location of Alignment in SEQ ID NO 1660: from 1 to 341
- Alignment No. 12894
- gi No. 3410961
- % Identity 81.1
- Alignment Length 391
- Location of Alignment in SEQ ID NO 1660: from 1 to 341
- Alignment No. 12895
- gi No. 66618
- % Identity 90.9
- Alignment Length 508
- Location of Alignment in SEQ ID NO 1660: from 1 to 341
- Alignment No. 12896
- gi No. 66619
- % Identity 78.1
- Alignment Length 493
- Location of Alignment in SEQ ID NO 1660: from 1 to 341

Maximum Length Sequence corresponding to clone ID 270102

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 1661
- Ceres seq_id 1500832
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 1662
- Ceres seq_id 1500833
- Location of start within SEQ ID NO 1661: at 298 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
- Alignment No. 12897
- UDP-glucuronosyl and UDP-glucosyl transferases
- Location within SEQ ID NO 1662: from 183 to 292 aa.
- (D) Related Amino Acid Sequences
- Alignment No. 12898
- gi No. 3582342
- % Identity 84.5
- Alignment Length 291
- Location of Alignment in SEQ ID NO 1662: from 2 to 292
- Alignment No. 12899
- gi No. 3582343
- % Identity 99.3
- Alignment Length 291
- Location of Alignment in SEQ ID NO 1662: from 2 to 292
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 1663
- Ceres seq_id 1500834
- Location of start within SEQ ID NO 1661: at 349 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
- Alignment No. 12900
- UDP-glucuronosyl and UDP-glucosyl transferases
- Location within SEQ ID NO 1663: from 166 to 275 aa.
- (D) Related Amino Acid Sequences
- Alignment No. 12901
- gi No. 3582342
- % Identity 84.5
- Alignment Length 291
- Location of Alignment in SEQ ID NO 1663: from 1 to 275
- Alignment No. 12902
- gi No. 3582343
- % Identity 99.3
- Alignment Length 291
- Location of Alignment in SEQ ID NO 1663: from 1 to 275
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 1664
- Ceres seq_id 1500835
- Location of start within SEQ ID NO 1661: at 424 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
- Alignment No. 12903
- UDP-glucuronosyl and UDP-glucosyl transferases
- Location within SEQ ID NO 1664: from 141 to 250 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12904
- gi No. 3582342
- % Identity 84.5
- Alignment Length 291
- Location of Alignment in SEQ ID NO 1664: from 1 to 250
- Alignment No. 12905
- gi No. 3582343
- % Identity 99.3
- Alignment Length 291
- Location of Alignment in SEQ ID NO 1664: from 1 to 250

Maximum Length Sequence corresponding to clone ID 270115

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1665
- Ceres seq_id 1500836

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1666
- Ceres seq_id 1500837
- Location of start within SEQ ID NO 1665: at 35 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12906
- pfkB family carbohydrate kinase
- Location within SEQ ID NO 1666: from 59 to 124 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1667
- Ceres seq_id 1500838
- Location of start within SEQ ID NO 1665: at 275 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 270512

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1668
- Ceres seq_id 1500847

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1669
- Ceres seq_id 1500848
- Location of start within SEQ ID NO 1668: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12907
- gi No. 2341040
- % Identity 97
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1669: from 12 to 111

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1670
- Ceres seq_id 1500849

- Location of start within SEQ ID NO 1668: at 35 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12908
- gi No. 2341040
- % Identity 97
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1670: from 1 to 100

Maximum Length Sequence corresponding to clone ID 270714

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1671
- Ceres seq_id 1500854

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1672
- Ceres seq_id 1500855
- Location of start within SEQ ID NO 1671: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12909
- gi No. 4115376
- % Identity 97.7
- Alignment Length 132
- Location of Alignment in SEQ ID NO 1672: from 1 to 132

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1673
- Ceres seq_id 1500856
- Location of start within SEQ ID NO 1671: at 62 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12910
- gi No. 4115376
- % Identity 97.7
- Alignment Length 132
- Location of Alignment in SEQ ID NO 1673: from 1 to 112

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1674
- Ceres seq_id 1500857
- Location of start within SEQ ID NO 1671: at 95 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12911
- gi No. 4115376
- % Identity 97.7
- Alignment Length 132
- Location of Alignment in SEQ ID NO 1674: from 1 to 101

Maximum Length Sequence corresponding to clone ID 271327

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1675
- Ceres seq_id 1500862

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1676
 - Ceres seq_id 1500863
 - Location of start within SEQ ID NO 1675: at 303 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 12912
 - gi No. 3063449
 - % Identity 100
 - Alignment Length 134
 - Location of Alignment in SEQ ID NO 1676: from 1 to 103

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1677
 - Ceres seq_id 1500864
 - Location of start within SEQ ID NO 1675: at 309 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 12913
 - gi No. 3063449
 - % Identity 100
 - Alignment Length 134
 - Location of Alignment in SEQ ID NO 1677: from 1 to 101

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1678
 - Ceres seq_id 1500865
 - Location of start within SEQ ID NO 1675: at 360 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 12914
 - gi No. 3063449
 - % Identity 100
 - Alignment Length 134
 - Location of Alignment in SEQ ID NO 1678: from 1 to 84

Maximum Length Sequence corresponding to clone ID 271605

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1679
 - Ceres seq_id 1500866
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1680
 - Ceres seq_id 1500867
 - Location of start within SEQ ID NO 1679: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 12915
 - gi No. 1350720
 - % Identity 97.3
 - Alignment Length 111
 - Location of Alignment in SEQ ID NO 1680: from 25 to 135
- Alignment No. 12916

- gi No. 1710539
- % Identity 81
- Alignment Length 42
- Location of Alignment in SEQ ID NO 1680: from 114 to 155
- Alignment No. 12917
- gi No. 3885519
- % Identity 88.6
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1680: from 121 to 155

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1681
- Ceres seq_id 1500868
- Location of start within SEQ ID NO 1679: at 69 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12918
- gi No. 1350720
- % Identity 97.3
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1681: from 3 to 113
- Alignment No. 12919
- gi No. 1710539
- % Identity 81
- Alignment Length 42
- Location of Alignment in SEQ ID NO 1681: from 92 to 133
- Alignment No. 12920
- gi No. 3885519
- % Identity 88.6
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1681: from 99 to 133

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1682
- Ceres seq_id 1500869
- Location of start within SEQ ID NO 1679: at 195 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12921
- gi No. 1350720
- % Identity 97.3
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1682: from 1 to 71
- Alignment No. 12922
- gi No. 1710539
- % Identity 81
- Alignment Length 42
- Location of Alignment in SEQ ID NO 1682: from 50 to 91
- Alignment No. 12923
- gi No. 3885519
- % Identity 88.6
- Alignment Length 35

- Location of Alignment in SEQ ID NO 1682: from 57 to 91

Maximum Length Sequence corresponding to clone ID 272234

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1683
- Ceres seq_id 1500877

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1684
- Ceres seq_id 1500878
- Location of start within SEQ ID NO 1683: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12924
- Zinc-binding dehydrogenases
- Location within SEQ ID NO 1684: from 66 to 160 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1685
- Ceres seq_id 1500879
- Location of start within SEQ ID NO 1683: at 125 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12925
- Zinc-binding dehydrogenases
- Location within SEQ ID NO 1685: from 25 to 119 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1686
- Ceres seq_id 1500880
- Location of start within SEQ ID NO 1683: at 209 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12926
- Zinc-binding dehydrogenases
- Location within SEQ ID NO 1686: from 1 to 91 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272243

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1687
- Ceres seq_id 1500881

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1688
- Ceres seq_id 1500882
- Location of start within SEQ ID NO 1687: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1689
- Ceres seq_id 1500883

- Location of start within SEQ ID NO 1687: at 115 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12927
- Biotin-requiring enzymes
- Location within SEQ ID NO 1689: from 75 to 139 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12928
- gi No. 4210332
- % Identity 74.7
- Alignment Length 79
- Location of Alignment in SEQ ID NO 1689: from 61 to 139
- Alignment No. 12929
- gi No. 4455214
- % Identity 76.7
- Alignment Length 60
- Location of Alignment in SEQ ID NO 1689: from 72 to 131

Maximum Length Sequence corresponding to clone ID 272277

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1690
- Ceres seq_id 1500884

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1691
- Ceres seq_id 1500885
- Location of start within SEQ ID NO 1690: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1692
- Ceres seq_id 1500886
- Location of start within SEQ ID NO 1690: at 63 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12930
- Mucin-like glycoprotein
- Location within SEQ ID NO 1692: from 25 to 90 aa.

- Alignment No. 12931
- Mucin-like glycoprotein
- Location within SEQ ID NO 1692: from 33 to 90 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1693
- Ceres seq_id 1500887
- Location of start within SEQ ID NO 1690: at 275 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 272304

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1694
- Ceres seq_id 1500888

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1695
- Ceres seq_id 1500889
- Location of start within SEQ ID NO 1694: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12932
- Protein phosphatase 2C
- Location within SEQ ID NO 1695: from 133 to 195 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12933
- gi No. 1914851
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1695: from 57 to 68
- Alignment No. 12934
- gi No. 3281853
- % Identity 75
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1695: from 126 to 196
- Alignment No. 12935
- gi No. 4808585
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1695: from 59 to 69

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1696
- Ceres seq_id 1500890
- Location of start within SEQ ID NO 1694: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1697
- Ceres seq_id 1500891
- Location of start within SEQ ID NO 1694: at 154 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12936
- Protein phosphatase 2C
- Location within SEQ ID NO 1697: from 82 to 144 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12937
- gi No. 1914851
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1697: from 6 to 17
- Alignment No. 12938

- gi No. 3281853
- % Identity 75
- Alignment Length 72
- Location of Alignment in SEQ ID NO 1697: from 75 to 145
- Alignment No. 12939
- gi No. 4808585
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1697: from 8 to 18

Maximum Length Sequence corresponding to clone ID 272501

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1698
- Ceres seq_id 1500900

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1699
- Ceres seq_id 1500901
- Location of start within SEQ ID NO 1698: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12940
- gi No. 2130028
- % Identity 87.5
- Alignment Length 64
- Location of Alignment in SEQ ID NO 1699: from 27 to 90
- Alignment No. 12941
- gi No. 2293568
- % Identity 93.7
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1699: from 28 to 90
- Alignment No. 12942
- gi No. 4530585
- % Identity 80.6
- Alignment Length 62
- Location of Alignment in SEQ ID NO 1699: from 29 to 90
- Alignment No. 12943
- gi No. 5541720
- % Identity 78
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1699: from 27 to 85

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1700
- Ceres seq_id 1500902
- Location of start within SEQ ID NO 1698: at 80 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12944
- gi No. 2130028
- % Identity 87.5
- Alignment Length 64
- Location of Alignment in SEQ ID NO 1700: from 1 to 64

- Alignment No. 12945
- gi No. 2293568
- % Identity 93.7
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1700: from 2 to 64
- Alignment No. 12946
- gi No. 4530585
- % Identity 80.6
- Alignment Length 62
- Location of Alignment in SEQ ID NO 1700: from 3 to 64
- Alignment No. 12947
- gi No. 5541720
- % Identity 78
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1700: from 1 to 59

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1701
- Ceres seq_id 1500903
- Location of start within SEQ ID NO 1698: at 286 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12948
- gi No. 3377850
- % Identity 70.7
- Alignment Length 82
- Location of Alignment in SEQ ID NO 1701: from 1 to 79

Maximum Length Sequence corresponding to clone ID 272512

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1702
- Ceres seq_id 1500907

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1703
- Ceres seq_id 1500908
- Location of start within SEQ ID NO 1702: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1704
- Ceres seq_id 1500909
- Location of start within SEQ ID NO 1702: at 161 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12949
- gi No. 1531758
- % Identity 75
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1704: from 6 to 52

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1705

- Ceres seq_id 1500910
- Location of start within SEQ ID NO 1702: at 316 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12950
- gi No. 1531758
- % Identity 71.2
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1705: from 1 to 49
- Alignment No. 12951
- gi No. 4803938
- % Identity 82.7
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1705: from 1 to 49

Maximum Length Sequence corresponding to clone ID 275375

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1706
- Ceres seq_id 1500915

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1707
- Ceres seq_id 1500916
- Location of start within SEQ ID NO 1706: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12952
- gi No. 3157951
- % Identity 97.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1707: from 147 to 181

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1708
- Ceres seq_id 1500917
- Location of start within SEQ ID NO 1706: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12953
- gi No. 462338
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1708: from 57 to 77

Maximum Length Sequence corresponding to clone ID 275391

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1709
- Ceres seq_id 1500926

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1710
- Ceres seq_id 1500927
- Location of start within SEQ ID NO 1709: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 12954
 - gi No. 2665536
 - % Identity 90.5
 - Alignment Length 179
 - Location of Alignment in SEQ ID NO 1710: from 33 to 209

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1711
 - Ceres seq_id 1500928
 - Location of start within SEQ ID NO 1709: at 227 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 12955
 - gi No. 2665536
 - % Identity 90.5
 - Alignment Length 179
 - Location of Alignment in SEQ ID NO 1711: from 1 to 134

Maximum Length Sequence corresponding to clone ID 275392

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1712
- Ceres seq_id 1500929

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1713
- Ceres seq_id 1500930
- Location of start within SEQ ID NO 1712: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12956
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1713: from 21 to 101 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1714
- Ceres seq_id 1500931
- Location of start within SEQ ID NO 1712: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1715
- Ceres seq_id 1500932
- Location of start within SEQ ID NO 1712: at 154 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 275421

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1716
- Ceres seq_id 1500945

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1717
- Ceres seq_id 1500946
- Location of start within SEQ ID NO 1716: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12957
- Hsp20/alpha crystallin family
- Location within SEQ ID NO 1717: from 34 to 126 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12958
- gi No. 3876261
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1717: from 113 to 126

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1718
- Ceres seq_id 1500947
- Location of start within SEQ ID NO 1716: at 72 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12959
- Hsp20/alpha crystallin family
- Location within SEQ ID NO 1718: from 11 to 103 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12960
- gi No. 3876261
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1718: from 90 to 103

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1719
- Ceres seq_id 1500948
- Location of start within SEQ ID NO 1716: at 116 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 275764

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1720
- Ceres seq_id 1500953

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1721
- Ceres seq_id 1500954
- Location of start within SEQ ID NO 1720: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12961
- Beta-ketoacyl synthase
- Location within SEQ ID NO 1721: from 93 to 172 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12962

- gi No. 119784
- % Identity 75.4
- Alignment Length 118
- Location of Alignment in SEQ ID NO 1721: from 58 to 172
- Alignment No. 12963
- gi No. 294668
- % Identity 83.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1721: from 78 to 172

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1722
- Ceres seq_id 1500955
- Location of start within SEQ ID NO 1720: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1723
- Ceres seq_id 1500956
- Location of start within SEQ ID NO 1720: at 133 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12964
- Beta-ketoacyl synthase
- Location within SEQ ID NO 1723: from 49 to 128 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12965
- gi No. 119784
- % Identity 75.4
- Alignment Length 118
- Location of Alignment in SEQ ID NO 1723: from 14 to 128
- Alignment No. 12966
- gi No. 294668
- % Identity 83.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 1723: from 34 to 128

Maximum Length Sequence corresponding to clone ID 276068

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1724
- Ceres seq_id 1500963

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1725
- Ceres seq_id 1500964
- Location of start within SEQ ID NO 1724: at 95 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1726
- Ceres seq_id 1500965
- Location of start within SEQ ID NO 1724: at 113 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1727
- Ceres seq_id 1500966
- Location of start within SEQ ID NO 1724: at 141 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12967
- Mucin-like glycoprotein
- Location within SEQ ID NO 1727: from 1 to 56 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 276186

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1728
- Ceres seq_id 1500974

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1729
- Ceres seq_id 1500975
- Location of start within SEQ ID NO 1728: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12968
- gi No. 2425066
- % Identity 100
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1729: from 61 to 81

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1730
- Ceres seq_id 1500976
- Location of start within SEQ ID NO 1728: at 62 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1731
- Ceres seq_id 1500977
- Location of start within SEQ ID NO 1728: at 146 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 279386

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1732
- Ceres seq_id 1500985

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1733
- Ceres seq_id 1500986

- Location of start within SEQ ID NO 1732: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1734
- Ceres seq_id 1500987
- Location of start within SEQ ID NO 1732: at 209 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12969
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1734: from 12 to 77 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12970
- gi No. 1777312
- % Identity 71.4
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1734: from 1 to 77
- Alignment No. 12971
- gi No. 2980770
- % Identity 71.8
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1734: from 7 to 77
- Alignment No. 12972
- gi No. 3256035
- % Identity 70.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1734: from 1 to 77

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1735
- Ceres seq_id 1500988
- Location of start within SEQ ID NO 1732: at 233 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 12973
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1735: from 4 to 69 aa.

(D) Related Amino Acid Sequences

- Alignment No. 12974
- gi No. 1777312
- % Identity 71.4
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1735: from 1 to 69
- Alignment No. 12975
- gi No. 2980770
- % Identity 71.8
- Alignment Length 71
- Location of Alignment in SEQ ID NO 1735: from 1 to 69
- Alignment No. 12976

- gi No. 3256035
- % Identity 70.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1735: from 1 to 69

Maximum Length Sequence corresponding to clone ID 280780

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1736
- Ceres seq_id 1500992

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1737
- Ceres seq_id 1500993
- Location of start within SEQ ID NO 1736: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12977
- gi No. 1041702
- % Identity 77.8
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1737: from 92 to 153

- Alignment No. 12978
- gi No. 1778097
- % Identity 84.6
- Alignment Length 39
- Location of Alignment in SEQ ID NO 1737: from 92 to 130

- Alignment No. 12979
- gi No. 1778099
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1737: from 92 to 153

- Alignment No. 12980
- gi No. 1778101
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1737: from 92 to 153

- Alignment No. 12981
- gi No. 1778107
- % Identity 89.5
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1737: from 92 to 129

- Alignment No. 12982
- gi No. 1778109
- % Identity 90.9
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1737: from 92 to 124

- Alignment No. 12983
- gi No. 1815681
- % Identity 73
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1737: from 92 to 153

- Alignment No. 12984
- gi No. 3461833

- % Identity 73
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1737: from 92 to 153

- Alignment No. 12985
- gi No. 3510538
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1737: from 92 to 153

- Alignment No. 12986
- gi No. 3510540
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1737: from 92 to 153

- Alignment No. 12987
- gi No. 4027897
- % Identity 73
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1737: from 92 to 153

- Alignment No. 12988
- gi No. 4027899
- % Identity 73
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1737: from 92 to 153

- Alignment No. 12989
- gi No. 4138914
- % Identity 71.4
- Alignment Length 65
- Location of Alignment in SEQ ID NO 1737: from 92 to 153

- Alignment No. 12990
- gi No. 4138916
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1737: from 92 to 153

- Alignment No. 12991
- gi No. 5524700
- % Identity 73
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1737: from 92 to 153

- Alignment No. 12992
- gi No. 5714392
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1737: from 92 to 153

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1738
- Ceres seq_id 1500994
- Location of start within SEQ ID NO 1736: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appin. SEQ ID NO 1739
- Ceres seq_id 1500995
- Location of start within SEQ ID NO 1736: at 79 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 12993
- gi No. 1041702
- % Identity 77.8
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1739: from 66 to 127
- Alignment No. 12994
- gi No. 1778097
- % Identity 84.6
- Alignment Length 39
- Location of Alignment in SEQ ID NO 1739: from 66 to 104
- Alignment No. 12995
- gi No. 1778099
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1739: from 66 to 127
- Alignment No. 12996
- gi No. 1778101
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1739: from 66 to 127
- Alignment No. 12997
- gi No. 1778107
- % Identity 89.5
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1739: from 66 to 103
- Alignment No. 12998
- gi No. 1778109
- % Identity 90.9
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1739: from 66 to 98
- Alignment No. 12999
- gi No. 1815681
- % Identity 73
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1739: from 66 to 127
- Alignment No. 13000
- gi No. 3461833
- % Identity 73
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1739: from 66 to 127
- Alignment No. 13001
- gi No. 3510538
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1739: from 66 to 127

- Alignment No. 13002
- gi No. 3510540
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1739: from 66 to 127

- Alignment No. 13003
- gi No. 4027897
- % Identity 73
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1739: from 66 to 127

- Alignment No. 13004
- gi No. 4027899
- % Identity 73
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1739: from 66 to 127

- Alignment No. 13005
- gi No. 4138914
- % Identity 71.4
- Alignment Length 65
- Location of Alignment in SEQ ID NO 1739: from 66 to 127

- Alignment No. 13006
- gi No. 4138916
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1739: from 66 to 127

- Alignment No. 13007
- gi No. 5524700
- % Identity 73
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1739: from 66 to 127

- Alignment No. 13008
- gi No. 5714392
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 1739: from 66 to 127

Maximum Length Sequence corresponding to clone ID 280829

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1740
- Ceres seq_id 1501005

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1741
- Ceres seq_id 1501006
- Location of start within SEQ ID NO 1740: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1742
- Ceres seq_id 1501007
- Location of start within SEQ ID NO 1740: at 99 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13009
- Sugar (and other) transporter
- Location within SEQ ID NO 1742: from 33 to 111 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1743
- Ceres seq_id 1501008
- Location of start within SEQ ID NO 1740: at 213 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13010
- Sugar (and other) transporter
- Location within SEQ ID NO 1743: from 1 to 73 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 280866

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1744
- Ceres seq_id 1501016

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1745
- Ceres seq_id 1501017
- Location of start within SEQ ID NO 1744: at 100 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13011
- Histone-like transcription factors (CBF/NF-Y) and archaeal histones.
- Location within SEQ ID NO 1745: from 10 to 73 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1746
- Ceres seq_id 1501018
- Location of start within SEQ ID NO 1744: at 151 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13012
- Histone-like transcription factors (CBF/NF-Y) and archaeal histones.
- Location within SEQ ID NO 1746: from 1 to 56 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 281118

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1747
- Ceres seq_id 1501023

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1748
- Ceres seq_id 1501024
- Location of start within SEQ ID NO 1747: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1749
- Ceres seq_id 1501025
- Location of start within SEQ ID NO 1747: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13013
- Lipase/Acylhydrolase with GDSL-like motif
- Location within SEQ ID NO 1749: from 96 to 148 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1750
- Ceres seq_id 1501026
- Location of start within SEQ ID NO 1747: at 165 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13014
- Lipase/Acylhydrolase with GDSL-like motif
- Location within SEQ ID NO 1750: from 42 to 94 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 281313

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1751
- Ceres seq_id 1501027

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1752
- Ceres seq_id 1501028
- Location of start within SEQ ID NO 1751: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13015
- gi No. 3153821
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1752: from 38 to 48

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1753
- Ceres seq_id 1501029
- Location of start within SEQ ID NO 1751: at 101 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 282233

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1754

- Ceres seq_id 1501037
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1755
 - Ceres seq_id 1501038
 - Location of start within SEQ ID NO 1754: at 148 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13016
- Adaptor complexes medium subunit family
- Location within SEQ ID NO 1755: from 8 to 121 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13017
- gi No. 2271477
- % Identity 95.9
- Alignment Length 122
- Location of Alignment in SEQ ID NO 1755: from 1 to 121

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1756
- Ceres seq_id 1501039
- Location of start within SEQ ID NO 1754: at 238 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13018
- Adaptor complexes medium subunit family
- Location within SEQ ID NO 1756: from 1 to 91 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13019
- gi No. 2271477
- % Identity 95.9
- Alignment Length 122
- Location of Alignment in SEQ ID NO 1756: from 1 to 91

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1757
- Ceres seq_id 1501040
- Location of start within SEQ ID NO 1754: at 256 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13020
- Adaptor complexes medium subunit family
- Location within SEQ ID NO 1757: from 1 to 85 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13021
- gi No. 2271477
- % Identity 95.9
- Alignment Length 122
- Location of Alignment in SEQ ID NO 1757: from 1 to 85

Maximum Length Sequence corresponding to clone ID 282427

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1758
- Ceres seq_id 1501058

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1759

- Ceres seq_id 1501059
- Location of start within SEQ ID NO 1758: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1760
- Ceres seq_id 1501060
- Location of start within SEQ ID NO 1758: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13022
- Mucin-like glycoprotein
- Location within SEQ ID NO 1760: from 20 to 133 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1761
- Ceres seq_id 1501061
- Location of start within SEQ ID NO 1758: at 91 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 282587

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1762
- Ceres seq_id 1501090

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1763
- Ceres seq_id 1501091
- Location of start within SEQ ID NO 1762: at 156 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13023
- BAH domain
- Location within SEQ ID NO 1763: from 30 to 115 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13024
- gi No. 3046693
- % Identity 78.2
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1763: from 30 to 115
- Alignment No. 13025
- gi No. 3377844
- % Identity 76.1
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1763: from 29 to 115

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1764
- Ceres seq_id 1501092
- Location of start within SEQ ID NO 1762: at 165 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13026
- BAH domain
- Location within SEQ ID NO 1764: from 27 to 112 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13027
- gi No. 3046693
- % Identity 78.2
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1764: from 27 to 112
- Alignment No. 13028
- gi No. 3377844
- % Identity 76.1
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1764: from 26 to 112

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1765
- Ceres seq_id 1501093
- Location of start within SEQ ID NO 1762: at 258 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13029
- BAH domain
- Location within SEQ ID NO 1765: from 1 to 81 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13030
- gi No. 3046693
- % Identity 78.2
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1765: from 1 to 81
- Alignment No. 13031
- gi No. 3377844
- % Identity 76.1
- Alignment Length 88
- Location of Alignment in SEQ ID NO 1765: from 1 to 81

Maximum Length Sequence corresponding to clone ID 282710

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1766
- Ceres seq_id 1501115

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1767
- Ceres seq_id 1501116
- Location of start within SEQ ID NO 1766: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13032
- gi No. 1742961
- % Identity 73.5
- Alignment Length 49
- Location of Alignment in SEQ ID NO 1767: from 43 to 91

- Alignment No. 13033
- gi No. 1791309
- % Identity 73.5
- Alignment Length 49
- Location of Alignment in SEQ ID NO 1767: from 43 to 91

- Alignment No. 13034
- gi No. 2198851
- % Identity 89
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1767: from 33 to 105

- Alignment No. 13035
- gi No. 2198851
- % Identity 73.8
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1767: from 80 to 107

- Alignment No. 13036
- gi No. 2198853
- % Identity 89
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1767: from 33 to 105

- Alignment No. 13037
- gi No. 2198853
- % Identity 73.8
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1767: from 80 to 107

- Alignment No. 13038
- gi No. 4959932
- % Identity 75.5
- Alignment Length 49
- Location of Alignment in SEQ ID NO 1767: from 45 to 91

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1768
- Ceres seq_id 1501117
- Location of start within SEQ ID NO 1766: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1769
- Ceres seq_id 1501118
- Location of start within SEQ ID NO 1766: at 97 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13039
- gi No. 1742961
- % Identity 73.5
- Alignment Length 49
- Location of Alignment in SEQ ID NO 1769: from 11 to 59

- Alignment No. 13040

- gi No. 1791309
- % Identity 73.5
- Alignment Length 49
- Location of Alignment in SEQ ID NO 1769: from 11 to 59

- Alignment No. 13041
- gi No. 2198851
- % Identity 89
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1769: from 1 to 73

- Alignment No. 13042
- gi No. 2198851
- % Identity 73.8
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1769: from 48 to 75

- Alignment No. 13043
- gi No. 2198853
- % Identity 89
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1769: from 1 to 73

- Alignment No. 13044
- gi No. 2198853
- % Identity 73.8
- Alignment Length 103
- Location of Alignment in SEQ ID NO 1769: from 48 to 75

- Alignment No. 13045
- gi No. 4959932
- % Identity 75.5
- Alignment Length 49
- Location of Alignment in SEQ ID NO 1769: from 13 to 59

Maximum Length Sequence corresponding to clone ID 282723

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1770
- Ceres seq_id 1501119

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1771
- Ceres seq_id 1501120
- Location of start within SEQ ID NO 1770: at 239 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13046
- Clathrin adaptor complex small chain
- Location within SEQ ID NO 1771: from 1 to 76 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1772
- Ceres seq_id 1501121
- Location of start within SEQ ID NO 1770: at 254 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13047
- Clathrin adaptor complex small chain

- Location within SEQ ID NO 1772: from 1 to 71 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1773
- Ceres seq_id 1501122
- Location of start within SEQ ID NO 1770: at 492 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13048
- Clathrin adaptor complex small chain
- Location within SEQ ID NO 1773: from 1 to 63 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13049
- gi No. 4835237
- % Identity 72.2
- Alignment Length 79
- Location of Alignment in SEQ ID NO 1773: from 1 to 61

Maximum Length Sequence corresponding to clone ID 282725

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1774
- Ceres seq_id 1501123

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1775
- Ceres seq_id 1501124
- Location of start within SEQ ID NO 1774: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1776
- Ceres seq_id 1501125
- Location of start within SEQ ID NO 1774: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13050
- gi No. 2688824
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1776: from 74 to 111

Maximum Length Sequence corresponding to clone ID 282757

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1777
- Ceres seq_id 1501137

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1778
- Ceres seq_id 1501138
- Location of start within SEQ ID NO 1777: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13051
- gi No. 103249
- % Identity 71
- Alignment Length 69
- Location of Alignment in SEQ ID NO 1778: from 90 to 157

- Alignment No. 13052
- gi No. 130831
- % Identity 71
- Alignment Length 69
- Location of Alignment in SEQ ID NO 1778: from 90 to 157

- Alignment No. 13053
- gi No. 1346784
- % Identity 77.6
- Alignment Length 67
- Location of Alignment in SEQ ID NO 1778: from 92 to 157

- Alignment No. 13054
- gi No. 2511580
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1778: from 89 to 157

- Alignment No. 13055
- gi No. 2529567
- % Identity 71
- Alignment Length 69
- Location of Alignment in SEQ ID NO 1778: from 90 to 157

- Alignment No. 13056
- gi No. 266839
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1778: from 89 to 157

- Alignment No. 13057
- gi No. 3024432
- % Identity 95.7
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1778: from 89 to 157

- Alignment No. 13058
- gi No. 3334299
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1778: from 89 to 157

- Alignment No. 13059
- gi No. 3421082
- % Identity 94.3
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1778: from 89 to 157

- Alignment No. 13060
- gi No. 3805978
- % Identity 77.6
- Alignment Length 67
- Location of Alignment in SEQ ID NO 1778: from 92 to 157

- Alignment No. 13061

- gi No. 3874776
- % Identity 71.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1778: from 89 to 157

- Alignment No. 13062
- gi No. 4092058
- % Identity 77.6
- Alignment Length 67
- Location of Alignment in SEQ ID NO 1778: from 92 to 157

- Alignment No. 13063
- gi No. 4506189
- % Identity 77.6
- Alignment Length 67
- Location of Alignment in SEQ ID NO 1778: from 92 to 157

- Alignment No. 13064
- gi No. 4586592
- % Identity 91.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 1778: from 89 to 157

- Alignment No. 13065
- gi No. 464459
- % Identity 82.6
- Alignment Length 69
- Location of Alignment in SEQ ID NO 1778: from 90 to 157

- Alignment No. 13066
- gi No. 485265
- % Identity 77.6
- Alignment Length 67
- Location of Alignment in SEQ ID NO 1778: from 92 to 157

Maximum Length Sequence corresponding to clone ID 282828

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1779
- Ceres seq_id 1501139

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1780
- Ceres seq_id 1501140
- Location of start within SEQ ID NO 1779: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13067
- Fatty acid desaturase
- Location within SEQ ID NO 1780: from 93 to 144 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13068
- gi No. 2194093
- % Identity 71.7
- Alignment Length 46
- Location of Alignment in SEQ ID NO 1780: from 99 to 144

- Alignment No. 13069
- gi No. 533082
- % Identity 71.2
- Alignment Length 52

- Location of Alignment in SEQ ID NO 1780: from 93 to 144

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1781
- Ceres seq_id 1501141
- Location of start within SEQ ID NO 1779: at 161 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13070
- Fatty acid desaturase
- Location within SEQ ID NO 1781: from 40 to 91 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13071
- gi No. 2194093
- % Identity 71.7
- Alignment Length 46
- Location of Alignment in SEQ ID NO 1781: from 46 to 91
- Alignment No. 13072
- gi No. 533082
- % Identity 71.2
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1781: from 40 to 91

Maximum Length Sequence corresponding to clone ID 282832

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1782
- Ceres seq_id 1501142

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1783
- Ceres seq_id 1501143
- Location of start within SEQ ID NO 1782: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1784
- Ceres seq_id 1501144
- Location of start within SEQ ID NO 1782: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1785
- Ceres seq_id 1501145
- Location of start within SEQ ID NO 1782: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13073
- gi No. 2358287
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1785: from 38 to 48

- Alignment No. 13074
- gi No. 3928704
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1785: from 10 to 23
- Alignment No. 13075
- gi No. 4508019
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1785: from 10 to 23
- Alignment No. 13076
- gi No. 545067
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1785: from 139 to 151

Maximum Length Sequence corresponding to clone ID 282932

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1786
- Ceres seq_id 1501163

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1787
- Ceres seq_id 1501164
- Location of start within SEQ ID NO 1786: at 139 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13077
- Histone deacetylase family
- Location within SEQ ID NO 1787: from 26 to 113 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13078
- gi No. 3023945
- % Identity 83.2
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1787: from 8 to 113

- Alignment No. 13079
- gi No. 3023947
- % Identity 95.6
- Alignment Length 114
- Location of Alignment in SEQ ID NO 1787: from 1 to 113

- Alignment No. 13080
- gi No. 4467119
- % Identity 84.1
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1787: from 8 to 113

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1788
- Ceres seq_id 1501165
- Location of start within SEQ ID NO 1786: at 268 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13081

- Histone deacetylase family
- Location within SEQ ID NO 1788: from 1 to 70 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13082
- gi No. 3023945
- % Identity 83.2
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1788: from 1 to 70
- Alignment No. 13083
- gi No. 3023947
- % Identity 95.6
- Alignment Length 114
- Location of Alignment in SEQ ID NO 1788: from 1 to 70
- Alignment No. 13084
- gi No. 4467119
- % Identity 84.1
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1788: from 1 to 70

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1789
- Ceres seq_id 1501166
- Location of start within SEQ ID NO 1786: at 289 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13085
- Histone deacetylase family
- Location within SEQ ID NO 1789: from 1 to 63 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13086
- gi No. 3023945
- % Identity 83.2
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1789: from 1 to 63
- Alignment No. 13087
- gi No. 3023947
- % Identity 95.6
- Alignment Length 114
- Location of Alignment in SEQ ID NO 1789: from 1 to 63
- Alignment No. 13088
- gi No. 4467119
- % Identity 84.1
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1789: from 1 to 63

Maximum Length Sequence corresponding to clone ID 283094

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1790
- Ceres seq_id 1501167

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1791
- Ceres seq_id 1501168
- Location of start within SEQ ID NO 1790: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13089
- gi No. 1170404
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1791: from 46 to 58

- Alignment No. 13090
- gi No. 1170404
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1791: from 44 to 58

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1792
- Ceres seq_id 1501169
- Location of start within SEQ ID NO 1790: at 30 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13091
- gi No. 1170404
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1792: from 37 to 49

- Alignment No. 13092
- gi No. 1170404
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1792: from 35 to 49

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1793
- Ceres seq_id 1501170
- Location of start within SEQ ID NO 1790: at 186 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 283333

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1794
- Ceres seq_id 1501203

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1795
- Ceres seq_id 1501204
- Location of start within SEQ ID NO 1794: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1796
- Ceres seq_id 1501205
- Location of start within SEQ ID NO 1794: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13093
- gi No. 102427
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1796: from 18 to 31

- Alignment No. 13094
- gi No. 102427
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1796: from 18 to 31

- Alignment No. 13095
- gi No. 4467884
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1796: from 19 to 29

- Alignment No. 13096
- gi No. 5123787
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 1796: from 17 to 31

- Alignment No. 13097
- gi No. 553165
- % Identity 92.9
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1796: from 18 to 31

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1797
- Ceres seq_id 1501206
- Location of start within SEQ ID NO 1794: at 146 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 283840

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1798
- Ceres seq_id 1501245

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1799
- Ceres seq_id 1501246
- Location of start within SEQ ID NO 1798: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13098
- gi No. 322759
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1799: from 15 to 25

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1800
 - Ceres seq_id 1501247
 - Location of start within SEQ ID NO 1798: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 13099
 - gi No. 688080
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 1800: from 93 to 103
 - Alignment No. 13100
 - gi No. 688080
 - % Identity 71.4
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 1800: from 90 to 103

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1801
 - Ceres seq_id 1501248
 - Location of start within SEQ ID NO 1798: at 226 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 283927

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1802
 - Ceres seq_id 1501259

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1803
 - Ceres seq_id 1501260
 - Location of start within SEQ ID NO 1802: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 13101
 - gi No. 1082871
 - % Identity 84.6
 - Alignment Length 26
 - Location of Alignment in SEQ ID NO 1803: from 28 to 53
 - Alignment No. 13102
 - gi No. 1352426
 - % Identity 84.6
 - Alignment Length 26
 - Location of Alignment in SEQ ID NO 1803: from 28 to 53
 - Alignment No. 13103
 - gi No. 1352427
 - % Identity 96.2
 - Alignment Length 26
 - Location of Alignment in SEQ ID NO 1803: from 28 to 53
 - Alignment No. 13104
 - gi No. 1794151

- % Identity 83.3
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1803: from 30 to 53

- Alignment No. 13105
- gi No. 2851524
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1803: from 28 to 53

- Alignment No. 13106
- gi No. 3024017
- % Identity 96.2
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1803: from 28 to 53

- Alignment No. 13107
- gi No. 3264536
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1803: from 28 to 53

- Alignment No. 13108
- gi No. 3746340
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1803: from 28 to 53

- Alignment No. 13109
- gi No. 3811355
- % Identity 75.9
- Alignment Length 29
- Location of Alignment in SEQ ID NO 1803: from 28 to 56

- Alignment No. 13110
- gi No. 4503499
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1803: from 28 to 53

- Alignment No. 13111
- gi No. 4587600
- % Identity 100
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1803: from 28 to 53

- Alignment No. 13112
- gi No. 4758254
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1803: from 28 to 53

- Alignment No. 13113
- gi No. 5690414
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1803: from 28 to 53

- Alignment No. 13114
- gi No. 626041
- % Identity 96

- Alignment Length 25
- Location of Alignment in SEQ ID NO 1803: from 29 to 53
- Alignment No. 13115
- gi No. 627817
- % Identity 84
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1803: from 29 to 53

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1804
- Ceres seq_id 1501261
- Location of start within SEQ ID NO 1802: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13116
- gi No. 1082871
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76
- Alignment No. 13117
- gi No. 1352426
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76
- Alignment No. 13118
- gi No. 1352427
- % Identity 100
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76
- Alignment No. 13119
- gi No. 1794151
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76
- Alignment No. 13120
- gi No. 2851524
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76
- Alignment No. 13121
- gi No. 3024017
- % Identity 95.5
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76
- Alignment No. 13122
- gi No. 3264536
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76
- Alignment No. 13123
- gi No. 3746340

- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76

- Alignment No. 13124
- gi No. 3811355
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1804: from 56 to 75

- Alignment No. 13125
- gi No. 4503499
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76

- Alignment No. 13126
- gi No. 4587600
- % Identity 95.5
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76

- Alignment No. 13127
- gi No. 4758254
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76

- Alignment No. 13128
- gi No. 5690414
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76

- Alignment No. 13129
- gi No. 626041
- % Identity 100
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76

- Alignment No. 13130
- gi No. 627817
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76

- Alignment No. 13131
- gi No. 729814
- % Identity 77.3
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1804: from 55 to 76

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1805
- Ceres seq_id 1501262
- Location of start within SEQ ID NO 1802: at 83 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 13132

- gi No. 1082871
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1805: from 1 to 26

- Alignment No. 13133
- gi No. 1352426
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1805: from 1 to 26

- Alignment No. 13134
- gi No. 1352427
- % Identity 96.2
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1805: from 1 to 26

- Alignment No. 13135
- gi No. 1794151
- % Identity 83.3
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1805: from 3 to 26

- Alignment No. 13136
- gi No. 2851524
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1805: from 1 to 26

- Alignment No. 13137
- gi No. 3024017
- % Identity 96.2
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1805: from 1 to 26

- Alignment No. 13138
- gi No. 3264536
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1805: from 1 to 26

- Alignment No. 13139
- gi No. 3746340
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1805: from 1 to 26

- Alignment No. 13140
- gi No. 3811355
- % Identity 75.9
- Alignment Length 29
- Location of Alignment in SEQ ID NO 1805: from 1 to 29

- Alignment No. 13141
- gi No. 4503499
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1805: from 1 to 26

- Alignment No. 13142
- gi No. 4587600

- % Identity 100
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1805: from 1 to 26

- Alignment No. 13143
- gi No. 4758254
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1805: from 1 to 26

- Alignment No. 13144
- gi No. 5690414
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 1805: from 1 to 26

- Alignment No. 13145
- gi No. 626041
- % Identity 96
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1805: from 2 to 26

- Alignment No. 13146
- gi No. 627817
- % Identity 84
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1805: from 2 to 26

Maximum Length Sequence corresponding to clone ID 283950

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1806
- Ceres seq_id 1501268

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1807
- Ceres seq_id 1501269
- Location of start within SEQ ID NO 1806: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13147
- gi No. 419789
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1807: from 146 to 158

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1808
- Ceres seq_id 1501270
- Location of start within SEQ ID NO 1806: at 116 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13148
- Glycosyl hydrolases family 17
- Location within SEQ ID NO 1808: from 29 to 109 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 284027

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1809
- Ceres seq_id 1501280
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1810
 - Ceres seq_id 1501281
 - Location of start within SEQ ID NO 1809: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 13149
 - gi No. 100931
 - % Identity 72.7
 - Alignment Length 22
 - Location of Alignment in SEQ ID NO 1810: from 44 to 64
 - Alignment No. 13150
 - gi No. 1045052
 - % Identity 71.8
 - Alignment Length 39
 - Location of Alignment in SEQ ID NO 1810: from 29 to 64
 - Alignment No. 13151
 - gi No. 1065516
 - % Identity 77.8
 - Alignment Length 36
 - Location of Alignment in SEQ ID NO 1810: from 29 to 64
 - Alignment No. 13152
 - gi No. 1078809
 - % Identity 76
 - Alignment Length 25
 - Location of Alignment in SEQ ID NO 1810: from 38 to 62
 - Alignment No. 13153
 - gi No. 1078810
 - % Identity 76
 - Alignment Length 25
 - Location of Alignment in SEQ ID NO 1810: from 38 to 62
 - Alignment No. 13154
 - gi No. 1101025
 - % Identity 86.1
 - Alignment Length 36
 - Location of Alignment in SEQ ID NO 1810: from 29 to 64
 - Alignment No. 13155
 - gi No. 1136120
 - % Identity 78.4
 - Alignment Length 37
 - Location of Alignment in SEQ ID NO 1810: from 29 to 64
 - Alignment No. 13156
 - gi No. 1136122
 - % Identity 86.5
 - Alignment Length 37
 - Location of Alignment in SEQ ID NO 1810: from 29 to 64
 - Alignment No. 13157
 - gi No. 1174592
 - % Identity 83.9

- Alignment Length 31
- Location of Alignment in SEQ ID NO 1810: from 29 to 59
- Alignment No. 13158
- gi No. 1174593
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13159
- gi No. 1223784
- % Identity 77.1
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1810: from 29 to 63
- Alignment No. 13160
- gi No. 1223786
- % Identity 84.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1810: from 29 to 57
- Alignment No. 13161
- gi No. 1245776
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13162
- gi No. 1279206
- % Identity 84.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1810: from 29 to 61
- Alignment No. 13163
- gi No. 1334748
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1810: from 29 to 63
- Alignment No. 13164
- gi No. 1351200
- % Identity 78.1
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1810: from 29 to 60
- Alignment No. 13165
- gi No. 135391
- % Identity 83.3
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13166
- gi No. 135392
- % Identity 71.9
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1810: from 29 to 60
- Alignment No. 13167
- gi No. 135393
- % Identity 70.3
- Alignment Length 37

- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13168
- gi No. 135394
- % Identity 75.7
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13169
- gi No. 135395
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13170
- gi No. 135396
- % Identity 72.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13171
- gi No. 135398
- % Identity 83.8
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13172
- gi No. 135399
- % Identity 91.7
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13173
- gi No. 135400
- % Identity 78.9
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13174
- gi No. 135401
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13175
- gi No. 135402
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1810: from 29 to 63
- Alignment No. 13176
- gi No. 135404
- % Identity 75.7
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13177
- gi No. 135406
- % Identity 91.7
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13178
- gi No. 135407
- % Identity 73.5
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1810: from 29 to 62

- Alignment No. 13179
- gi No. 135409
- % Identity 75.7
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13180
- gi No. 135411
- % Identity 81.1
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13181
- gi No. 135412
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13182
- gi No. 135413
- % Identity 77.8
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1810: from 29 to 55

- Alignment No. 13183
- gi No. 135414
- % Identity 84.4
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1810: from 29 to 60

- Alignment No. 13184
- gi No. 135415
- % Identity 88.9
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1810: from 29 to 55

- Alignment No. 13185
- gi No. 135416
- % Identity 72.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13186
- gi No. 135417
- % Identity 80.6
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13187
- gi No. 135418
- % Identity 72.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13188
- gi No. 135419
- % Identity 72.4
- Alignment Length 29
- Location of Alignment in SEQ ID NO 1810: from 29 to 57

- Alignment No. 13189
- gi No. 135420
- % Identity 78.1
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1810: from 29 to 60

- Alignment No. 13190
- gi No. 135422
- % Identity 74.3
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1810: from 29 to 63

- Alignment No. 13191
- gi No. 135423
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1810: from 29 to 63

- Alignment No. 13192
- gi No. 135424
- % Identity 75
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13193
- gi No. 135425
- % Identity 77.8
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13194
- gi No. 135426
- % Identity 84.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1810: from 29 to 60

- Alignment No. 13195
- gi No. 135427
- % Identity 72.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13196
- gi No. 135428
- % Identity 82.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1810: from 29 to 62

- Alignment No. 13197
- gi No. 135430
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13198

- gi No. 135431
- % Identity 77.1
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1810: from 29 to 63

- Alignment No. 13199
- gi No. 135431
- % Identity 73.7
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1810: from 29 to 63

- Alignment No. 13200
- gi No. 135432
- % Identity 73
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13201
- gi No. 135433
- % Identity 84.4
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1810: from 29 to 60

- Alignment No. 13202
- gi No. 135434
- % Identity 84.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1810: from 29 to 60

- Alignment No. 13203
- gi No. 135435
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13204
- gi No. 135436
- % Identity 82.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1810: from 29 to 61

- Alignment No. 13205
- gi No. 135437
- % Identity 85.3
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1810: from 29 to 61

- Alignment No. 13206
- gi No. 135438
- % Identity 84.4
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1810: from 29 to 60

- Alignment No. 13207
- gi No. 135439
- % Identity 76.9
- Alignment Length 39
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13208
- gi No. 135440

- % Identity 78.4
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13209
- gi No. 135441
- % Identity 80.6
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13210
- gi No. 1362559
- % Identity 75.7
- Alignment Length 39
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13211
- gi No. 1460090
- % Identity 82.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1810: from 29 to 62

- Alignment No. 13212
- gi No. 1460092
- % Identity 82.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1810: from 29 to 62

- Alignment No. 13213
- gi No. 1477428
- % Identity 100
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13214
- gi No. 1527170
- % Identity 73
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13215
- gi No. 1527172
- % Identity 73
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13216
- gi No. 1556446
- % Identity 86.5
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13217
- gi No. 1619297
- % Identity 86.5
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13218
- gi No. 1729834
- % Identity 79.3

- Alignment Length 29
- Location of Alignment in SEQ ID NO 1810: from 29 to 57

- Alignment No. 13219
- gi No. 1729835
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 1810: from 29 to 57

- Alignment No. 13220
- gi No. 1729837
- % Identity 72.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13221
- gi No. 1729838
- % Identity 79.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1810: from 29 to 62

- Alignment No. 13222
- gi No. 1729839
- % Identity 77.8
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13223
- gi No. 1729841
- % Identity 72.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13224
- gi No. 1729842
- % Identity 77.8
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13225
- gi No. 173058
- % Identity 73.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 1810: from 29 to 57

- Alignment No. 13226
- gi No. 1854669
- % Identity 77.8
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13227
- gi No. 202223
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13228
- gi No. 202225
- % Identity 70.3
- Alignment Length 37

- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13229
- gi No. 2088848
- % Identity 77.8
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13230
- gi No. 2098751
- % Identity 75.7
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13231
- gi No. 2098753
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13232
- gi No. 2098757
- % Identity 78.4
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13233
- gi No. 2119263
- % Identity 75
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13234
- gi No. 2119268
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13235
- gi No. 2119269
- % Identity 72.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13236
- gi No. 212836
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13237
- gi No. 223280
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13238
- gi No. 223556
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13239
- gi No. 225587
- % Identity 77.8
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13240
- gi No. 226261
- % Identity 83.3
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13241
- gi No. 2401255
- % Identity 77.8
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13242
- gi No. 2511531
- % Identity 83.8
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13243
- gi No. 2511533
- % Identity 81.3
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1810: from 29 to 60

- Alignment No. 13244
- gi No. 2511535
- % Identity 97.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13245
- gi No. 2522334
- % Identity 77.1
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 63

- Alignment No. 13246
- gi No. 2522336
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13247
- gi No. 2599500
- % Identity 77.8
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13248
- gi No. 2613143
- % Identity 78.4
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13249
- gi No. 2625154
- % Identity 78.4
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13250
- gi No. 2625156
- % Identity 75.7
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13251
- gi No. 267069
- % Identity 88.9
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13252
- gi No. 267070
- % Identity 88.9
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13253
- gi No. 283503
- % Identity 82.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1810: from 29 to 62
- Alignment No. 13254
- gi No. 2842514
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1810: from 29 to 63
- Alignment No. 13255
- gi No. 2843123
- % Identity 72.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13256
- gi No. 3024695
- % Identity 72.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13257
- gi No. 306451
- % Identity 72.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13258
- gi No. 3163946
- % Identity 83.8
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13259

- gi No. 32015
- % Identity 74.3
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1810: from 29 to 63
- Alignment No. 13260
- gi No. 320182
- % Identity 72.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 63
- Alignment No. 13261
- gi No. 320192
- % Identity 78.9
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13262
- gi No. 320960
- % Identity 85.3
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1810: from 29 to 61
- Alignment No. 13263
- gi No. 3334365
- % Identity 74.4
- Alignment Length 39
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13264
- gi No. 3334366
- % Identity 85.3
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1810: from 29 to 62
- Alignment No. 13265
- gi No. 3334366
- % Identity 76.9
- Alignment Length 39
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13266
- gi No. 3348122
- % Identity 72.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13267
- gi No. 3745821
- % Identity 87.5
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1810: from 29 to 52
- Alignment No. 13268
- gi No. 3876026
- % Identity 71.9
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1810: from 29 to 60
- Alignment No. 13269
- gi No. 3876416

- % Identity 75.7
- Alignment Length 39
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13270
- gi No. 3880320
- % Identity 80
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1810: from 29 to 63

- Alignment No. 13271
- gi No. 3915082
- % Identity 81.1
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13272
- gi No. 3915086
- % Identity 75.7
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13273
- gi No. 3915092
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13274
- gi No. 3915094
- % Identity 75.7
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13275
- gi No. 401161
- % Identity 100
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13276
- gi No. 4050007
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13277
- gi No. 4090251
- % Identity 72.7
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1810: from 29 to 61

- Alignment No. 13278
- gi No. 4090271
- % Identity 77.1
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1810: from 29 to 63

- Alignment No. 13279
- gi No. 4098272
- % Identity 83.8

- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13280
- gi No. 416222
- % Identity 81.1
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13281
- gi No. 4165488
- % Identity 83.8
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13282
- gi No. 4206112
- % Identity 91.9
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13283
- gi No. 421757
- % Identity 81.1
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13284
- gi No. 4416179
- % Identity 84.4
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1810: from 29 to 60

- Alignment No. 13285
- gi No. 4583673
- % Identity 81.5
- Alignment Length 27
- Location of Alignment in SEQ ID NO 1810: from 29 to 55

- Alignment No. 13286
- gi No. 464840
- % Identity 83.8
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13287
- gi No. 464841
- % Identity 83.3
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13288
- gi No. 464846
- % Identity 100
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13289
- gi No. 464847
- % Identity 81.1
- Alignment Length 37

- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13290
- gi No. 464849
- % Identity 88.9
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13291
- gi No. 4741827
- % Identity 73
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13292
- gi No. 477233
- % Identity 75.7
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13293
- gi No. 477265
- % Identity 77.8
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13294
- gi No. 4929136
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13295
- gi No. 5174477
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13296
- gi No. 5174733
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13297
- gi No. 539933
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13298
- gi No. 542179
- % Identity 81.1
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13299
- gi No. 549051
- % Identity 73
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13300
- gi No. 549052
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13301
- gi No. 55775
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13302
- gi No. 586073
- % Identity 84.4
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1810: from 29 to 60

- Alignment No. 13303
- gi No. 586074
- % Identity 84.4
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1810: from 29 to 60

- Alignment No. 13304
- gi No. 606648
- % Identity 78.4
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13305
- gi No. 630460
- % Identity 77.1
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1810: from 29 to 63

- Alignment No. 13306
- gi No. 630460
- % Identity 73.7
- Alignment Length 38
- Location of Alignment in SEQ ID NO 1810: from 29 to 63

- Alignment No. 13307
- gi No. 65165
- % Identity 80.6
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13308
- gi No. 71575
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

- Alignment No. 13309
- gi No. 71577
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1810: from 29 to 63

- Alignment No. 13310
- gi No. 730899
- % Identity 84.4
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1810: from 29 to 60
- Alignment No. 13311
- gi No. 84169
- % Identity 77.8
- Alignment Length 36
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13312
- gi No. 84373
- % Identity 78.1
- Alignment Length 32
- Location of Alignment in SEQ ID NO 1810: from 29 to 60
- Alignment No. 13313
- gi No. 90217
- % Identity 75.7
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64
- Alignment No. 13314
- gi No. 942596
- % Identity 73
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1810: from 29 to 64

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1811
- Ceres seq_id 1501282
- Location of start within SEQ ID NO 1809: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 284113

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1812
- Ceres seq_id 1501306

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1813
- Ceres seq_id 1501307
- Location of start within SEQ ID NO 1812: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1814
- Ceres seq_id 1501308
- Location of start within SEQ ID NO 1812: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1815
 - Ceres seq_id 1501309
 - Location of start within SEQ ID NO 1812: at 146 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 13315
 - gi No. 3935169
 - % Identity 80.9
 - Alignment Length 68
 - Location of Alignment in SEQ ID NO 1815: from 1 to 68
- Alignment No. 13316
 - gi No. 3935171
 - % Identity 77.4
 - Alignment Length 53
 - Location of Alignment in SEQ ID NO 1815: from 1 to 53

Maximum Length Sequence corresponding to clone ID 284115

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1816
 - Ceres seq_id 1501310

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1817
 - Ceres seq_id 1501311
 - Location of start within SEQ ID NO 1816: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 13317
 - gi No. 3894190
 - % Identity 72.7
 - Alignment Length 22
 - Location of Alignment in SEQ ID NO 1817: from 69 to 90

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1818
 - Ceres seq_id 1501312
 - Location of start within SEQ ID NO 1816: at 16 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 13318
 - gi No. 3894190
 - % Identity 72.7
 - Alignment Length 22
 - Location of Alignment in SEQ ID NO 1818: from 64 to 85

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1819
 - Ceres seq_id 1501313
 - Location of start within SEQ ID NO 1816: at 61 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 13319

- gi No. 3894190
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 1819: from 49 to 70

Maximum Length Sequence corresponding to clone ID 284319

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1820
- Ceres seq_id 1501318

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1821
- Ceres seq_id 1501319
- Location of start within SEQ ID NO 1820: at 182 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13320
- gi No. 1743354
- % Identity 75
- Alignment Length 28
- Location of Alignment in SEQ ID NO 1821: from 28 to 55

Maximum Length Sequence corresponding to clone ID 284342

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1822
- Ceres seq_id 1501324

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1823
- Ceres seq_id 1501325
- Location of start within SEQ ID NO 1822: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13321
- gi No. 2385410
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1823: from 144 to 179

- Alignment No. 13322
- gi No. 586324
- % Identity 71.8
- Alignment Length 39
- Location of Alignment in SEQ ID NO 1823: from 142 to 179

Maximum Length Sequence corresponding to clone ID 284346

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1824
- Ceres seq_id 1501326

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1825
- Ceres seq_id 1501327
- Location of start within SEQ ID NO 1824: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13323
- Initiation factor 2 subunit
- Location within SEQ ID NO 1825: from 92 to 177 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13324
- gi No. 1085819
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1825: from 70 to 80

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1826
- Ceres seq_id 1501328
- Location of start within SEQ ID NO 1824: at 62 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13325
- Initiation factor 2 subunit
- Location within SEQ ID NO 1826: from 72 to 157 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13326
- gi No. 1085819
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1826: from 50 to 60

Maximum Length Sequence corresponding to clone ID 284539

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1827
- Ceres seq_id 1501329

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1828
- Ceres seq_id 1501330
- Location of start within SEQ ID NO 1827: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1829
- Ceres seq_id 1501331
- Location of start within SEQ ID NO 1827: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13327
- Glycosyl hydrolase family 1
- Location within SEQ ID NO 1829: from 48 to 162 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 284568

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1830
- Ceres seq_id 1501339

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1831
- Ceres seq_id 1501340
- Location of start within SEQ ID NO 1830: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 13328
- Purine/pyrimidine phosphoribosyl transferases
- Location within SEQ ID NO 1831: from 51 to 135 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1832
- Ceres seq_id 1501341
- Location of start within SEQ ID NO 1830: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1833
- Ceres seq_id 1501342
- Location of start within SEQ ID NO 1830: at 73 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 13329
- Purine/pyrimidine phosphoribosyl transferases
- Location within SEQ ID NO 1833: from 27 to 111 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 284741

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1834
- Ceres seq_id 1501345

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1835
- Ceres seq_id 1501346
- Location of start within SEQ ID NO 1834: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13330
- gi No. 1644232
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1835: from 43 to 53
- Alignment No. 13331
- gi No. 4505323
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1835: from 43 to 53

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1836
- Ceres seq_id 1501347
- Location of start within SEQ ID NO 1834: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1837
- Ceres seq_id 1501348
- Location of start within SEQ ID NO 1834: at 80 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 284789

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1838
- Ceres seq_id 1501364

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1839
- Ceres seq_id 1501365
- Location of start within SEQ ID NO 1838: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1840
- Ceres seq_id 1501366
- Location of start within SEQ ID NO 1838: at 131 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13332
- Aldo/keto reductase family
- Location within SEQ ID NO 1840: from 13 to 126 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13333
- gi No. 1935911
- % Identity 90.4
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1840: from 76 to 126

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1841
- Ceres seq_id 1501367
- Location of start within SEQ ID NO 1838: at 212 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13334
- Aldo/keto reductase family
- Location within SEQ ID NO 1841: from 1 to 99 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13335
- gi No. 1935911
- % Identity 90.4
- Alignment Length 52
- Location of Alignment in SEQ ID NO 1841: from 49 to 99

Maximum Length Sequence corresponding to clone ID 285304

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1842
- Ceres seq_id 1501400

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1843
- Ceres seq_id 1501401
- Location of start within SEQ ID NO 1842: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1844
- Ceres seq_id 1501402
- Location of start within SEQ ID NO 1842: at 330 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13336
- gi No. 2997589
- % Identity 100
- Alignment Length 62
- Location of Alignment in SEQ ID NO 1844: from 1 to 61

Maximum Length Sequence corresponding to clone ID 285353

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1845
- Ceres seq_id 1501416

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1846
- Ceres seq_id 1501417
- Location of start within SEQ ID NO 1845: at 140 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13337
- Helix-loop-helix DNA-binding domain
- Location within SEQ ID NO 1846: from 65 to 113 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1847
- Ceres seq_id 1501418
- Location of start within SEQ ID NO 1845: at 143 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13338
- Helix-loop-helix DNA-binding domain
- Location within SEQ ID NO 1847: from 64 to 112 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 285545

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1848
- Ceres seq_id 1501439

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1849
- Ceres seq_id 1501440
- Location of start within SEQ ID NO 1848: at 87 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13339
- Pyruvate kinase
- Location within SEQ ID NO 1849: from 25 to 143 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1850
- Ceres seq_id 1501441
- Location of start within SEQ ID NO 1848: at 231 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13340
- Pyruvate kinase
- Location within SEQ ID NO 1850: from 1 to 95 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1851
- Ceres seq_id 1501442
- Location of start within SEQ ID NO 1848: at 261 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13341
- Pyruvate kinase
- Location within SEQ ID NO 1851: from 1 to 85 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 285623

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1852
- Ceres seq_id 1501471

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1853
- Ceres seq_id 1501472
- Location of start within SEQ ID NO 1852: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13342
- DNA topoisomerase II (N-terminal region)
- Location within SEQ ID NO 1853: from 1 to 117 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 285664

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1854
- Ceres seq_id 1501485

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1855

- Ceres seq_id 1501486
- Location of start within SEQ ID NO 1854: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 13343
 - gi No. 2134209
 - % Identity 70.4
 - Alignment Length 27
 - Location of Alignment in SEQ ID NO 1855: from 64 to 90

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1856
- Ceres seq_id 1501487
- Location of start within SEQ ID NO 1854: at 88 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13344
- Aspartate/ornithine carbamoyltransferase
- Location within SEQ ID NO 1856: from 70 to 141 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1857
- Ceres seq_id 1501488
- Location of start within SEQ ID NO 1854: at 91 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13345
- Aspartate/ornithine carbamoyltransferase
- Location within SEQ ID NO 1857: from 69 to 140 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 285671

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1858
- Ceres seq_id 1501489

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1859
- Ceres seq_id 1501490
- Location of start within SEQ ID NO 1858: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13346
- gi No. 2507155
- % Identity 81.8
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1859: from 1 to 11

- Alignment No. 13347
- gi No. 3122386
- % Identity 85.5
- Alignment Length 145
- Location of Alignment in SEQ ID NO 1859: from 48 to 191

- Alignment No. 13348
- gi No. 3122387
- % Identity 84.1
- Alignment Length 145
- Location of Alignment in SEQ ID NO 1859: from 48 to 191

- Alignment No. 13349
- gi No. 439289
- % Identity 81.8
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1859: from 1 to 11

- Alignment No. 13350
- gi No. 465445
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1859: from 5 to 15

- Alignment No. 13351
- gi No. 871535
- % Identity 81.8
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1859: from 1 to 11

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1860
- Ceres seq_id 1501491
- Location of start within SEQ ID NO 1858: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 285805

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1861
- Ceres seq_id 1501515

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1862
- Ceres seq_id 1501516
- Location of start within SEQ ID NO 1861: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13352
- Elongation factor 1 (beta/delta chain)
- Location within SEQ ID NO 1862: from 126 to 251 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13353
- gi No. 232031
- % Identity 85.2
- Alignment Length 225
- Location of Alignment in SEQ ID NO 1862: from 33 to 251

- Alignment No. 13354
- gi No. 232033
- % Identity 82.6
- Alignment Length 223
- Location of Alignment in SEQ ID NO 1862: from 33 to 251

- Alignment No. 13355
- gi No. 461073
- % Identity 86.7
- Alignment Length 30
- Location of Alignment in SEQ ID NO 1862: from 180 to 209

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1863
- Ceres seq_id 1501517
- Location of start within SEQ ID NO 1861: at 99 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13356
- Elongation factor 1 (beta/delta chain)
- Location within SEQ ID NO 1863: from 94 to 219 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13357
- gi No. 232031
- % Identity 85.2
- Alignment Length 225
- Location of Alignment in SEQ ID NO 1863: from 1 to 219

- Alignment No. 13358
- gi No. 232033
- % Identity 82.6
- Alignment Length 223
- Location of Alignment in SEQ ID NO 1863: from 1 to 219

- Alignment No. 13359
- gi No. 461073
- % Identity 86.7
- Alignment Length 30
- Location of Alignment in SEQ ID NO 1863: from 148 to 177

Maximum Length Sequence corresponding to clone ID 285925

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1864
- Ceres seq_id 1501543

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1865
- Ceres seq_id 1501544
- Location of start within SEQ ID NO 1864: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13360
- gi No. 1155261
- % Identity 90.1
- Alignment Length 151
- Location of Alignment in SEQ ID NO 1865: from 44 to 193

- Alignment No. 13361
- gi No. 135054
- % Identity 74.1
- Alignment Length 147
- Location of Alignment in SEQ ID NO 1865: from 48 to 193

- Alignment No. 13362
- gi No. 1542845
- % Identity 83
- Alignment Length 53
- Location of Alignment in SEQ ID NO 1865: from 142 to 193

- Alignment No. 13363
- gi No. 2315514
- % Identity 79.2
- Alignment Length 144
- Location of Alignment in SEQ ID NO 1865: from 51 to 193

- Alignment No. 13364
- gi No. 2996008
- % Identity 80.4
- Alignment Length 153
- Location of Alignment in SEQ ID NO 1865: from 44 to 193

- Alignment No. 13365
- gi No. 338687
- % Identity 81.2
- Alignment Length 149
- Location of Alignment in SEQ ID NO 1865: from 46 to 193

- Alignment No. 13366
- gi No. 3845214
- % Identity 75.7
- Alignment Length 144
- Location of Alignment in SEQ ID NO 1865: from 51 to 193

- Alignment No. 13367
- gi No. 468605
- % Identity 74.8
- Alignment Length 147
- Location of Alignment in SEQ ID NO 1865: from 48 to 193

- Alignment No. 13368
- gi No. 4759034
- % Identity 81.9
- Alignment Length 149
- Location of Alignment in SEQ ID NO 1865: from 46 to 193

- Alignment No. 13369
- gi No. 549010
- % Identity 91.4
- Alignment Length 151
- Location of Alignment in SEQ ID NO 1865: from 44 to 193

- Alignment No. 13370
- gi No. 549011
- % Identity 81.9
- Alignment Length 149
- Location of Alignment in SEQ ID NO 1865: from 46 to 193

- Alignment No. 13371
- gi No. 626763
- % Identity 74.8
- Alignment Length 147
- Location of Alignment in SEQ ID NO 1865: from 48 to 193

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1866
- Ceres seq_id 1501545
- Location of start within SEQ ID NO 1866: at 131 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13372
- gi No. 1155261
- % Identity 90.1
- Alignment Length 151
- Location of Alignment in SEQ ID NO 1866: from 1 to 150

- Alignment No. 13373
- gi No. 135054
- % Identity 74.1
- Alignment Length 147
- Location of Alignment in SEQ ID NO 1866: from 5 to 150

- Alignment No. 13374
- gi No. 1542845
- % Identity 83
- Alignment Length 53
- Location of Alignment in SEQ ID NO 1866: from 99 to 150

- Alignment No. 13375
- gi No. 2315514
- % Identity 79.2
- Alignment Length 144
- Location of Alignment in SEQ ID NO 1866: from 8 to 150

- Alignment No. 13376
- gi No. 2996008
- % Identity 80.4
- Alignment Length 153
- Location of Alignment in SEQ ID NO 1866: from 1 to 150

- Alignment No. 13377
- gi No. 338687
- % Identity 81.2
- Alignment Length 149
- Location of Alignment in SEQ ID NO 1866: from 3 to 150

- Alignment No. 13378
- gi No. 3845214
- % Identity 75.7
- Alignment Length 144
- Location of Alignment in SEQ ID NO 1866: from 8 to 150

- Alignment No. 13379
- gi No. 468605
- % Identity 74.8
- Alignment Length 147
- Location of Alignment in SEQ ID NO 1866: from 5 to 150

- Alignment No. 13380
- gi No. 4759034
- % Identity 81.9
- Alignment Length 149
- Location of Alignment in SEQ ID NO 1866: from 3 to 150

- Alignment No. 13381
- gi No. 549010
- % Identity 91.4
- Alignment Length 151
- Location of Alignment in SEQ ID NO 1866: from 1 to 150
- Alignment No. 13382
- gi No. 549011
- % Identity 81.9
- Alignment Length 149
- Location of Alignment in SEQ ID NO 1866: from 3 to 150
- Alignment No. 13383
- gi No. 626763
- % Identity 74.8
- Alignment Length 147
- Location of Alignment in SEQ ID NO 1866: from 5 to 150

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1867
- Ceres seq_id 1501546
- Location of start within SEQ ID NO 1864: at 227 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13384
- gi No. 1155261
- % Identity 90.1
- Alignment Length 151
- Location of Alignment in SEQ ID NO 1867: from 1 to 118
- Alignment No. 13385
- gi No. 135054
- % Identity 74.1
- Alignment Length 147
- Location of Alignment in SEQ ID NO 1867: from 1 to 118
- Alignment No. 13386
- gi No. 1542845
- % Identity 83
- Alignment Length 53
- Location of Alignment in SEQ ID NO 1867: from 67 to 118
- Alignment No. 13387
- gi No. 2315514
- % Identity 79.2
- Alignment Length 144
- Location of Alignment in SEQ ID NO 1867: from 1 to 118
- Alignment No. 13388
- gi No. 2996008
- % Identity 80.4
- Alignment Length 153
- Location of Alignment in SEQ ID NO 1867: from 1 to 118
- Alignment No. 13389
- gi No. 338687
- % Identity 81.2
- Alignment Length 149
- Location of Alignment in SEQ ID NO 1867: from 1 to 118

- Alignment No. 13390
- gi No. 3845214
- % Identity 75.7
- Alignment Length 144
- Location of Alignment in SEQ ID NO 1867: from 1 to 118

- Alignment No. 13391
- gi No. 468605
- % Identity 74.8
- Alignment Length 147
- Location of Alignment in SEQ ID NO 1867: from 1 to 118

- Alignment No. 13392
- gi No. 4759034
- % Identity 81.9
- Alignment Length 149
- Location of Alignment in SEQ ID NO 1867: from 1 to 118

- Alignment No. 13393
- gi No. 549010
- % Identity 91.4
- Alignment Length 151
- Location of Alignment in SEQ ID NO 1867: from 1 to 118

- Alignment No. 13394
- gi No. 549011
- % Identity 81.9
- Alignment Length 149
- Location of Alignment in SEQ ID NO 1867: from 1 to 118

- Alignment No. 13395
- gi No. 626763
- % Identity 74.8
- Alignment Length 147
- Location of Alignment in SEQ ID NO 1867: from 1 to 118

Maximum Length Sequence corresponding to clone ID 286066

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1868
- Ceres seq_id 1501547

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1869
- Ceres seq_id 1501548
- Location of start within SEQ ID NO 1868: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13396
- Nucleoside diphosphate kinases
- Location within SEQ ID NO 1869: from 94 to 241 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13397
- gi No. 1076713
- % Identity 87.5
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1869: from 91 to 114

- Alignment No. 13398
- gi No. 1304478

- % Identity 70
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1869: from 91 to 130

- Alignment No. 13399
- gi No. 1729427
- % Identity 70
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1869: from 91 to 130

- Alignment No. 13400
- gi No. 2129487
- % Identity 81
- Alignment Length 153
- Location of Alignment in SEQ ID NO 1869: from 91 to 243

- Alignment No. 13401
- gi No. 2829275
- % Identity 71.2
- Alignment Length 230
- Location of Alignment in SEQ ID NO 1869: from 15 to 243

- Alignment No. 13402
- gi No. 4972094
- % Identity 72.5
- Alignment Length 229
- Location of Alignment in SEQ ID NO 1869: from 15 to 243

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1870
- Ceres seq_id 1501549
- Location of start within SEQ ID NO 1868: at 17 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13403
- Nucleoside diphosphate kinases
- Location within SEQ ID NO 1870: from 89 to 236 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13404
- gi No. 1076713
- % Identity 87.5
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1870: from 86 to 109

- Alignment No. 13405
- gi No. 1304478
- % Identity 70
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1870: from 86 to 125

- Alignment No. 13406
- gi No. 1729427
- % Identity 70
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1870: from 86 to 125

- Alignment No. 13407
- gi No. 2129487
- % Identity 81

- Alignment Length 153
- Location of Alignment in SEQ ID NO 1870: from 86 to 238
- Alignment No. 13408
- gi No. 2829275
- % Identity 71.2
- Alignment Length 230
- Location of Alignment in SEQ ID NO 1870: from 10 to 238
- Alignment No. 13409
- gi No. 4972094
- % Identity 72.5
- Alignment Length 229
- Location of Alignment in SEQ ID NO 1870: from 10 to 238

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1871
- Ceres seq_id 1501550
- Location of start within SEQ ID NO 1868: at 245 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13410
- Nucleoside diphosphate kinases
- Location within SEQ ID NO 1871: from 13 to 160 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13411
- gi No. 1076713
- % Identity 87.5
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1871: from 10 to 33
- Alignment No. 13412
- gi No. 1304478
- % Identity 70
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1871: from 10 to 49
- Alignment No. 13413
- gi No. 1729427
- % Identity 70
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1871: from 10 to 49
- Alignment No. 13414
- gi No. 2129487
- % Identity 81
- Alignment Length 153
- Location of Alignment in SEQ ID NO 1871: from 10 to 162
- Alignment No. 13415
- gi No. 2829275
- % Identity 71.2
- Alignment Length 230
- Location of Alignment in SEQ ID NO 1871: from 1 to 162
- Alignment No. 13416
- gi No. 4972094
- % Identity 72.5
- Alignment Length 229

- Location of Alignment in SEQ ID NO 1871: from 1 to 162

Maximum Length Sequence corresponding to clone ID 286096

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1872
- Ceres seq_id 1501565

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1873
- Ceres seq_id 1501566
- Location of start within SEQ ID NO 1872: at 457 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13417
- gi No. 1002689
- % Identity 72
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1873: from 7 to 31
- Alignment No. 13418
- gi No. 1172600
- % Identity 82.9
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1873: from 1 to 34
- Alignment No. 13419
- gi No. 130847
- % Identity 78.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1873: from 1 to 33
- Alignment No. 13420
- gi No. 130860
- % Identity 88.2
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1873: from 1 to 34
- Alignment No. 13421
- gi No. 2621771
- % Identity 72
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1873: from 7 to 31
- Alignment No. 13422
- gi No. 2650136
- % Identity 72
- Alignment Length 25
- Location of Alignment in SEQ ID NO 1873: from 7 to 31
- Alignment No. 13423
- gi No. 3080509
- % Identity 73.5
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1873: from 1 to 34
- Alignment No. 13424
- gi No. 3114275
- % Identity 79.3
- Alignment Length 29
- Location of Alignment in SEQ ID NO 1873: from 5 to 33

- Alignment No. 13425
- gi No. 3421096
- % Identity 94.3
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1873: from 1 to 34

- Alignment No. 13426
- gi No. 3914413
- % Identity 93.9
- Alignment Length 33
- Location of Alignment in SEQ ID NO 1873: from 3 to 34

- Alignment No. 13427
- gi No. 3914424
- % Identity 91.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1873: from 1 to 34

- Alignment No. 13428
- gi No. 3914431
- % Identity 94.3
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1873: from 1 to 34

- Alignment No. 13429
- gi No. 3914438
- % Identity 88.2
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1873: from 1 to 34

- Alignment No. 13430
- gi No. 3914440
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1873: from 1 to 34

- Alignment No. 13431
- gi No. 4506183
- % Identity 88.2
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1873: from 1 to 34

- Alignment No. 13432
- gi No. 542655
- % Identity 88.2
- Alignment Length 34
- Location of Alignment in SEQ ID NO 1873: from 1 to 34

- Alignment No. 13433
- gi No. 585729
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1873: from 8 to 31

Maximum Length Sequence corresponding to clone ID 286125

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1874
- Ceres seq_id 1501567

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1875

- Ceres seq_id 1501568
- Location of start within SEQ ID NO 1874: at 46 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1876
- Ceres seq_id 1501569
- Location of start within SEQ ID NO 1874: at 176 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13434
- Ribosomal protein S11
- Location within SEQ ID NO 1876: from 29 to 129 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13435
- gi No. 1173200
- % Identity 95.3
- Alignment Length 64
- Location of Alignment in SEQ ID NO 1876: from 67 to 129
- Alignment No. 13436
- gi No. 1173201
- % Identity 86.5
- Alignment Length 126
- Location of Alignment in SEQ ID NO 1876: from 5 to 129
- Alignment No. 13437
- gi No. 131772
- % Identity 96.9
- Alignment Length 130
- Location of Alignment in SEQ ID NO 1876: from 1 to 129
- Alignment No. 13438
- gi No. 131773
- % Identity 94.5
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1876: from 3 to 129
- Alignment No. 13439
- gi No. 133771
- % Identity 81.7
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1876: from 1 to 129
- Alignment No. 13440
- gi No. 133777
- % Identity 78.2
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1876: from 21 to 129
- Alignment No. 13441
- gi No. 133782
- % Identity 78.8
- Alignment Length 132
- Location of Alignment in SEQ ID NO 1876: from 1 to 129

- Alignment No. 13442
- gi No. 133785
- % Identity 84
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1876: from 1 to 129

- Alignment No. 13443
- gi No. 133789
- % Identity 70.2
- Alignment Length 121
- Location of Alignment in SEQ ID NO 1876: from 10 to 129

- Alignment No. 13444
- gi No. 1346941
- % Identity 76.4
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1876: from 21 to 129

- Alignment No. 13445
- gi No. 1350935
- % Identity 78.8
- Alignment Length 132
- Location of Alignment in SEQ ID NO 1876: from 1 to 129

- Alignment No. 13446
- gi No. 1350937
- % Identity 77.9
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1876: from 1 to 129

- Alignment No. 13447
- gi No. 2350992
- % Identity 76
- Alignment Length 104
- Location of Alignment in SEQ ID NO 1876: from 27 to 129

- Alignment No. 13448
- gi No. 2414647
- % Identity 80.9
- Alignment Length 115
- Location of Alignment in SEQ ID NO 1876: from 16 to 129

- Alignment No. 13449
- gi No. 2500443
- % Identity 97.8
- Alignment Length 46
- Location of Alignment in SEQ ID NO 1876: from 85 to 129

- Alignment No. 13450
- gi No. 3097244
- % Identity 85.5
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1876: from 1 to 129

- Alignment No. 13451
- gi No. 3122785
- % Identity 90
- Alignment Length 130
- Location of Alignment in SEQ ID NO 1876: from 1 to 129

- Alignment No. 13452

- gi No. 4574240
- % Identity 84.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1876: from 21 to 129

- Alignment No. 13453
- gi No. 4588920
- % Identity 81.7
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1876: from 1 to 129

- Alignment No. 13454
- gi No. 4678226
- % Identity 90.8
- Alignment Length 130
- Location of Alignment in SEQ ID NO 1876: from 1 to 129

- Alignment No. 13455
- gi No. 4886269
- % Identity 91.5
- Alignment Length 130
- Location of Alignment in SEQ ID NO 1876: from 1 to 129

- Alignment No. 13456
- gi No. 5032051
- % Identity 84.7
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1876: from 1 to 129

- Alignment No. 13457
- gi No. 5441523
- % Identity 98.3
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1876: from 72 to 129

- Alignment No. 13458
- gi No. 547604
- % Identity 77.3
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1876: from 21 to 129

- Alignment No. 13459
- gi No. 70946
- % Identity 76.4
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1876: from 21 to 129

- Alignment No. 13460
- gi No. 730453
- % Identity 77.3
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1876: from 21 to 129

- Alignment No. 13461
- gi No. 730633
- % Identity 82.4
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1876: from 1 to 129

- Alignment No. 13462
- gi No. 83794

- % Identity 80
- Alignment Length 130
- Location of Alignment in SEQ ID NO 1876: from 1 to 129

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1877
- Ceres seq_id 1501570
- Location of start within SEQ ID NO 1874: at 350 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13463
- Ribosomal protein S11
- Location within SEQ ID NO 1877: from 1 to 71 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13464
- gi No. 1173200
- % Identity 95.3
- Alignment Length 64
- Location of Alignment in SEQ ID NO 1877: from 9 to 71
- Alignment No. 13465
- gi No. 1173201
- % Identity 86.5
- Alignment Length 126
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13466
- gi No. 131772
- % Identity 96.9
- Alignment Length 130
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13467
- gi No. 131773
- % Identity 94.5
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13468
- gi No. 133771
- % Identity 81.7
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13469
- gi No. 133777
- % Identity 78.2
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13470
- gi No. 133782
- % Identity 78.8
- Alignment Length 132
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13471
- gi No. 133785
- % Identity 84

- Alignment Length 131
- Location of Alignment in SEQ ID NO 1877: from 1 to 71

- Alignment No. 13472
- gi No. 133789
- % Identity 70.2
- Alignment Length 121
- Location of Alignment in SEQ ID NO 1877: from 1 to 71

- Alignment No. 13473
- gi No. 1346941
- % Identity 76.4
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1877: from 1 to 71

- Alignment No. 13474
- gi No. 1350935
- % Identity 78.8
- Alignment Length 132
- Location of Alignment in SEQ ID NO 1877: from 1 to 71

- Alignment No. 13475
- gi No. 1350937
- % Identity 77.9
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1877: from 1 to 71

- Alignment No. 13476
- gi No. 2350992
- % Identity 76
- Alignment Length 104
- Location of Alignment in SEQ ID NO 1877: from 1 to 71

- Alignment No. 13477
- gi No. 2414647
- % Identity 80.9
- Alignment Length 115
- Location of Alignment in SEQ ID NO 1877: from 1 to 71

- Alignment No. 13478
- gi No. 2500443
- % Identity 97.8
- Alignment Length 46
- Location of Alignment in SEQ ID NO 1877: from 27 to 71

- Alignment No. 13479
- gi No. 3097244
- % Identity 85.5
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1877: from 1 to 71

- Alignment No. 13480
- gi No. 3122785
- % Identity 90
- Alignment Length 130
- Location of Alignment in SEQ ID NO 1877: from 1 to 71

- Alignment No. 13481
- gi No. 4574240
- % Identity 84.5
- Alignment Length 110

- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13482
- gi No. 4588920
- % Identity 81.7
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13483
- gi No. 4678226
- % Identity 90.8
- Alignment Length 130
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13484
- gi No. 4886269
- % Identity 91.5
- Alignment Length 130
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13485
- gi No. 5032051
- % Identity 84.7
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13486
- gi No. 5441523
- % Identity 98.3
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1877: from 14 to 71
- Alignment No. 13487
- gi No. 547604
- % Identity 77.3
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13488
- gi No. 70946
- % Identity 76.4
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13489
- gi No. 730453
- % Identity 77.3
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13490
- gi No. 730633
- % Identity 82.4
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1877: from 1 to 71
- Alignment No. 13491
- gi No. 83794
- % Identity 80
- Alignment Length 130
- Location of Alignment in SEQ ID NO 1877: from 1 to 71

Maximum Length Sequence corresponding to clone ID 286127

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1878
- Ceres seq_id 1501571

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1879
- Ceres seq_id 1501572
- Location of start within SEQ ID NO 1878: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13492
- gi No. 4506093
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1879: from 27 to 37
- Alignment No. 13493
- gi No. 973307
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1879: from 27 to 37

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1880
- Ceres seq_id 1501573
- Location of start within SEQ ID NO 1878: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13494
- gi No. 2493240
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 1880: from 145 to 158
- Alignment No. 13495
- gi No. 4808162
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1880: from 145 to 157
- Alignment No. 13496
- gi No. 4808164
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1880: from 145 to 157
- Alignment No. 13497
- gi No. 4808166
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1880: from 145 to 157
- Alignment No. 13498
- gi No. 4808177
- % Identity 76.9
- Alignment Length 13

- Location of Alignment in SEQ ID NO 1880: from 145 to 157

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1881
- Ceres seq_id 1501574
- Location of start within SEQ ID NO 1878: at 125 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13499
- gi No. 2493240
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 1881: from 104 to 117
- Alignment No. 13500
- gi No. 4808162
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1881: from 104 to 116
- Alignment No. 13501
- gi No. 4808164
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1881: from 104 to 116
- Alignment No. 13502
- gi No. 4808166
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1881: from 104 to 116
- Alignment No. 13503
- gi No. 4808177
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1881: from 104 to 116

Maximum Length Sequence corresponding to clone ID 286161

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1882
- Ceres seq_id 1501582

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1883
- Ceres seq_id 1501583
- Location of start within SEQ ID NO 1882: at 268 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13504
- gi No. 2655291
- % Identity 84.4
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1883: from 1 to 76

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1884
- Ceres seq_id 1501584

- Location of start within SEQ ID NO 1882: at 352 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13505
- gi No. 2655291
- % Identity 84.4
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1884: from 1 to 48

Maximum Length Sequence corresponding to clone ID 286175

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1885
- Ceres seq_id 1501589

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1886
- Ceres seq_id 1501590
- Location of start within SEQ ID NO 1885: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1887
- Ceres seq_id 1501591
- Location of start within SEQ ID NO 1885: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13506
- Lysyl oxidase
- Location within SEQ ID NO 1887: from 53 to 170 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1888
- Ceres seq_id 1501592
- Location of start within SEQ ID NO 1885: at 108 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13507
- Lysyl oxidase
- Location within SEQ ID NO 1888: from 18 to 135 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 286275

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1889
- Ceres seq_id 1501609

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1890
- Ceres seq_id 1501610
- Location of start within SEQ ID NO 1889: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1891
- Ceres seq_id 1501611
- Location of start within SEQ ID NO 1889: at 26 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1892
- Ceres seq_id 1501612
- Location of start within SEQ ID NO 1889: at 324 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13508
- Glycosyl hydrolase family 9
- Location within SEQ ID NO 1892: from 3 to 42 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13509
- gi No. 2765531
- % Identity 76.7
- Alignment Length 30
- Location of Alignment in SEQ ID NO 1892: from 1 to 15

Maximum Length Sequence corresponding to clone ID 286426

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1893
- Ceres seq_id 1501624

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1894
- Ceres seq_id 1501625
- Location of start within SEQ ID NO 1893: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13510
- gi No. 2135765
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1894: from 53 to 64

- Alignment No. 13511
- gi No. 4505285
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1894: from 53 to 64

- Alignment No. 13512
- gi No. 542994
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1894: from 21 to 34

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1895

- Ceres seq_id 1501626
- Location of start within SEQ ID NO 1893: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13513
- gi No. 2224619
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1895: from 58 to 68

- Alignment No. 13514
- gi No. 418612
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1895: from 57 to 68

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1896
- Ceres seq_id 1501627
- Location of start within SEQ ID NO 1893: at 82 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13515
- gi No. 2135765
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1896: from 26 to 37

- Alignment No. 13516
- gi No. 4505285
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1896: from 26 to 37

Maximum Length Sequence corresponding to clone ID 286438

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1897
- Ceres seq_id 1501632

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1898
- Ceres seq_id 1501633
- Location of start within SEQ ID NO 1897: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13517
- gi No. 2204081
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1898: from 67 to 80

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1899
- Ceres seq_id 1501634
- Location of start within SEQ ID NO 1897: at 119 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13518
- gi No. 2204081
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1899: from 28 to 41

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1900
- Ceres seq_id 1501635
- Location of start within SEQ ID NO 1897: at 146 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13519
- gi No. 2204081
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1900: from 19 to 32

Maximum Length Sequence corresponding to clone ID 286538

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1901
- Ceres seq_id 1501639

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1902
- Ceres seq_id 1501640
- Location of start within SEQ ID NO 1901: at 165 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1903
- Ceres seq_id 1501641
- Location of start within SEQ ID NO 1901: at 198 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1904
- Ceres seq_id 1501642
- Location of start within SEQ ID NO 1901: at 362 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13520
- gi No. 2894559
- % Identity 89.1
- Alignment Length 46
- Location of Alignment in SEQ ID NO 1904: from 1 to 45
- Alignment No. 13521
- gi No. 4115936

- % Identity 87
- Alignment Length 46
- Location of Alignment in SEQ ID NO 1904: from 1 to 45

Maximum Length Sequence corresponding to clone ID 286545

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1905
- Ceres seq_id 1501643

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1906
- Ceres seq_id 1501644
- Location of start within SEQ ID NO 1905: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13522
- Ezrin/radixin/moesin family
- Location within SEQ ID NO 1906: from 1 to 145 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1907
- Ceres seq_id 1501645
- Location of start within SEQ ID NO 1905: at 167 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13523
- Ezrin/radixin/moesin family
- Location within SEQ ID NO 1907: from 1 to 90 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1908
- Ceres seq_id 1501646
- Location of start within SEQ ID NO 1905: at 399 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 286676

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1909
- Ceres seq_id 1501689

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1910
- Ceres seq_id 1501690
- Location of start within SEQ ID NO 1909: at 152 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13524
- Ubiquitin family
- Location within SEQ ID NO 1910: from 1 to 74 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1911
- Ceres seq_id 1501691
- Location of start within SEQ ID NO 1909: at 284 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1912
- Ceres seq_id 1501692
- Location of start within SEQ ID NO 1909: at 368 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 286738

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1913
- Ceres seq_id 1501701

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1914
- Ceres seq_id 1501702
- Location of start within SEQ ID NO 1913: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1915
- Ceres seq_id 1501703
- Location of start within SEQ ID NO 1913: at 110 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13525
- gi No. 2244980
- % Identity 75
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1915: from 31 to 53

- Alignment No. 13526
- gi No. 4587539
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1915: from 31 to 50

- Alignment No. 13527
- gi No. 4914386
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1915: from 31 to 53

Maximum Length Sequence corresponding to clone ID 286767

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1916
- Ceres seq_id 1501710

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1917
- Ceres seq_id 1501711
- Location of start within SEQ ID NO 1916: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13528
- Protein phosphatase 2C
- Location within SEQ ID NO 1917: from 32 to 84 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1918
- Ceres seq_id 1501712
- Location of start within SEQ ID NO 1916: at 295 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13529
- Protein phosphatase 2C
- Location within SEQ ID NO 1918: from 20 to 85 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1919
- Ceres seq_id 1501713
- Location of start within SEQ ID NO 1916: at 346 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13530
- Protein phosphatase 2C
- Location within SEQ ID NO 1919: from 3 to 68 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 286773

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1920
- Ceres seq_id 1501718

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1921
- Ceres seq_id 1501719
- Location of start within SEQ ID NO 1920: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13531
- gi No. 1093503
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1921: from 149 to 168

- Alignment No. 13532
- gi No. 1340178
- % Identity 73.9
- Alignment Length 23
- Location of Alignment in SEQ ID NO 1921: from 147 to 168

- Alignment No. 13533
- gi No. 1498185
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1921: from 149 to 168

- Alignment No. 13534
- gi No. 2146900
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1921: from 149 to 168

- Alignment No. 13535
- gi No. 416764
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1921: from 149 to 168

- Alignment No. 13536
- gi No. 416766
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1921: from 149 to 168

- Alignment No. 13537
- gi No. 416767
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1921: from 149 to 168

- Alignment No. 13538
- gi No. 479893
- % Identity 83.3
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1921: from 149 to 166

- Alignment No. 13539
- gi No. 479895
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1921: from 149 to 166

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1922
- Ceres seq_id 1501720
- Location of start within SEQ ID NO 1920: at 49 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13540
- gi No. 1093503
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1922: from 133 to 152

- Alignment No. 13541
- gi No. 1340178
- % Identity 73.9
- Alignment Length 23

- Location of Alignment in SEQ ID NO 1922: from 131 to 152
- Alignment No. 13542
- gi No. 1498185
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1922: from 133 to 152
- Alignment No. 13543
- gi No. 2146900
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1922: from 133 to 152
- Alignment No. 13544
- gi No. 416764
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1922: from 133 to 152
- Alignment No. 13545
- gi No. 416766
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1922: from 133 to 152
- Alignment No. 13546
- gi No. 416767
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1922: from 133 to 152
- Alignment No. 13547
- gi No. 479893
- % Identity 83.3
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1922: from 133 to 150
- Alignment No. 13548
- gi No. 479895
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1922: from 133 to 150

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1923
- Ceres seq_id 1501721
- Location of start within SEQ ID NO 1920: at 223 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13549
- gi No. 1093503
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1923: from 75 to 94
- Alignment No. 13550
- gi No. 1340178
- % Identity 73.9

- Alignment Length 23
- Location of Alignment in SEQ ID NO 1923: from 73 to 94
- Alignment No. 13551
- gi No. 1498185
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1923: from 75 to 94
- Alignment No. 13552
- gi No. 2146900
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1923: from 75 to 94
- Alignment No. 13553
- gi No. 416764
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1923: from 75 to 94
- Alignment No. 13554
- gi No. 416766
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1923: from 75 to 94
- Alignment No. 13555
- gi No. 416767
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1923: from 75 to 94
- Alignment No. 13556
- gi No. 479893
- % Identity 83.3
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1923: from 75 to 92
- Alignment No. 13557
- gi No. 479895
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1923: from 75 to 92

Maximum Length Sequence corresponding to clone ID 286777

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1924
- Ceres seq_id 1501722

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1925
- Ceres seq_id 1501723
- Location of start within SEQ ID NO 1924: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1926
- Ceres seq_id 1501724

- Location of start within SEQ ID NO 1924: at 41 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1927
- Ceres seq_id 1501725
- Location of start within SEQ ID NO 1924: at 312 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13558
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 1927: from 1 to 55 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 286992

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1928
- Ceres seq_id 1501730

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1929
- Ceres seq_id 1501731
- Location of start within SEQ ID NO 1928: at 137 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13559
- Collagen triple helix repeat (20 copies)
- Location within SEQ ID NO 1929: from 33 to 96 aa.

- Alignment No. 13560
- Collagen triple helix repeat (20 copies)
- Location within SEQ ID NO 1929: from 45 to 102 aa.

- Alignment No. 13561
- Collagen triple helix repeat (20 copies)
- Location within SEQ ID NO 1929: from 45 to 106 aa.

- Alignment No. 13562
- Collagen triple helix repeat (20 copies)
- Location within SEQ ID NO 1929: from 62 to 108 aa.

- Alignment No. 13563
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1929: from 32 to 100 aa.

- Alignment No. 13564
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1929: from 32 to 106 aa.

- Alignment No. 13565
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1929: from 32 to 108 aa.

- Alignment No. 13566
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1929: from 33 to 94 aa.

- Alignment No. 13567
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1929: from 33 to 106 aa.

- Alignment No. 13568
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1929: from 33 to 108 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1930
- Ceres seq_id 1501732
- Location of start within SEQ ID NO 1928: at 347 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1931
- Ceres seq_id 1501733
- Location of start within SEQ ID NO 1928: at 389 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 287753

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1932
- Ceres seq_id 1501737

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1933
- Ceres seq_id 1501738
- Location of start within SEQ ID NO 1932: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1934
- Ceres seq_id 1501739
- Location of start within SEQ ID NO 1932: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13569
- Collagen triple helix repeat (20 copies)
- Location within SEQ ID NO 1934: from 34 to 83 aa.

- Alignment No. 13570
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1934: from 5 to 83 aa.

- Alignment No. 13571
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1934: from 21 to 83 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13572
- gi No. 3327046
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1934: from 67 to 83

- Alignment No. 13573
- gi No. 3745837
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1934: from 65 to 83

- Alignment No. 13574
- gi No. 4028930
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1934: from 67 to 83

- Alignment No. 13575
- gi No. 4775349
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1934: from 72 to 82

- Alignment No. 13576
- gi No. 4775349
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1934: from 72 to 82

- Alignment No. 13577
- gi No. 4996894
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1934: from 72 to 82

- Alignment No. 13578
- gi No. 4996894
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1934: from 72 to 82

- Alignment No. 13579
- gi No. 688080
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1934: from 65 to 78

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1935
- Ceres seq_id 1501740
- Location of start within SEQ ID NO 1932: at 64 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 287760

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1936

- Ceres_seq_id 1501741
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1937
 - Ceres_seq_id 1501742
 - Location of start within SEQ ID NO 1936: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13580
- DnaJ domain
- Location within SEQ ID NO 1937: from 36 to 81 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13581
- gi No. 1125691
- % Identity 84.5
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1937: from 24 to 81

- Alignment No. 13582
- gi No. 1169382
- % Identity 82.8
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1937: from 24 to 81

- Alignment No. 13583
- gi No. 1169383
- % Identity 76.3
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1937: from 24 to 81

- Alignment No. 13584
- gi No. 1169384
- % Identity 86.2
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1937: from 24 to 81

- Alignment No. 13585
- gi No. 2129577
- % Identity 79.7
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1937: from 24 to 81

- Alignment No. 13586
- gi No. 2370312
- % Identity 78
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1937: from 24 to 81

- Alignment No. 13587
- gi No. 2641638
- % Identity 79.7
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1937: from 24 to 81

- Alignment No. 13588
- gi No. 2984709
- % Identity 89.7
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1937: from 24 to 81

- Alignment No. 13589
- gi No. 39890
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1937: from 37 to 55

- Alignment No. 13590
- gi No. 4008159
- % Identity 89.7
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1937: from 24 to 81

- Alignment No. 13591
- gi No. 4097575
- % Identity 86.2
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1937: from 24 to 81

- Alignment No. 13592
- gi No. 4097577
- % Identity 82.8
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1937: from 24 to 81

- Alignment No. 13593
- gi No. 4210948
- % Identity 91.4
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1937: from 24 to 81

- Alignment No. 13594
- gi No. 421809
- % Identity 89.7
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1937: from 24 to 81

- Alignment No. 13595
- gi No. 4589726
- % Identity 81
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1937: from 24 to 81

- Alignment No. 13596
- gi No. 461942
- % Identity 86.5
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1937: from 45 to 81

- Alignment No. 13597
- gi No. 461944
- % Identity 89.7
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1937: from 24 to 81

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1938
- Ceres seq_id 1501743
- Location of start within SEQ ID NO 1936: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appin. SEQ ID NO 1939
- Ceres seq_id 1501744
- Location of start within SEQ ID NO 1936: at 70 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13598
- DnaJ domain
- Location within SEQ ID NO 1939: from 13 to 58 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13599
- gi No. 1125691
- % Identity 84.5
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1939: from 1 to 58

- Alignment No. 13600
- gi No. 1169382
- % Identity 82.8
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1939: from 1 to 58

- Alignment No. 13601
- gi No. 1169383
- % Identity 76.3
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1939: from 1 to 58

- Alignment No. 13602
- gi No. 1169384
- % Identity 86.2
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1939: from 1 to 58

- Alignment No. 13603
- gi No. 2129577
- % Identity 79.7
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1939: from 1 to 58

- Alignment No. 13604
- gi No. 2370312
- % Identity 78
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1939: from 1 to 58

- Alignment No. 13605
- gi No. 2641638
- % Identity 79.7
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1939: from 1 to 58

- Alignment No. 13606
- gi No. 2984709
- % Identity 89.7
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1939: from 1 to 58

- Alignment No. 13607
- gi No. 39890
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1939: from 14 to 32

- Alignment No. 13608
- gi No. 4008159
- % Identity 89.7
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1939: from 1 to 58

- Alignment No. 13609
- gi No. 4097575
- % Identity 86.2
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1939: from 1 to 58

- Alignment No. 13610
- gi No. 4097577
- % Identity 82.8
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1939: from 1 to 58

- Alignment No. 13611
- gi No. 4210948
- % Identity 91.4
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1939: from 1 to 58

- Alignment No. 13612
- gi No. 421809
- % Identity 89.7
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1939: from 1 to 58

- Alignment No. 13613
- gi No. 4589726
- % Identity 81
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1939: from 1 to 58

- Alignment No. 13614
- gi No. 461942
- % Identity 86.5
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1939: from 22 to 58

- Alignment No. 13615
- gi No. 461944
- % Identity 89.7
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1939: from 1 to 58

Maximum Length Sequence corresponding to clone ID 288024

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1940
- Ceres seq_id 1501755

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1941

- Ceres seq_id 1501756
- Location of start within SEQ ID NO 1940: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1942
- Ceres seq_id 1501757
- Location of start within SEQ ID NO 1940: at 155 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1943
- Ceres seq_id 1501758
- Location of start within SEQ ID NO 1940: at 207 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13616
- gi No. 2342735
- % Identity 81.8
- Alignment Length 55
- Location of Alignment in SEQ ID NO 1943: from 37 to 91

Maximum Length Sequence corresponding to clone ID 288145

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1944
- Ceres seq_id 1501763

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1945
- Ceres seq_id 1501764
- Location of start within SEQ ID NO 1944: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13617
- Ribosomal protein L14
- Location within SEQ ID NO 1945: from 28 to 149 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13618
- gi No. 103355
- % Identity 79.9
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1945: from 10 to 148

- Alignment No. 13619
- gi No. 132744
- % Identity 75.9
- Alignment Length 133
- Location of Alignment in SEQ ID NO 1945: from 17 to 149

- Alignment No. 13620
- gi No. 1350671
- % Identity 74.8

- Alignment Length 139
- Location of Alignment in SEQ ID NO 1945: from 10 to 148

- Alignment No. 13621
- gi No. 1350673
- % Identity 77
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1945: from 10 to 148

- Alignment No. 13622
- gi No. 1710495
- % Identity 95.4
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1945: from 10 to 96

- Alignment No. 13623
- gi No. 1710496
- % Identity 75
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1945: from 10 to 57

- Alignment No. 13624
- gi No. 2341028
- % Identity 96.3
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1945: from 14 to 149

- Alignment No. 13625
- gi No. 2459420
- % Identity 96.4
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1945: from 10 to 149

- Alignment No. 13626
- gi No. 2500265
- % Identity 77
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1945: from 10 to 148

- Alignment No. 13627
- gi No. 2706454
- % Identity 77.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 1945: from 13 to 149

- Alignment No. 13628
- gi No. 279650
- % Identity 82.7
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1945: from 10 to 148

- Alignment No. 13629
- gi No. 2982289
- % Identity 99.2
- Alignment Length 133
- Location of Alignment in SEQ ID NO 1945: from 17 to 149

- Alignment No. 13630
- gi No. 3851618
- % Identity 74.6
- Alignment Length 130

- Location of Alignment in SEQ ID NO 1945: from 20 to 149
- Alignment No. 13631
- gi No. 4028025
- % Identity 83.2
- Alignment Length 125
- Location of Alignment in SEQ ID NO 1945: from 14 to 138
- Alignment No. 13632
- gi No. 4506605
- % Identity 83.5
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1945: from 10 to 148
- Alignment No. 13633
- gi No. 4574244
- % Identity 90
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1945: from 10 to 149
- Alignment No. 13634
- gi No. 4583511
- % Identity 82.7
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1945: from 10 to 148
- Alignment No. 13635
- gi No. 5441537
- % Identity 82.7
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1945: from 10 to 148
- Alignment No. 13636
- gi No. 546005
- % Identity 75.5
- Alignment Length 49
- Location of Alignment in SEQ ID NO 1945: from 10 to 58
- Alignment No. 13637
- gi No. 730536
- % Identity 96.4
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1945: from 10 to 149

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1946
- Ceres seq_id 1501765
- Location of start within SEQ ID NO 1944: at 29 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13638
- Ribosomal protein L14
- Location within SEQ ID NO 1946: from 19 to 140 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13639
- gi No. 103355
- % Identity 79.9
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1946: from 1 to 139

- Alignment No. 13640
- gi No. 132744
- % Identity 75.9
- Alignment Length 133
- Location of Alignment in SEQ ID NO 1946: from 8 to 140

- Alignment No. 13641
- gi No. 1350671
- % Identity 74.8
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1946: from 1 to 139

- Alignment No. 13642
- gi No. 1350673
- % Identity 77
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1946: from 1 to 139

- Alignment No. 13643
- gi No. 1710495
- % Identity 95.4
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1946: from 1 to 87

- Alignment No. 13644
- gi No. 1710496
- % Identity 75
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1946: from 1 to 48

- Alignment No. 13645
- gi No. 2341028
- % Identity 96.3
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1946: from 5 to 140

- Alignment No. 13646
- gi No. 2459420
- % Identity 96.4
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1946: from 1 to 140

- Alignment No. 13647
- gi No. 2500265
- % Identity 77
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1946: from 1 to 139

- Alignment No. 13648
- gi No. 2706454
- % Identity 77.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 1946: from 4 to 140

- Alignment No. 13649
- gi No. 279650
- % Identity 82.7
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1946: from 1 to 139

- Alignment No. 13650
- gi No. 2982289
- % Identity 99.2
- Alignment Length 133
- Location of Alignment in SEQ ID NO 1946: from 8 to 140
- Alignment No. 13651
- gi No. 3851618
- % Identity 74.6
- Alignment Length 130
- Location of Alignment in SEQ ID NO 1946: from 11 to 140
- Alignment No. 13652
- gi No. 4028025
- % Identity 83.2
- Alignment Length 125
- Location of Alignment in SEQ ID NO 1946: from 5 to 129
- Alignment No. 13653
- gi No. 4506605
- % Identity 83.5
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1946: from 1 to 139
- Alignment No. 13654
- gi No. 4574244
- % Identity 90
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1946: from 1 to 140
- Alignment No. 13655
- gi No. 4583511
- % Identity 82.7
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1946: from 1 to 139
- Alignment No. 13656
- gi No. 5441537
- % Identity 82.7
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1946: from 1 to 139
- Alignment No. 13657
- gi No. 546005
- % Identity 75.5
- Alignment Length 49
- Location of Alignment in SEQ ID NO 1946: from 1 to 49
- Alignment No. 13658
- gi No. 730536
- % Identity 96.4
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1946: from 1 to 140

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1947
- Ceres seq_id 1501766
- Location of start within SEQ ID NO 1944: at 74 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 13659
- Ribosomal protein L14
- Location within SEQ ID NO 1947: from 4 to 125 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13660
- gi No. 103355
- % Identity 79.9
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1947: from 1 to 124
- Alignment No. 13661
- gi No. 132744
- % Identity 75.9
- Alignment Length 133
- Location of Alignment in SEQ ID NO 1947: from 1 to 125
- Alignment No. 13662
- gi No. 1350671
- % Identity 74.8
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1947: from 1 to 124
- Alignment No. 13663
- gi No. 1350673
- % Identity 77
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1947: from 1 to 124
- Alignment No. 13664
- gi No. 1710495
- % Identity 95.4
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1947: from 1 to 72
- Alignment No. 13665
- gi No. 1710496
- % Identity 75
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1947: from 1 to 33
- Alignment No. 13666
- gi No. 2341028
- % Identity 96.3
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1947: from 1 to 125
- Alignment No. 13667
- gi No. 2459420
- % Identity 96.4
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1947: from 1 to 125
- Alignment No. 13668
- gi No. 2500265
- % Identity 77
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1947: from 1 to 124
- Alignment No. 13669
- gi No. 2706454

- % Identity 77.4
- Alignment Length 137
- Location of Alignment in SEQ ID NO 1947: from 1 to 125

- Alignment No. 13670
- gi No. 279650
- % Identity 82.7
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1947: from 1 to 124

- Alignment No. 13671
- gi No. 2982289
- % Identity 99.2
- Alignment Length 133
- Location of Alignment in SEQ ID NO 1947: from 1 to 125

- Alignment No. 13672
- gi No. 3851618
- % Identity 74.6
- Alignment Length 130
- Location of Alignment in SEQ ID NO 1947: from 1 to 125

- Alignment No. 13673
- gi No. 4028025
- % Identity 83.2
- Alignment Length 125
- Location of Alignment in SEQ ID NO 1947: from 1 to 114

- Alignment No. 13674
- gi No. 4506605
- % Identity 83.5
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1947: from 1 to 124

- Alignment No. 13675
- gi No. 4574244
- % Identity 90
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1947: from 1 to 125

- Alignment No. 13676
- gi No. 4583511
- % Identity 82.7
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1947: from 1 to 124

- Alignment No. 13677
- gi No. 5441537
- % Identity 82.7
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1947: from 1 to 124

- Alignment No. 13678
- gi No. 546005
- % Identity 75.5
- Alignment Length 49
- Location of Alignment in SEQ ID NO 1947: from 1 to 34

- Alignment No. 13679
- gi No. 730536
- % Identity 96.4

- Alignment Length 140
- Location of Alignment in SEQ ID NO 1947: from 1 to 125

Maximum Length Sequence corresponding to clone ID 288149

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1948
- Ceres seq_id 1501771

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1949
- Ceres seq_id 1501772
- Location of start within SEQ ID NO 1948: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13680
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1949: from 88 to 176 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1950
- Ceres seq_id 1501773
- Location of start within SEQ ID NO 1948: at 136 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13681
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1950: from 43 to 131 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1951
- Ceres seq_id 1501774
- Location of start within SEQ ID NO 1948: at 241 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13682
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1951: from 8 to 96 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 288431

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1952
- Ceres seq_id 1501786

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1953
- Ceres seq_id 1501787
- Location of start within SEQ ID NO 1952: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13683
- gi No. 1184100
- % Identity 90.9

- Alignment Length 11
- Location of Alignment in SEQ ID NO 1953: from 40 to 50
- Alignment No. 13684
- gi No. 1914851
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1953: from 41 to 51
- Alignment No. 13685
- gi No. 688080
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1953: from 40 to 50

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1954
- Ceres seq_id 1501788
- Location of start within SEQ ID NO 1952: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13686
- gi No. 19917
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1954: from 30 to 40
- Alignment No. 13687
- gi No. 322760
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1954: from 30 to 40

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1955
- Ceres seq_id 1501789
- Location of start within SEQ ID NO 1952: at 26 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13688
- gi No. 19917
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1955: from 22 to 32
- Alignment No. 13689
- gi No. 322760
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1955: from 22 to 32

Maximum Length Sequence corresponding to clone ID 288440

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1956
- Ceres seq_id 1501794

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1957

- Ceres seq_id 1501795
- Location of start within SEQ ID NO 1956: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1958
- Ceres seq_id 1501796
- Location of start within SEQ ID NO 1956: at 182 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13690
- gi No. 4521249
- % Identity 71
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1958: from 1 to 92

- Alignment No. 13691
- gi No. 4587311
- % Identity 71
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1958: from 1 to 92

- Alignment No. 13692
- gi No. 4929561
- % Identity 71
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1958: from 1 to 92

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1959
- Ceres seq_id 1501797
- Location of start within SEQ ID NO 1956: at 209 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13693
- gi No. 4521249
- % Identity 71
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1959: from 1 to 83

- Alignment No. 13694
- gi No. 4587311
- % Identity 71
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1959: from 1 to 83

- Alignment No. 13695
- gi No. 4929561
- % Identity 71
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1959: from 1 to 83

Maximum Length Sequence corresponding to clone ID 288752

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1960
- Ceres seq_id 1501804
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1961
 - Ceres seq_id 1501805
 - Location of start within SEQ ID NO 1960: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13696
 - gi No. 1076501
 - % Identity 75
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 1961: from 62 to 73
- Alignment No. 13697
 - gi No. 1076501
 - % Identity 76.9
 - Alignment Length 13
 - Location of Alignment in SEQ ID NO 1961: from 62 to 73
- Alignment No. 13698
 - gi No. 1155068
 - % Identity 71.4
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 1961: from 62 to 73
- Alignment No. 13699
 - gi No. 1155068
 - % Identity 71.4
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 1961: from 62 to 73
- Alignment No. 13700
 - gi No. 1155068
 - % Identity 70.6
 - Alignment Length 17
 - Location of Alignment in SEQ ID NO 1961: from 62 to 74
- Alignment No. 13701
 - gi No. 1155068
 - % Identity 70.6
 - Alignment Length 17
 - Location of Alignment in SEQ ID NO 1961: from 62 to 74
- Alignment No. 13702
 - gi No. 2226329
 - % Identity 84.7
 - Alignment Length 59
 - Location of Alignment in SEQ ID NO 1961: from 34 to 91
- Alignment No. 13703
 - gi No. 399204
 - % Identity 86.4
 - Alignment Length 59
 - Location of Alignment in SEQ ID NO 1961: from 34 to 91
- Alignment No. 13704
 - gi No. 688422
 - % Identity 71.4

- Alignment Length 14
- Location of Alignment in SEQ ID NO 1961: from 79 to 91

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1962
- Ceres seq_id 1501806
- Location of start within SEQ ID NO 1960: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13705
- Plant lipid transfer protein family
- Location within SEQ ID NO 1962: from 81 to 137 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13706
- gi No. 1092083
- % Identity 76.5
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1962: from 112 to 128

- Alignment No. 13707
- gi No. 2226329
- % Identity 82
- Alignment Length 50
- Location of Alignment in SEQ ID NO 1962: from 89 to 136

- Alignment No. 13708
- gi No. 399204
- % Identity 81.6
- Alignment Length 49
- Location of Alignment in SEQ ID NO 1962: from 89 to 137

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1963
- Ceres seq_id 1501807
- Location of start within SEQ ID NO 1960: at 158 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 288760

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1964
- Ceres seq_id 1501810

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1965
- Ceres seq_id 1501811
- Location of start within SEQ ID NO 1964: at 115 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13709
- gi No. 1076418
- % Identity 77
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1965: from 11 to 109
- Alignment No. 13710

- gi No. 1717779
- % Identity 70.3
- Alignment Length 101
- Location of Alignment in SEQ ID NO 1965: from 9 to 109
- Alignment No. 13711
- gi No. 1942055
- % Identity 77
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1965: from 11 to 109
- Alignment No. 13712
- gi No. 2262173
- % Identity 72.3
- Alignment Length 101
- Location of Alignment in SEQ ID NO 1965: from 10 to 109
- Alignment No. 13713
- gi No. 2500128
- % Identity 70.2
- Alignment Length 94
- Location of Alignment in SEQ ID NO 1965: from 12 to 105
- Alignment No. 13714
- gi No. 2500129
- % Identity 71
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1965: from 11 to 109
- Alignment No. 13715
- gi No. 2500130
- % Identity 70.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1965: from 34 to 109

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1966
- Ceres seq_id 1501812
- Location of start within SEQ ID NO 1964: at 241 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13716
- gi No. 1076418
- % Identity 77
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1966: from 1 to 67
- Alignment No. 13717
- gi No. 1717779
- % Identity 70.3
- Alignment Length 101
- Location of Alignment in SEQ ID NO 1966: from 1 to 67
- Alignment No. 13718
- gi No. 1942055
- % Identity 77
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1966: from 1 to 67

- Alignment No. 13719
- gi No. 2262173
- % Identity 72.3
- Alignment Length 101
- Location of Alignment in SEQ ID NO 1966: from 1 to 67
- Alignment No. 13720
- gi No. 2500128
- % Identity 70.2
- Alignment Length 94
- Location of Alignment in SEQ ID NO 1966: from 1 to 63
- Alignment No. 13721
- gi No. 2500129
- % Identity 71
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1966: from 1 to 67
- Alignment No. 13722
- gi No. 2500130
- % Identity 70.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1966: from 1 to 67

Maximum Length Sequence corresponding to clone ID 288771

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1967
- Ceres seq_id 1501813

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1968
- Ceres seq_id 1501814
- Location of start within SEQ ID NO 1967: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13723
- gi No. 3128181
- % Identity 74.6
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1968: from 42 to 100

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1969
- Ceres seq_id 1501815
- Location of start within SEQ ID NO 1967: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1970
- Ceres seq_id 1501816
- Location of start within SEQ ID NO 1967: at 124 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13724
- gi No. 3128181

- % Identity 74.6
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1970: from 1 to 59

Maximum Length Sequence corresponding to clone ID 289873

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1971
- Ceres seq_id 1501824

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1972
- Ceres seq_id 1501825
- Location of start within SEQ ID NO 1971: at 304 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13725
- GDP dissociation inhibitor
- Location within SEQ ID NO 1972: from 1 to 100 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13726
- gi No. 2384758
- % Identity 70.1
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1972: from 1 to 100

- Alignment No. 13727
- gi No. 2384760
- % Identity 70.9
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1972: from 1 to 100

- Alignment No. 13728
- gi No. 2501850
- % Identity 74.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 1972: from 1 to 100

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1973
- Ceres seq_id 1501826
- Location of start within SEQ ID NO 1971: at 319 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13729
- GDP dissociation inhibitor
- Location within SEQ ID NO 1973: from 1 to 95 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13730
- gi No. 2384758
- % Identity 70.1
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1973: from 1 to 95

- Alignment No. 13731
- gi No. 2384760
- % Identity 70.9
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1973: from 1 to 95

- Alignment No. 13732
- gi No. 2501850
- % Identity 74.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 1973: from 1 to 95

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1974
- Ceres seq_id 1501827
- Location of start within SEQ ID NO 1971: at 322 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13733
- GDP dissociation inhibitor
- Location within SEQ ID NO 1974: from 1 to 94 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13734
- gi No. 2384758
- % Identity 70.1
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1974: from 1 to 94

- Alignment No. 13735
- gi No. 2384760
- % Identity 70.9
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1974: from 1 to 94

- Alignment No. 13736
- gi No. 2501850
- % Identity 74.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 1974: from 1 to 94

Maximum Length Sequence corresponding to clone ID 289892

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1975
- Ceres seq_id 1501828

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1976
- Ceres seq_id 1501829
- Location of start within SEQ ID NO 1975: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13737
- gi No. 3860272
- % Identity 85.6
- Alignment Length 105
- Location of Alignment in SEQ ID NO 1976: from 62 to 163

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1977
- Ceres seq_id 1501830
- Location of start within SEQ ID NO 1975: at 186 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13738
- gi No. 3860272
- % Identity 85.6
- Alignment Length 105
- Location of Alignment in SEQ ID NO 1977: from 1 to 102

Maximum Length Sequence corresponding to clone ID 291908

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1978
- Ceres seq_id 1501850

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1979
- Ceres seq_id 1501851
- Location of start within SEQ ID NO 1978: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1980
- Ceres seq_id 1501852
- Location of start within SEQ ID NO 1978: at 12 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1981
- Ceres seq_id 1501853
- Location of start within SEQ ID NO 1978: at 101 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 13739
- Thioredoxin
- Location within SEQ ID NO 1981: from 31 to 139 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13740
- gi No. 1848212
- % Identity 75.4
- Alignment Length 138
- Location of Alignment in SEQ ID NO 1981: from 7 to 143
- Alignment No. 13741
- gi No. 2529680
- % Identity 74.6
- Alignment Length 138
- Location of Alignment in SEQ ID NO 1981: from 7 to 143
- Alignment No. 13742
- gi No. 729442
- % Identity 74.3
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1981: from 5 to 143

- Alignment No. 13743
- gi No. 99991
- % Identity 89.5
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1981: from 52 to 70

- Alignment No. 13744
- gi No. 99991
- % Identity 100
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1981: from 51 to 70

Maximum Length Sequence corresponding to clone ID 292482

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1982
- Ceres seq_id 1501862

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1983
- Ceres seq_id 1501863
- Location of start within SEQ ID NO 1982: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1984
- Ceres seq_id 1501864
- Location of start within SEQ ID NO 1982: at 76 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13745
- Ribosomal protein L13e
- Location within SEQ ID NO 1984: from 6 to 82 aa.

- Alignment No. 13746
- Fatty acid desaturase
- Location within SEQ ID NO 1984: from 77 to 131 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13747
- gi No. 1350664
- % Identity 89
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1984: from 10 to 82

- Alignment No. 13748
- gi No. 2662188
- % Identity 70.6
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1984: from 1 to 84

- Alignment No. 13749
- gi No. 730449
- % Identity 86.9
- Alignment Length 84
- Location of Alignment in SEQ ID NO 1984: from 2 to 84

- Alignment No. 13750
- gi No. 730450

- % Identity 88.9
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1984: from 2 to 82
- Alignment No. 13751
- gi No. 730526
- % Identity 88.9
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1984: from 2 to 82

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1985
- Ceres seq_id 1501865
- Location of start within SEQ ID NO 1982: at 274 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13752
- Fatty acid desaturase
- Location within SEQ ID NO 1985: from 11 to 65 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13753
- gi No. 1350664
- % Identity 89
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1985: from 1 to 16
- Alignment No. 13754
- gi No. 2662188
- % Identity 70.6
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1985: from 1 to 18
- Alignment No. 13755
- gi No. 730449
- % Identity 86.9
- Alignment Length 84
- Location of Alignment in SEQ ID NO 1985: from 1 to 18
- Alignment No. 13756
- gi No. 730450
- % Identity 88.9
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1985: from 1 to 16
- Alignment No. 13757
- gi No. 730526
- % Identity 88.9
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1985: from 1 to 16

Maximum Length Sequence corresponding to clone ID 293228

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1986
- Ceres seq_id 1501872

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1987
- Ceres seq_id 1501873
- Location of start within SEQ ID NO 1986: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1988
- Ceres seq_id 1501874
- Location of start within SEQ ID NO 1986: at 92 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13758
- Oleosin
- Location within SEQ ID NO 1988: from 1 to 78 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1989
- Ceres seq_id 1501875
- Location of start within SEQ ID NO 1986: at 161 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13759
- Oleosin
- Location within SEQ ID NO 1989: from 1 to 55 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 293659

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1990
- Ceres seq_id 1501884

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1991
- Ceres seq_id 1501885
- Location of start within SEQ ID NO 1990: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1992
- Ceres seq_id 1501886
- Location of start within SEQ ID NO 1990: at 217 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13760
- gi No. 166410
- % Identity 78.8
- Alignment Length 113
- Location of Alignment in SEQ ID NO 1992: from 1 to 112
- Alignment No. 13761
- gi No. 3894178
- % Identity 81.4
- Alignment Length 102

- Location of Alignment in SEQ ID NO 1992: from 12 to 112
- Alignment No. 13762
- gi No. 4091080
- % Identity 79.3
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1992: from 3 to 112
- Alignment No. 13763
- gi No. 4091117
- % Identity 79.3
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1992: from 3 to 112
- Alignment No. 13764
- gi No. 4884860
- % Identity 75.7
- Alignment Length 115
- Location of Alignment in SEQ ID NO 1992: from 3 to 112

(B) Polypeptide Sequence

- Pat. Appin. SEQ ID NO 1993
- Ceres seq_id 1501887
- Location of start within SEQ ID NO 1990: at 346 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13765
- gi No. 166410
- % Identity 78.8
- Alignment Length 113
- Location of Alignment in SEQ ID NO 1993: from 1 to 69
- Alignment No. 13766
- gi No. 3894178
- % Identity 81.4
- Alignment Length 102
- Location of Alignment in SEQ ID NO 1993: from 1 to 69
- Alignment No. 13767
- gi No. 4091080
- % Identity 79.3
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1993: from 1 to 69
- Alignment No. 13768
- gi No. 4091117
- % Identity 79.3
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1993: from 1 to 69
- Alignment No. 13769
- gi No. 4884860
- % Identity 75.7
- Alignment Length 115
- Location of Alignment in SEQ ID NO 1993: from 1 to 69

Maximum Length Sequence corresponding to clone ID 293683

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1994

- Ceres seq_id 1501888
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1995
 - Ceres seq_id 1501889
 - Location of start within SEQ ID NO 1994: at 203 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13770
- Aminotransferases class-I
- Location within SEQ ID NO 1995: from 16 to 109 aa.

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1996
 - Ceres seq_id 1501890
 - Location of start within SEQ ID NO 1994: at 257 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13771
- Aminotransferases class-I
- Location within SEQ ID NO 1996: from 1 to 91 aa.

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1997
 - Ceres seq_id 1501891
 - Location of start within SEQ ID NO 1994: at 299 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13772
- Aminotransferases class-I
- Location within SEQ ID NO 1997: from 1 to 77 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 293689

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 1998
 - Ceres seq_id 1501895
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 1999
 - Ceres seq_id 1501896
 - Location of start within SEQ ID NO 1998: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13773
- DnaJ domain
- Location within SEQ ID NO 1999: from 5 to 51 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13774
- gi No. 126757
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1999: from 13 to 47

- Alignment No. 13775
- gi No. 30851
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1999: from 24 to 47

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2000
- Ceres seq_id 1501897
- Location of start within SEQ ID NO 1998: at 29 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13776
- gi No. 126757
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2000: from 4 to 38

- Alignment No. 13777
- gi No. 30851
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2000: from 15 to 38

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2001
- Ceres seq_id 1501898
- Location of start within SEQ ID NO 1998: at 86 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13778
- gi No. 126757
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2001: from 1 to 19

- Alignment No. 13779
- gi No. 30851
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2001: from 1 to 19

Maximum Length Sequence corresponding to clone ID 293692

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2002
- Ceres seq_id 1501899

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2003
- Ceres seq_id 1501900
- Location of start within SEQ ID NO 2002: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13780
- Pyruvate kinase
- Location within SEQ ID NO 2003: from 110 to 143 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13781
- gi No. 125606
- % Identity 90
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2003: from 105 to 143

- Alignment No. 13782
- gi No. 2497538
- % Identity 87.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2003: from 105 to 143

- Alignment No. 13783
- gi No. 2497543
- % Identity 91.7
- Alignment Length 36
- Location of Alignment in SEQ ID NO 2003: from 109 to 143

- Alignment No. 13784
- gi No. 322787
- % Identity 90
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2003: from 105 to 143

- Alignment No. 13785
- gi No. 4033431
- % Identity 86.1
- Alignment Length 36
- Location of Alignment in SEQ ID NO 2003: from 109 to 143

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2004
- Ceres seq_id 1501901
- Location of start within SEQ ID NO 2002: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13786
- gi No. 2134206
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2004: from 53 to 63

Maximum Length Sequence corresponding to clone ID 293697

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2005
- Ceres seq_id 1501902

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2006
- Ceres seq_id 1501903
- Location of start within SEQ ID NO 2005: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13787
- gi No. 1947160
- % Identity 72.7

- Alignment Length 11
- Location of Alignment in SEQ ID NO 2006: from 24 to 34
- Alignment No. 13788
- gi No. 3858883
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2006: from 18 to 28
- Alignment No. 13789
- gi No. 4996894
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2006: from 24 to 34

(B) Polypeptide Sequence

- Pat. Appn. SEQ ID NO 2007
- Ceres seq_id 1501904
- Location of start within SEQ ID NO 2005: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13790
- Syndecan domain
- Location within SEQ ID NO 2007: from 39 to 141 aa.
- Alignment No. 13791
- Assemblin (Peptidase family S21)
- Location within SEQ ID NO 2007: from 24 to 139 aa.
- Alignment No. 13792
- Mucin-like glycoprotein
- Location within SEQ ID NO 2007: from 35 to 140 aa.
- Alignment No. 13793
- Mucin-like glycoprotein
- Location within SEQ ID NO 2007: from 35 to 141 aa.
- Alignment No. 13794
- Mucin-like glycoprotein
- Location within SEQ ID NO 2007: from 41 to 139 aa.
- Alignment No. 13795
- Mucin-like glycoprotein
- Location within SEQ ID NO 2007: from 59 to 139 aa.
- Alignment No. 13796
- Mucin-like glycoprotein
- Location within SEQ ID NO 2007: from 76 to 139 aa.
- Alignment No. 13797
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2007: from 21 to 137 aa.
- Alignment No. 13798
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2007: from 21 to 141 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13799
- gi No. 585527

- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2007: from 128 to 141

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2008
- Ceres seq_id 1501905
- Location of start within SEQ ID NO 2005: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13800
- gi No. 113928
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2008: from 7 to 18
- Alignment No. 13801
- gi No. 1914853
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2008: from 18 to 28
- Alignment No. 13802
- gi No. 2077900
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2008: from 17 to 27
- Alignment No. 13803
- gi No. 280655
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2008: from 7 to 18

Maximum Length Sequence corresponding to clone ID 293718

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2009
- Ceres seq_id 1501906

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2010
- Ceres seq_id 1501907
- Location of start within SEQ ID NO 2009: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13804
- gi No. 2909522
- % Identity 75
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2010: from 1 to 28

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2011
- Ceres seq_id 1501908
- Location of start within SEQ ID NO 2009: at 388 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2012
- Ceres seq_id 1501909
- Location of start within SEQ ID NO 2009: at 407 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 293854

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2013
- Ceres seq_id 1501922

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2014
- Ceres seq_id 1501923
- Location of start within SEQ ID NO 2013: at 208 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13805
- Peroxidase
- Location within SEQ ID NO 2014: from 48 to 113 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2015
- Ceres seq_id 1501924
- Location of start within SEQ ID NO 2013: at 223 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13806
- Peroxidase
- Location within SEQ ID NO 2015: from 43 to 108 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2016
- Ceres seq_id 1501925
- Location of start within SEQ ID NO 2013: at 226 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13807
- Peroxidase
- Location within SEQ ID NO 2016: from 42 to 107 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 293858

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2017
- Ceres seq_id 1501926

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2018
- Ceres seq_id 1501927

- Location of start within SEQ ID NO 2017: at 190 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13808
- Synaptobrevin
- Location within SEQ ID NO 2018: from 62 to 121 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13809
- gi No. 3157951
- % Identity 88.5
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2018: from 62 to 121

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2019
- Ceres seq_id 1501928
- Location of start within SEQ ID NO 2017: at 205 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13810
- Synaptobrevin
- Location within SEQ ID NO 2019: from 57 to 116 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13811
- gi No. 3157951
- % Identity 88.5
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2019: from 57 to 116

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2020
- Ceres seq_id 1501929
- Location of start within SEQ ID NO 2017: at 346 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13812
- Synaptobrevin
- Location within SEQ ID NO 2020: from 10 to 69 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13813
- gi No. 3157951
- % Identity 88.5
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2020: from 10 to 69

Maximum Length Sequence corresponding to clone ID 293863

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2021
- Ceres seq_id 1501930

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2022
- Ceres seq_id 1501931
- Location of start within SEQ ID NO 2021: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2023
- Ceres seq_id 1501932
- Location of start within SEQ ID NO 2021: at 97 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13814
- gi No. 2213626
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2023: from 9 to 27
- Alignment No. 13815
- gi No. 4850408
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2023: from 13 to 31

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2024
- Ceres seq_id 1501933
- Location of start within SEQ ID NO 2021: at 240 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 293882

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2025
- Ceres seq_id 1501949

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2026
- Ceres seq_id 1501950
- Location of start within SEQ ID NO 2025: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2027
- Ceres seq_id 1501951
- Location of start within SEQ ID NO 2025: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2028
- Ceres seq_id 1501952
- Location of start within SEQ ID NO 2025: at 96 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 13816
- ABC transporter
- Location within SEQ ID NO 2028: from 83 to 147 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 297023

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2029
- Ceres seq_id 1501976

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2030
- Ceres seq_id 1501977
- Location of start within SEQ ID NO 2029: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2031
- Ceres seq_id 1501978
- Location of start within SEQ ID NO 2029: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13817
- gi No. 4678325
- % Identity 78.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 2031: from 41 to 110

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2032
- Ceres seq_id 1501979
- Location of start within SEQ ID NO 2029: at 75 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13818
- gi No. 4678325
- % Identity 78.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 2032: from 17 to 86

Maximum Length Sequence corresponding to clone ID 297685

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2033
- Ceres seq_id 1502003

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2034
- Ceres seq_id 1502004
- Location of start within SEQ ID NO 2033: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2035
- Ceres seq_id 1502005
- Location of start within SEQ ID NO 2033: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13819
- Gag polyprotein, inner coat protein p12
- Location within SEQ ID NO 2035: from 35 to 89 aa.
- Alignment No. 13820
- Mucin-like glycoprotein
- Location within SEQ ID NO 2035: from 12 to 130 aa.
- Alignment No. 13821
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2035: from 27 to 85 aa.
- Alignment No. 13822
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2035: from 27 to 93 aa.
- Alignment No. 13823
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2035: from 33 to 116 aa.
- Alignment No. 13824
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2035: from 34 to 116 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13825
- gi No. 2134206
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2035: from 136 to 146
- Alignment No. 13826
- gi No. 2134208
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2035: from 136 to 146
- Alignment No. 13827
- gi No. 2134209
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2035: from 136 to 146
- Alignment No. 13828
- gi No. 2507155
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2035: from 45 to 55
- Alignment No. 13829
- gi No. 439289
- % Identity 72.7
- Alignment Length 11

- Location of Alignment in SEQ ID NO 2035: from 45 to 55
- Alignment No. 13830
- gi No. 871535
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2035: from 45 to 55
- Alignment No. 13831
- gi No. 93144
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2035: from 32 to 52
- Alignment No. 13832
- gi No. 93144
- % Identity 73.9
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2035: from 32 to 54

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2036
- Ceres seq_id 1502006
- Location of start within SEQ ID NO 2033: at 116 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 297707

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2037
- Ceres seq_id 1502011

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2038
- Ceres seq_id 1502012
- Location of start within SEQ ID NO 2037: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13833
- gi No. 3915131
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 2038: from 24 to 61

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2039
- Ceres seq_id 1502013
- Location of start within SEQ ID NO 2037: at 210 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13834
- GMC oxidoreductases
- Location within SEQ ID NO 2039: from 1 to 55 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13835
- gi No. 4903006

- % Identity 71.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 2039: from 1 to 63

- Alignment No. 13836
- gi No. 4903018
- % Identity 71.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 2039: from 1 to 63

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2040
- Ceres seq_id 1502014
- Location of start within SEQ ID NO 2037: at 575 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 297709

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2041
- Ceres seq_id 1502015

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2042
- Ceres seq_id 1502016
- Location of start within SEQ ID NO 2041: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2043
- Ceres seq_id 1502017
- Location of start within SEQ ID NO 2041: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13837
- gi No. 82087
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2043: from 41 to 54

- Alignment No. 13838
- gi No. 82087
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2043: from 41 to 54

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2044
- Ceres seq_id 1502018
- Location of start within SEQ ID NO 2041: at 78 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13839

- gi No. 82087
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2044: from 16 to 29

- Alignment No. 13840
- gi No. 82087
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2044: from 16 to 29

Maximum Length Sequence corresponding to clone ID 297786

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2045
- Ceres seq_id 1502023

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2046
- Ceres seq_id 1502024
- Location of start within SEQ ID NO 2045: at 126 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13841
- Zinc finger, C3HC4 type (RING finger)
- Location within SEQ ID NO 2046: from 78 to 129 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2047
- Ceres seq_id 1502025
- Location of start within SEQ ID NO 2045: at 289 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2048
- Ceres seq_id 1502026
- Location of start within SEQ ID NO 2045: at 298 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 297797

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2049
- Ceres seq_id 1502027

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2050
- Ceres seq_id 1502028
- Location of start within SEQ ID NO 2049: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2051

- Ceres seq_id 1502029
- Location of start within SEQ ID NO 2049: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2052
- Ceres seq_id 1502030
- Location of start within SEQ ID NO 2049: at 256 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13842
- Ubiquitin-conjugating enzyme
- Location within SEQ ID NO 2052: from 1 to 81 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13843
- gi No. 1174852
- % Identity 78.9
- Alignment Length 76
- Location of Alignment in SEQ ID NO 2052: from 7 to 81

- Alignment No. 13844
- gi No. 136647
- % Identity 86.7
- Alignment Length 60
- Location of Alignment in SEQ ID NO 2052: from 23 to 81

- Alignment No. 13845
- gi No. 2129758
- % Identity 83.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2052: from 6 to 81

- Alignment No. 13846
- gi No. 2624417
- % Identity 98.8
- Alignment Length 82
- Location of Alignment in SEQ ID NO 2052: from 1 to 81

- Alignment No. 13847
- gi No. 2641619
- % Identity 89
- Alignment Length 82
- Location of Alignment in SEQ ID NO 2052: from 1 to 81

- Alignment No. 13848
- gi No. 992706
- % Identity 80.5
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2052: from 6 to 81

Maximum Length Sequence corresponding to clone ID 297802

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2053
- Ceres seq_id 1502031

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2054

- Ceres_seq_id 1502032
- Location of start within SEQ ID NO 2053: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13849
- Aminotransferases class-III pyridoxal-phosphate
- Location within SEQ ID NO 2054: from 110 to 174 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13850
- gi No. 100332
- % Identity 70.4
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2054: from 35 to 174

- Alignment No. 13851
- gi No. 1170029
- % Identity 85.7
- Alignment Length 154
- Location of Alignment in SEQ ID NO 2054: from 22 to 174

- Alignment No. 13852
- gi No. 1170031
- % Identity 71.4
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2054: from 29 to 174

- Alignment No. 13853
- gi No. 1170032
- % Identity 74
- Alignment Length 104
- Location of Alignment in SEQ ID NO 2054: from 72 to 174

- Alignment No. 13854
- gi No. 2492858
- % Identity 76.1
- Alignment Length 92
- Location of Alignment in SEQ ID NO 2054: from 84 to 174

- Alignment No. 13855
- gi No. 2492862
- % Identity 77.2
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2054: from 53 to 174

- Alignment No. 13856
- gi No. 2982001
- % Identity 74
- Alignment Length 104
- Location of Alignment in SEQ ID NO 2054: from 72 to 174

- Alignment No. 13857
- gi No. 399785
- % Identity 78
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2054: from 53 to 174

- Alignment No. 13858
- gi No. 97570
- % Identity 75

- Alignment Length 104
- Location of Alignment in SEQ ID NO 2054: from 72 to 174

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2055
- Ceres seq_id 1502033
- Location of start within SEQ ID NO 2053: at 64 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13859
- Aminotransferases class-III pyridoxal-phosphate
- Location within SEQ ID NO 2055: from 89 to 153 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13860
- gi No. 100332
- % Identity 70.4
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2055: from 14 to 153
- Alignment No. 13861
- gi No. 1170029
- % Identity 85.7
- Alignment Length 154
- Location of Alignment in SEQ ID NO 2055: from 1 to 153
- Alignment No. 13862
- gi No. 1170031
- % Identity 71.4
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2055: from 8 to 153
- Alignment No. 13863
- gi No. 1170032
- % Identity 74
- Alignment Length 104
- Location of Alignment in SEQ ID NO 2055: from 51 to 153
- Alignment No. 13864
- gi No. 2492858
- % Identity 76.1
- Alignment Length 92
- Location of Alignment in SEQ ID NO 2055: from 63 to 153
- Alignment No. 13865
- gi No. 2492862
- % Identity 77.2
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2055: from 32 to 153
- Alignment No. 13866
- gi No. 2982001
- % Identity 74
- Alignment Length 104
- Location of Alignment in SEQ ID NO 2055: from 51 to 153
- Alignment No. 13867
- gi No. 399785
- % Identity 78
- Alignment Length 123

- Location of Alignment in SEQ ID NO 2055: from 32 to 153
- Alignment No. 13868
- gi No. 97570
- % Identity 75
- Alignment Length 104
- Location of Alignment in SEQ ID NO 2055: from 51 to 153

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2056
- Ceres seq_id 1502034
- Location of start within SEQ ID NO 2053: at 124 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13869
- Aminotransferases class-III pyridoxal-phosphate
- Location within SEQ ID NO 2056: from 69 to 133 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13870
- gi No. 100332
- % Identity 70.4
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2056: from 1 to 133
- Alignment No. 13871
- gi No. 1170029
- % Identity 85.7
- Alignment Length 154
- Location of Alignment in SEQ ID NO 2056: from 1 to 133
- Alignment No. 13872
- gi No. 1170031
- % Identity 71.4
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2056: from 1 to 133
- Alignment No. 13873
- gi No. 1170032
- % Identity 74
- Alignment Length 104
- Location of Alignment in SEQ ID NO 2056: from 31 to 133
- Alignment No. 13874
- gi No. 2492858
- % Identity 76.1
- Alignment Length 92
- Location of Alignment in SEQ ID NO 2056: from 43 to 133
- Alignment No. 13875
- gi No. 2492862
- % Identity 77.2
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2056: from 12 to 133
- Alignment No. 13876
- gi No. 2982001
- % Identity 74
- Alignment Length 104
- Location of Alignment in SEQ ID NO 2056: from 31 to 133

- Alignment No. 13877
- gi No. 399785
- % Identity 78
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2056: from 12 to 133

- Alignment No. 13878
- gi No. 97570
- % Identity 75
- Alignment Length 104
- Location of Alignment in SEQ ID NO 2056: from 31 to 133

Maximum Length Sequence corresponding to clone ID 297826

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2057
- Ceres seq_id 1502035

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2058
- Ceres seq_id 1502036
- Location of start within SEQ ID NO 2057: at 72 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13879
- Bowman-Birk serine protease inhibitor family
- Location within SEQ ID NO 2058: from 67 to 119 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2059
- Ceres seq_id 1502037
- Location of start within SEQ ID NO 2057: at 78 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13880
- Bowman-Birk serine protease inhibitor family
- Location within SEQ ID NO 2059: from 65 to 117 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2060
- Ceres seq_id 1502038
- Location of start within SEQ ID NO 2057: at 102 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13881
- Bowman-Birk serine protease inhibitor family
- Location within SEQ ID NO 2060: from 57 to 109 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 298533

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2061
- Ceres seq_id 1502048

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2062
- Ceres seq_id 1502049
- Location of start within SEQ ID NO 2061: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2063
- Ceres seq_id 1502050
- Location of start within SEQ ID NO 2061: at 109 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13882
- Sugar (and other) transporter
- Location within SEQ ID NO 2063: from 26 to 175 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 298547

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2064
- Ceres seq_id 1502056

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2065
- Ceres seq_id 1502057
- Location of start within SEQ ID NO 2064: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2066
- Ceres seq_id 1502058
- Location of start within SEQ ID NO 2064: at 330 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13883
- gi No. 3402683
- % Identity 81.5
- Alignment Length 27
- Location of Alignment in SEQ ID NO 2066: from 22 to 48

- Alignment No. 13884

- gi No. 4678298

- % Identity 95.7

- Alignment Length 23

- Location of Alignment in SEQ ID NO 2066: from 22 to 44

- Alignment No. 13885

- gi No. 4914404

- % Identity 79.3

- Alignment Length 29

- Location of Alignment in SEQ ID NO 2066: from 24 to 52

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2067
- Ceres seq_id 1502059
- Location of start within SEQ ID NO 2064: at 348 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13886
- gi No. 3402683
- % Identity 81.5
- Alignment Length 27
- Location of Alignment in SEQ ID NO 2067: from 16 to 42
- Alignment No. 13887
- gi No. 4678298
- % Identity 95.7
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2067: from 16 to 38
- Alignment No. 13888
- gi No. 4914404
- % Identity 79.3
- Alignment Length 29
- Location of Alignment in SEQ ID NO 2067: from 18 to 46

Maximum Length Sequence corresponding to clone ID 298567

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2068
- Ceres seq_id 1502066

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2069
- Ceres seq_id 1502067
- Location of start within SEQ ID NO 2068: at 140 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13889
- DnaJ domain
- Location within SEQ ID NO 2069: from 12 to 79 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 298580

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2070
- Ceres seq_id 1502074

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2071
- Ceres seq_id 1502075
- Location of start within SEQ ID NO 2070: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13890
- Collagen triple helix repeat (20 copies)
- Location within SEQ ID NO 2071: from 70 to 120 aa.
- Alignment No. 13891
- Mucin-like glycoprotein
- Location within SEQ ID NO 2071: from 34 to 153 aa.

- Alignment No. 13892
- Mucin-like glycoprotein
- Location within SEQ ID NO 2071: from 58 to 148 aa.
- Alignment No. 13893
- Mucin-like glycoprotein
- Location within SEQ ID NO 2071: from 58 to 151 aa.
- Alignment No. 13894
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2071: from 41 to 153 aa.
- Alignment No. 13895
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2071: from 48 to 153 aa.
- Alignment No. 13896
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2071: from 59 to 134 aa.
- Alignment No. 13897
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2071: from 61 to 116 aa.
- Alignment No. 13898
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2071: from 61 to 140 aa.
- Alignment No. 13899
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2071: from 61 to 147 aa.
- Alignment No. 13900
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2071: from 61 to 150 aa.
- Alignment No. 13901
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2071: from 61 to 153 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13902
- gi No. 100687
- % Identity 70.6
- Alignment Length 138
- Location of Alignment in SEQ ID NO 2071: from 32 to 153
- Alignment No. 13903
- gi No. 228937
- % Identity 91.5
- Alignment Length 136
- Location of Alignment in SEQ ID NO 2071: from 28 to 153
- Alignment No. 13904
- gi No. 228938
- % Identity 93.3
- Alignment Length 134
- Location of Alignment in SEQ ID NO 2071: from 28 to 153
- Alignment No. 13905
- gi No. 283032

- % Identity 96.2
- Alignment Length 130
- Location of Alignment in SEQ ID NO 2071: from 28 to 153
- Alignment No. 13906
- gi No. 283045
- % Identity 91.9
- Alignment Length 136
- Location of Alignment in SEQ ID NO 2071: from 28 to 153
- Alignment No. 13907
- gi No. 458468
- % Identity 71.8
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2071: from 107 to 141
- Alignment No. 13908
- gi No. 458468
- % Identity 75.7
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2071: from 118 to 153
- Alignment No. 13909
- gi No. 458468
- % Identity 76.3
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2071: from 112 to 149
- Alignment No. 13910
- gi No. 458468
- % Identity 75
- Alignment Length 43
- Location of Alignment in SEQ ID NO 2071: from 112 to 151
- Alignment No. 13911
- gi No. 458468
- % Identity 72.5
- Alignment Length 43
- Location of Alignment in SEQ ID NO 2071: from 112 to 151
- Alignment No. 13912
- gi No. 458468
- % Identity 71.4
- Alignment Length 44
- Location of Alignment in SEQ ID NO 2071: from 107 to 148
- Alignment No. 13913
- gi No. 82698
- % Identity 91.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 2071: from 28 to 153

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2072
- Ceres seq_id 1502076
- Location of start within SEQ ID NO 2070: at 80 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13914
- Collagen triple helix repeat (20 copies)

- Location within SEQ ID NO 2072: from 44 to 94 aa.
- Alignment No. 13915
- Mucin-like glycoprotein
- Location within SEQ ID NO 2072: from 8 to 127 aa.
- Alignment No. 13916
- Mucin-like glycoprotein
- Location within SEQ ID NO 2072: from 32 to 122 aa.
- Alignment No. 13917
- Mucin-like glycoprotein
- Location within SEQ ID NO 2072: from 32 to 125 aa.
- Alignment No. 13918
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2072: from 15 to 127 aa.
- Alignment No. 13919
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2072: from 22 to 127 aa.
- Alignment No. 13920
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2072: from 33 to 108 aa.
- Alignment No. 13921
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2072: from 35 to 90 aa.
- Alignment No. 13922
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2072: from 35 to 114 aa.
- Alignment No. 13923
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2072: from 35 to 121 aa.
- Alignment No. 13924
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2072: from 35 to 124 aa.
- Alignment No. 13925
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2072: from 35 to 127 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13926
- gi No. 100687
- % Identity 70.6
- Alignment Length 138
- Location of Alignment in SEQ ID NO 2072: from 6 to 127
- Alignment No. 13927
- gi No. 228937
- % Identity 91.5
- Alignment Length 136
- Location of Alignment in SEQ ID NO 2072: from 2 to 127
- Alignment No. 13928
- gi No. 228938

- % Identity 93.3
- Alignment Length 134
- Location of Alignment in SEQ ID NO 2072: from 2 to 127

- Alignment No. 13929
- gi No. 283032
- % Identity 96.2
- Alignment Length 130
- Location of Alignment in SEQ ID NO 2072: from 2 to 127

- Alignment No. 13930
- gi No. 283045
- % Identity 91.9
- Alignment Length 136
- Location of Alignment in SEQ ID NO 2072: from 2 to 127

- Alignment No. 13931
- gi No. 458468
- % Identity 71.8
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2072: from 81 to 115

- Alignment No. 13932
- gi No. 458468
- % Identity 75.7
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2072: from 92 to 127

- Alignment No. 13933
- gi No. 458468
- % Identity 76.3
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2072: from 86 to 123

- Alignment No. 13934
- gi No. 458468
- % Identity 75
- Alignment Length 43
- Location of Alignment in SEQ ID NO 2072: from 86 to 125

- Alignment No. 13935
- gi No. 458468
- % Identity 72.5
- Alignment Length 43
- Location of Alignment in SEQ ID NO 2072: from 86 to 125

- Alignment No. 13936
- gi No. 458468
- % Identity 71.4
- Alignment Length 44
- Location of Alignment in SEQ ID NO 2072: from 81 to 122

- Alignment No. 13937
- gi No. 82698
- % Identity 91.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 2072: from 2 to 127

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2073
- Ceres seq_id 1502077

- Location of start within SEQ ID NO 2070: at 83 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13938
 - Collagen triple helix repeat (20 copies)
 - Location within SEQ ID NO 2073: from 43 to 93 aa.
- Alignment No. 13939
 - Mucin-like glycoprotein
 - Location within SEQ ID NO 2073: from 7 to 126 aa.
- Alignment No. 13940
 - Mucin-like glycoprotein
 - Location within SEQ ID NO 2073: from 31 to 121 aa.
- Alignment No. 13941
 - Mucin-like glycoprotein
 - Location within SEQ ID NO 2073: from 31 to 124 aa.
- Alignment No. 13942
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 2073: from 14 to 126 aa.
- Alignment No. 13943
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 2073: from 21 to 126 aa.
- Alignment No. 13944
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 2073: from 32 to 107 aa.
- Alignment No. 13945
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 2073: from 34 to 89 aa.
- Alignment No. 13946
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 2073: from 34 to 113 aa.
- Alignment No. 13947
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 2073: from 34 to 120 aa.
- Alignment No. 13948
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 2073: from 34 to 123 aa.
- Alignment No. 13949
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 2073: from 34 to 126 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13950
 - gi No. 100687
 - % Identity 70.6
 - Alignment Length 138
 - Location of Alignment in SEQ ID NO 2073: from 5 to 126
- Alignment No. 13951
 - gi No. 228937

- % Identity 91.5
- Alignment Length 136
- Location of Alignment in SEQ ID NO 2073: from 1 to 126

- Alignment No. 13952
- gi No. 228938
- % Identity 93.3
- Alignment Length 134
- Location of Alignment in SEQ ID NO 2073: from 1 to 126

- Alignment No. 13953
- gi No. 283032
- % Identity 96.2
- Alignment Length 130
- Location of Alignment in SEQ ID NO 2073: from 1 to 126

- Alignment No. 13954
- gi No. 283045
- % Identity 91.9
- Alignment Length 136
- Location of Alignment in SEQ ID NO 2073: from 1 to 126

- Alignment No. 13955
- gi No. 458468
- % Identity 71.8
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2073: from 80 to 114

- Alignment No. 13956
- gi No. 458468
- % Identity 75.7
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2073: from 91 to 126

- Alignment No. 13957
- gi No. 458468
- % Identity 76.3
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2073: from 85 to 122

- Alignment No. 13958
- gi No. 458468
- % Identity 75
- Alignment Length 43
- Location of Alignment in SEQ ID NO 2073: from 85 to 124

- Alignment No. 13959
- gi No. 458468
- % Identity 72.5
- Alignment Length 43
- Location of Alignment in SEQ ID NO 2073: from 85 to 124

- Alignment No. 13960
- gi No. 458468
- % Identity 71.4
- Alignment Length 44
- Location of Alignment in SEQ ID NO 2073: from 80 to 121

- Alignment No. 13961
- gi No. 82698
- % Identity 91.6

- Alignment Length 137
- Location of Alignment in SEQ ID NO 2073: from 1 to 126

Maximum Length Sequence corresponding to clone ID 300006

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2074
- Ceres seq_id 1502086

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2075
- Ceres seq_id 1502087
- Location of start within SEQ ID NO 2074: at 222 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13962
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 2075: from 35 to 112 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13963
- gi No. 3850816
- % Identity 77.3
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2075: from 3 to 112

- Alignment No. 13964
- gi No. 3850818
- % Identity 84.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2075: from 3 to 112

- Alignment No. 13965
- gi No. 3850819
- % Identity 84.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2075: from 3 to 112

- Alignment No. 13966
- gi No. 5668775
- % Identity 78.2
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2075: from 3 to 112

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2076
- Ceres seq_id 1502088
- Location of start within SEQ ID NO 2074: at 294 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13967
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 2076: from 11 to 88 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13968
- gi No. 3850816
- % Identity 77.3
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2076: from 1 to 88

- Alignment No. 13969
- gi No. 3850818
- % Identity 84.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2076: from 1 to 88

- Alignment No. 13970
- gi No. 3850819
- % Identity 84.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2076: from 1 to 88

- Alignment No. 13971
- gi No. 5668775
- % Identity 78.2
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2076: from 1 to 88

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2077
- Ceres seq_id 1502089
- Location of start within SEQ ID NO 2074: at 312 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13972
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 2077: from 5 to 82 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13973
- gi No. 3850816
- % Identity 77.3
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2077: from 1 to 82

- Alignment No. 13974
- gi No. 3850818
- % Identity 84.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2077: from 1 to 82

- Alignment No. 13975
- gi No. 3850819
- % Identity 84.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2077: from 1 to 82

- Alignment No. 13976
- gi No. 5668775
- % Identity 78.2
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2077: from 1 to 82

Maximum Length Sequence corresponding to clone ID 300011

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2078
- Ceres seq_id 1502090

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2079
- Ceres seq_id 1502091

- Location of start within SEQ ID NO 2078: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13977
 - gi No. 2134207
 - % Identity 72.7
 - Alignment Length 22
 - Location of Alignment in SEQ ID NO 2079: from 71 to 92
- Alignment No. 13978
 - gi No. 2134208
 - % Identity 72.7
 - Alignment Length 22
 - Location of Alignment in SEQ ID NO 2079: from 71 to 92
- Alignment No. 13979
 - gi No. 2134209
 - % Identity 72.7
 - Alignment Length 22
 - Location of Alignment in SEQ ID NO 2079: from 71 to 92
- Alignment No. 13980
 - gi No. 2134210
 - % Identity 70.8
 - Alignment Length 24
 - Location of Alignment in SEQ ID NO 2079: from 71 to 92
- Alignment No. 13981
 - gi No. 2134211
 - % Identity 72.7
 - Alignment Length 22
 - Location of Alignment in SEQ ID NO 2079: from 71 to 92

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2080
- Ceres seq_id 1502092
- Location of start within SEQ ID NO 2078: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2081
- Ceres seq_id 1502093
- Location of start within SEQ ID NO 2078: at 137 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 300014

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2082
- Ceres seq_id 1502094

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2083
- Ceres seq_id 1502095
- Location of start within SEQ ID NO 2082: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13982
- Glutathione S-transferases.
- Location within SEQ ID NO 2083: from 32 to 211 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2084
- Ceres seq_id 1502096
- Location of start within SEQ ID NO 2082: at 20 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13983
- Glutathione S-transferases.
- Location within SEQ ID NO 2084: from 26 to 205 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2085
- Ceres seq_id 1502097
- Location of start within SEQ ID NO 2082: at 50 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13984
- Glutathione S-transferases.
- Location within SEQ ID NO 2085: from 16 to 195 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 300700

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2086
- Ceres seq_id 1502100

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2087
- Ceres seq_id 1502101
- Location of start within SEQ ID NO 2086: at 53 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2088
- Ceres seq_id 1502102
- Location of start within SEQ ID NO 2086: at 171 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13985
- Pentapeptide repeats (8 copies)
- Location within SEQ ID NO 2088: from 101 to 135 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 302706

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2089
- Ceres seq_id 1502130

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2090
- Ceres seq_id 1502131
- Location of start within SEQ ID NO 2089: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13986
- gi No. 1352442
- % Identity 79.4
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2090: from 55 to 155
- Alignment No. 13987
- gi No. 170753
- % Identity 79.4
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2090: from 55 to 155
- Alignment No. 13988
- gi No. 3342823
- % Identity 84.8
- Alignment Length 99
- Location of Alignment in SEQ ID NO 2090: from 58 to 155
- Alignment No. 13989
- gi No. 547713
- % Identity 79.4
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2090: from 55 to 155

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2091
- Ceres seq_id 1502132
- Location of start within SEQ ID NO 2089: at 163 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13990
- gi No. 1352442
- % Identity 79.4
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2091: from 1 to 101
- Alignment No. 13991
- gi No. 170753
- % Identity 79.4
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2091: from 1 to 101
- Alignment No. 13992
- gi No. 3342823
- % Identity 84.8
- Alignment Length 99
- Location of Alignment in SEQ ID NO 2091: from 4 to 101

- Alignment No. 13993
- gi No. 547713
- % Identity 79.4
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2091: from 1 to 101

Maximum Length Sequence corresponding to clone ID 302718

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2092
- Ceres seq_id 1502133

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2093
- Ceres seq_id 1502134
- Location of start within SEQ ID NO 2092: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2094
- Ceres seq_id 1502135
- Location of start within SEQ ID NO 2092: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13994
- Protamine Pl
- Location within SEQ ID NO 2094: from 22 to 94 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2095
- Ceres seq_id 1502136
- Location of start within SEQ ID NO 2092: at 247 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13995
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 2095: from 23 to 88 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13996
- gi No. 266410
- % Identity 82.9
- Alignment Length 82
- Location of Alignment in SEQ ID NO 2095: from 7 to 88

Maximum Length Sequence corresponding to clone ID 302744

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2096
- Ceres seq_id 1502153

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2097
- Ceres seq_id 1502154
- Location of start within SEQ ID NO 2096: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13997
- Cytochrome P450
- Location within SEQ ID NO 2097: from 66 to 173 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13998
- gi No. 1870203
- % Identity 99.4
- Alignment Length 165
- Location of Alignment in SEQ ID NO 2097: from 10 to 173
- Alignment No. 13999
- gi No. 5420116
- % Identity 99.4
- Alignment Length 164
- Location of Alignment in SEQ ID NO 2097: from 11 to 173

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2098
- Ceres seq_id 1502155
- Location of start within SEQ ID NO 2096: at 28 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14000
- Cytochrome P450
- Location within SEQ ID NO 2098: from 57 to 164 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14001
- gi No. 1870203
- % Identity 99.4
- Alignment Length 165
- Location of Alignment in SEQ ID NO 2098: from 1 to 164
- Alignment No. 14002
- gi No. 5420116
- % Identity 99.4
- Alignment Length 164
- Location of Alignment in SEQ ID NO 2098: from 2 to 164

Maximum Length Sequence corresponding to clone ID 303152

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2099
- Ceres seq_id 1502165

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2100
- Ceres seq_id 1502166
- Location of start within SEQ ID NO 2099: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2101
- Ceres seq_id 1502167
- Location of start within SEQ ID NO 2099: at 177 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14003
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 2101: from 60 to 126 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 303165

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2102
- Ceres seq_id 1502168

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2103
- Ceres seq_id 1502169
- Location of start within SEQ ID NO 2102: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14004
- 3-beta hydroxysteroid dehydrogenase/isomerase family
- Location within SEQ ID NO 2103: from 18 to 153 aa.

- Alignment No. 14005
- NAD dependent epimerase/dehydratase family
- Location within SEQ ID NO 2103: from 21 to 140 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14006
- gi No. 3269286
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 2103: from 19 to 52

- Alignment No. 14007
- gi No. 553035
- % Identity 74.2
- Alignment Length 31
- Location of Alignment in SEQ ID NO 2103: from 20 to 50

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2104
- Ceres seq_id 1502170
- Location of start within SEQ ID NO 2102: at 42 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14008
- 3-beta hydroxysteroid dehydrogenase/isomerase family
- Location within SEQ ID NO 2104: from 5 to 140 aa.

- Alignment No. 14009
- NAD dependent epimerase/dehydratase family
- Location within SEQ ID NO 2104: from 8 to 127 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14010
- gi No. 3269286
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 2104: from 6 to 39

- Alignment No. 14011
- gi No. 553035
- % Identity 74.2
- Alignment Length 31
- Location of Alignment in SEQ ID NO 2104: from 7 to 37

Maximum Length Sequence corresponding to clone ID 303456

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2105
- Ceres seq_id 1502189

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2106
- Ceres seq_id 1502190
- Location of start within SEQ ID NO 2105: at 192 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

- Alignment No. 14012
- Eukaryotic ribosomal protein L18
- Location within SEQ ID NO 2106: from 14 to 165 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14013
- gi No. 1172977
- % Identity 80.9
- Alignment Length 152
- Location of Alignment in SEQ ID NO 2106: from 14 to 165
- Alignment No. 14014
- gi No. 2529670
- % Identity 76.5
- Alignment Length 153
- Location of Alignment in SEQ ID NO 2106: from 14 to 165
- Alignment No. 14015
- gi No. 3021348
- % Identity 80.3
- Alignment Length 152
- Location of Alignment in SEQ ID NO 2106: from 14 to 165

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2107
- Ceres seq_id 1502191
- Location of start within SEQ ID NO 2105: at 285 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

- Alignment No. 14016
- Eukaryotic ribosomal protein L18
- Location within SEQ ID NO 2107: from 1 to 134 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14017
- gi No. 1172977
- % Identity 80.9
- Alignment Length 152
- Location of Alignment in SEQ ID NO 2107: from 1 to 134
- Alignment No. 14018
- gi No. 2529670

- % Identity 76.5
- Alignment Length 153
- Location of Alignment in SEQ ID NO 2107: from 1 to 134
- Alignment No. 14019
- gi No. 3021348
- % Identity 80.3
- Alignment Length 152
- Location of Alignment in SEQ ID NO 2107: from 1 to 134

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2108
- Ceres seq_id 1502192
- Location of start within SEQ ID NO 2105: at 315 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14020
- Eukaryotic ribosomal protein L18
- Location within SEQ ID NO 2108: from 1 to 124 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14021
- gi No. 1172977
- % Identity 80.9
- Alignment Length 152
- Location of Alignment in SEQ ID NO 2108: from 1 to 124
- Alignment No. 14022
- gi No. 2529670
- % Identity 76.5
- Alignment Length 153
- Location of Alignment in SEQ ID NO 2108: from 1 to 124
- Alignment No. 14023
- gi No. 3021348
- % Identity 80.3
- Alignment Length 152
- Location of Alignment in SEQ ID NO 2108: from 1 to 124

Maximum Length Sequence corresponding to clone ID 303464

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2109
- Ceres seq_id 1502193

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2110
- Ceres seq_id 1502194
- Location of start within SEQ ID NO 2109: at 70 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14024
- gi No. 100219
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2110: from 7 to 24
- Alignment No. 14025
- gi No. 100219
- % Identity 73.7

- Alignment Length 19
- Location of Alignment in SEQ ID NO 2110: from 7 to 25
- Alignment No. 14026
- gi No. 100219
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2110: from 7 to 25

Maximum Length Sequence corresponding to clone ID 303902

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2111
- Ceres seq_id 1502205

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2112
- Ceres seq_id 1502206
- Location of start within SEQ ID NO 2111: at 195 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14027
- Glutathione peroxidases
- Location within SEQ ID NO 2112: from 9 to 98 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14028
- gi No. 1362150
- % Identity 87
- Alignment Length 46
- Location of Alignment in SEQ ID NO 2112: from 53 to 98
- Alignment No. 14029
- gi No. 1708062
- % Identity 71.7
- Alignment Length 99
- Location of Alignment in SEQ ID NO 2112: from 1 to 98
- Alignment No. 14030
- gi No. 2274857
- % Identity 71.7
- Alignment Length 99
- Location of Alignment in SEQ ID NO 2112: from 1 to 98
- Alignment No. 14031
- gi No. 232190
- % Identity 74.7
- Alignment Length 99
- Location of Alignment in SEQ ID NO 2112: from 1 to 98
- Alignment No. 14032
- gi No. 2388885
- % Identity 76.8
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2112: from 4 to 98
- Alignment No. 14033
- gi No. 2388887
- % Identity 72.4
- Alignment Length 29
- Location of Alignment in SEQ ID NO 2112: from 70 to 98

- Alignment No. 14034
- gi No. 2392021
- % Identity 75
- Alignment Length 100
- Location of Alignment in SEQ ID NO 2112: from 1 to 98
- Alignment No. 14035
- gi No. 2632109
- % Identity 71.1
- Alignment Length 90
- Location of Alignment in SEQ ID NO 2112: from 9 to 98
- Alignment No. 14036
- gi No. 2746232
- % Identity 74
- Alignment Length 100
- Location of Alignment in SEQ ID NO 2112: from 1 to 98
- Alignment No. 14037
- gi No. 2760606
- % Identity 86.7
- Alignment Length 98
- Location of Alignment in SEQ ID NO 2112: from 1 to 98
- Alignment No. 14038
- gi No. 3023912
- % Identity 94.1
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2112: from 59 to 75
- Alignment No. 14039
- gi No. 3913793
- % Identity 81.4
- Alignment Length 86
- Location of Alignment in SEQ ID NO 2112: from 13 to 98
- Alignment No. 14040
- gi No. 3913794
- % Identity 71.4
- Alignment Length 98
- Location of Alignment in SEQ ID NO 2112: from 1 to 98
- Alignment No. 14041
- gi No. 4138608
- % Identity 91.7
- Alignment Length 72
- Location of Alignment in SEQ ID NO 2112: from 1 to 72
- Alignment No. 14042
- gi No. 4584526
- % Identity 73.7
- Alignment Length 99
- Location of Alignment in SEQ ID NO 2112: from 1 to 98
- Alignment No. 14043
- gi No. 485512
- % Identity 79.2
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2112: from 3 to 98
- Alignment No. 14044

- gi No. 544437
- % Identity 80.2
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2112: from 3 to 98

Maximum Length Sequence corresponding to clone ID 304670

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2113
- Ceres seq_id 1502220

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2114
- Ceres seq_id 1502221
- Location of start within SEQ ID NO 2113: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14045
- gi No. 1172637
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2114: from 94 to 173

- Alignment No. 14046
- gi No. 1172638
- % Identity 75
- Alignment Length 80
- Location of Alignment in SEQ ID NO 2114: from 95 to 173

- Alignment No. 14047
- gi No. 1709797
- % Identity 70.4
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2114: from 94 to 173

- Alignment No. 14048
- gi No. 2492517
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2114: from 94 to 173

- Alignment No. 14049
- gi No. 263099
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2114: from 94 to 173

- Alignment No. 14050
- gi No. 2791680
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2114: from 94 to 173

- Alignment No. 14051
- gi No. 3450955
- % Identity 70.4
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2114: from 94 to 173

- Alignment No. 14052
- gi No. 687927

- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2114: from 106 to 125

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2115
- Ceres seq_id 1502222
- Location of start within SEQ ID NO 2113: at 11 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14053
- gi No. 1172637
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2115: from 91 to 170

- Alignment No. 14054
- gi No. 1172638
- % Identity 75
- Alignment Length 80
- Location of Alignment in SEQ ID NO 2115: from 92 to 170

- Alignment No. 14055
- gi No. 1709797
- % Identity 70.4
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2115: from 91 to 170

- Alignment No. 14056
- gi No. 2492517
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2115: from 91 to 170

- Alignment No. 14057
- gi No. 263099
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2115: from 91 to 170

- Alignment No. 14058
- gi No. 2791680
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2115: from 91 to 170

- Alignment No. 14059
- gi No. 3450955
- % Identity 70.4
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2115: from 91 to 170

- Alignment No. 14060
- gi No. 687927
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2115: from 103 to 122

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2116
- Ceres seq_id 1502223
- Location of start within SEQ ID NO 2113: at 173 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14061
- gi No. 1172637
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2116: from 37 to 116
- Alignment No. 14062
- gi No. 1172638
- % Identity 75
- Alignment Length 80
- Location of Alignment in SEQ ID NO 2116: from 38 to 116
- Alignment No. 14063
- gi No. 1709797
- % Identity 70.4
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2116: from 37 to 116
- Alignment No. 14064
- gi No. 2492517
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2116: from 37 to 116
- Alignment No. 14065
- gi No. 263099
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2116: from 37 to 116
- Alignment No. 14066
- gi No. 2791680
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2116: from 37 to 116
- Alignment No. 14067
- gi No. 3450955
- % Identity 70.4
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2116: from 37 to 116
- Alignment No. 14068
- gi No. 687927
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2116: from 49 to 68

Maximum Length Sequence corresponding to clone ID 304673

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2117
- Ceres seq_id 1502224

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2118

- Ceres seq_id 1502225
- Location of start within SEQ ID NO 2117: at 167 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14069
- Acetyltransferase (GNAT) family
- Location within SEQ ID NO 2118: from 110 to 183 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2119
- Ceres seq_id 1502226
- Location of start within SEQ ID NO 2117: at 209 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14070
- Acetyltransferase (GNAT) family
- Location within SEQ ID NO 2119: from 96 to 169 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2120
- Ceres seq_id 1502227
- Location of start within SEQ ID NO 2117: at 272 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14071
- Acetyltransferase (GNAT) family
- Location within SEQ ID NO 2120: from 75 to 148 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 304677

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2121
- Ceres seq_id 1502228

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2122
- Ceres seq_id 1502229
- Location of start within SEQ ID NO 2121: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2123
- Ceres seq_id 1502230
- Location of start within SEQ ID NO 2121: at 79 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14072
- Pollen allergen
- Location within SEQ ID NO 2123: from 28 to 105 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2124
- Ceres seq_id 1502231
- Location of start within SEQ ID NO 2121: at 115 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14073
- Pollen allergen
- Location within SEQ ID NO 2124: from 16 to 93 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 311105

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2125
- Ceres seq_id 1502270

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2126
- Ceres seq_id 1502271
- Location of start within SEQ ID NO 2125: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14074
- Ras family
- Location within SEQ ID NO 2126: from 31 to 158 aa.
- Alignment No. 14075
- ADP-ribosylation factor family
- Location within SEQ ID NO 2126: from 31 to 148 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14076
- gi No. 1370172
- % Identity 72.9
- Alignment Length 140
- Location of Alignment in SEQ ID NO 2126: from 20 to 158
- Alignment No. 14077
- gi No. 2723477
- % Identity 75.2
- Alignment Length 141
- Location of Alignment in SEQ ID NO 2126: from 19 to 158

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2127
- Ceres seq_id 1502272
- Location of start within SEQ ID NO 2125: at 54 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14078
- Ras family
- Location within SEQ ID NO 2127: from 14 to 141 aa.
- Alignment No. 14079
- ADP-ribosylation factor family
- Location within SEQ ID NO 2127: from 14 to 131 aa.

- (D) Related Amino Acid Sequences
 - Alignment No. 14080
 - gi No. 1370172
 - % Identity 72.9
 - Alignment Length 140
 - Location of Alignment in SEQ ID NO 2127: from 3 to 141
- Alignment No. 14081
- gi No. 2723477
- % Identity 75.2
- Alignment Length 141
- Location of Alignment in SEQ ID NO 2127: from 2 to 141

Maximum Length Sequence corresponding to clone ID 311199

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2128
- Ceres seq_id 1502285

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2129
- Ceres seq_id 1502286
- Location of start within SEQ ID NO 2128: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14082
- gi No. 1002380
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2129: from 94 to 112

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2130
- Ceres seq_id 1502287
- Location of start within SEQ ID NO 2128: at 54 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14083
- gi No. 1002380
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2130: from 77 to 95

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2131
- Ceres seq_id 1502288
- Location of start within SEQ ID NO 2128: at 66 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14084
- gi No. 1002380
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2131: from 73 to 91

Maximum Length Sequence corresponding to clone ID 311212

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 2132
- Ceres seq_id 1502297
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 2133
- Ceres seq_id 1502298
- Location of start within SEQ ID NO 2132: at 2 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
- (D) Related Amino Acid Sequences
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 2134
- Ceres seq_id 1502299
- Location of start within SEQ ID NO 2132: at 3 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
- (D) Related Amino Acid Sequences
- Alignment No. 14085
- gi No. 102706
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2134: from 81 to 96
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 2135
- Ceres seq_id 1502300
- Location of start within SEQ ID NO 2132: at 48 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
- (D) Related Amino Acid Sequences
- Alignment No. 14086
- gi No. 102706
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2135: from 66 to 81
- Maximum Length Sequence corresponding to clone ID 311293
- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 2136
- Ceres seq_id 1502315
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 2137
- Ceres seq_id 1502316
- Location of start within SEQ ID NO 2136: at 63 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
- (D) Related Amino Acid Sequences
- Alignment No. 14087
- gi No. 2739368
- % Identity 71.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 2137: from 56 to 130
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 2138
- Ceres seq_id 1502317

- Location of start within SEQ ID NO 2136: at 228 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 14088
 - gi No. 2739368
 - % Identity 71.1
 - Alignment Length 76
 - Location of Alignment in SEQ ID NO 2138: from 1 to 75

Maximum Length Sequence corresponding to clone ID 311422

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2139
- Ceres seq_id 1502363

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2140
- Ceres seq_id 1502364
- Location of start within SEQ ID NO 2139: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 14089
 - gi No. 396749
 - % Identity 71.4
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2140: from 84 to 101

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2141
- Ceres seq_id 1502365
- Location of start within SEQ ID NO 2139: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2142
- Ceres seq_id 1502366
- Location of start within SEQ ID NO 2139: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14090
 - gi No. 2828285
 - % Identity 76.2
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2142: from 138 to 157
-
- Alignment No. 14091
 - gi No. 2832638
 - % Identity 76.2
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2142: from 138 to 157

Maximum Length Sequence corresponding to clone ID 311431

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2143

- Ceres seq id 1502367
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2144
 - Ceres seq id 1502368
 - Location of start within SEQ ID NO 2143: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14092
- Kinesin motor domain
- Location within SEQ ID NO 2144: from 1 to 78 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14093
- gi No. 1170619
- % Identity 89.7
- Alignment Length 78
- Location of Alignment in SEQ ID NO 2144: from 1 to 78

- Alignment No. 14094
- gi No. 1170620
- % Identity 88.5
- Alignment Length 78
- Location of Alignment in SEQ ID NO 2144: from 1 to 78

- Alignment No. 14095
- gi No. 1170621
- % Identity 87.2
- Alignment Length 78
- Location of Alignment in SEQ ID NO 2144: from 1 to 78

- Alignment No. 14096
- gi No. 125477
- % Identity 70.9
- Alignment Length 79
- Location of Alignment in SEQ ID NO 2144: from 1 to 77

- Alignment No. 14097
- gi No. 2826849
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2144: from 1 to 15

- Alignment No. 14098
- gi No. 3023586
- % Identity 70.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2144: from 1 to 77

- Alignment No. 14099
- gi No. 3913957
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2144: from 1 to 15

- Alignment No. 14100
- gi No. 4490714
- % Identity 88.5
- Alignment Length 78
- Location of Alignment in SEQ ID NO 2144: from 1 to 78

- Alignment No. 14101
- gi No. 4504869
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2144: from 1 to 15

Maximum Length Sequence corresponding to clone ID 311460

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2145
- Ceres seq_id 1502373

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2146
- Ceres seq_id 1502374
- Location of start within SEQ ID NO 2145: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2147
- Ceres seq_id 1502375
- Location of start within SEQ ID NO 2145: at 188 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14102
- gi No. 2655291
- % Identity 82.1
- Alignment Length 67
- Location of Alignment in SEQ ID NO 2147: from 1 to 66

- Alignment No. 14103
- gi No. 2979494
- % Identity 73
- Alignment Length 37
- Location of Alignment in SEQ ID NO 2147: from 22 to 58

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2148
- Ceres seq_id 1502376
- Location of start within SEQ ID NO 2145: at 272 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14104
- gi No. 2655291
- % Identity 82.1
- Alignment Length 67
- Location of Alignment in SEQ ID NO 2148: from 1 to 38

- Alignment No. 14105
- gi No. 2979494
- % Identity 73
- Alignment Length 37
- Location of Alignment in SEQ ID NO 2148: from 1 to 30

Maximum Length Sequence corresponding to clone ID 311474

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2149
- Ceres seq_id 1502381
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2150
 - Ceres seq_id 1502382
 - Location of start within SEQ ID NO 2149: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14106
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 2150: from 1 to 131 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14107
- gi No. 1066501
- % Identity 70.2
- Alignment Length 132
- Location of Alignment in SEQ ID NO 2150: from 3 to 131

- Alignment No. 14108
- gi No. 1168470
- % Identity 73.9
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2150: from 1 to 131

- Alignment No. 14109
- gi No. 1168471
- % Identity 77.4
- Alignment Length 94
- Location of Alignment in SEQ ID NO 2150: from 42 to 131

- Alignment No. 14110
- gi No. 1778444
- % Identity 75.6
- Alignment Length 45
- Location of Alignment in SEQ ID NO 2150: from 88 to 131

- Alignment No. 14111
- gi No. 2852447
- % Identity 72
- Alignment Length 133
- Location of Alignment in SEQ ID NO 2150: from 1 to 131

- Alignment No. 14112
- gi No. 2852449
- % Identity 71.2
- Alignment Length 133
- Location of Alignment in SEQ ID NO 2150: from 1 to 131

- Alignment No. 14113
- gi No. 3075390
- % Identity 76.2
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2150: from 3 to 131

- Alignment No. 14114
- gi No. 3461835
- % Identity 73.1
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2150: from 1 to 131

- Alignment No. 14115
- gi No. 3805765
- % Identity 70.8
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2150: from 3 to 131

- Alignment No. 14116
- gi No. 4006829
- % Identity 74.6
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2150: from 3 to 131

- Alignment No. 14117
- gi No. 4432889
- % Identity 77.4
- Alignment Length 94
- Location of Alignment in SEQ ID NO 2150: from 42 to 131

- Alignment No. 14118
- gi No. 4585873
- % Identity 73.1
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2150: from 3 to 131

- Alignment No. 14119
- gi No. 4753653
- % Identity 71
- Alignment Length 62
- Location of Alignment in SEQ ID NO 2150: from 69 to 130

- Alignment No. 14120
- gi No. 5091529
- % Identity 83.3
- Alignment Length 132
- Location of Alignment in SEQ ID NO 2150: from 1 to 131

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2151
- Ceres seq_id 1502383
- Location of start within SEQ ID NO 2149: at 160 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14121
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 2151: from 1 to 78 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14122
- gi No. 1066501
- % Identity 70.2
- Alignment Length 132
- Location of Alignment in SEQ ID NO 2151: from 1 to 78

- Alignment No. 14123
- gi No. 1168470
- % Identity 73.9
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2151: from 1 to 78

- Alignment No. 14124
- gi No. 1168471
- % Identity 77.4
- Alignment Length 94
- Location of Alignment in SEQ ID NO 2151: from 1 to 78

- Alignment No. 14125
- gi No. 1778444
- % Identity 75.6
- Alignment Length 45
- Location of Alignment in SEQ ID NO 2151: from 35 to 78

- Alignment No. 14126
- gi No. 2852447
- % Identity 72
- Alignment Length 133
- Location of Alignment in SEQ ID NO 2151: from 1 to 78

- Alignment No. 14127
- gi No. 2852449
- % Identity 71.2
- Alignment Length 133
- Location of Alignment in SEQ ID NO 2151: from 1 to 78

- Alignment No. 14128
- gi No. 3075390
- % Identity 76.2
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2151: from 1 to 78

- Alignment No. 14129
- gi No. 3461835
- % Identity 73.1
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2151: from 1 to 78

- Alignment No. 14130
- gi No. 3805765
- % Identity 70.8
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2151: from 1 to 78

- Alignment No. 14131
- gi No. 4006829
- % Identity 74.6
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2151: from 1 to 78

- Alignment No. 14132
- gi No. 4432889
- % Identity 77.4
- Alignment Length 94
- Location of Alignment in SEQ ID NO 2151: from 1 to 78

- Alignment No. 14133
- gi No. 4585873
- % Identity 73.1
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2151: from 1 to 78

- Alignment No. 14134

- gi No. 4753653
- % Identity 71
- Alignment Length 62
- Location of Alignment in SEQ ID NO 2151: from 16 to 77
- Alignment No. 14135
- gi No. 5091529
- % Identity 83.3
- Alignment Length 132
- Location of Alignment in SEQ ID NO 2151: from 1 to 78

Maximum Length Sequence corresponding to clone ID 311490

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2152
- Ceres seq_id 1502387

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2153
- Ceres seq_id 1502388
- Location of start within SEQ ID NO 2152: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14136
- Ribosomal protein L5
- Location within SEQ ID NO 2153: from 65 to 100 aa.
- Alignment No. 14137
- ribosomal L5P family C-terminus
- Location within SEQ ID NO 2153: from 104 to 158 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14138
- gi No. 1125808
- % Identity 84.2
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
- Alignment No. 14139
- gi No. 1172816
- % Identity 96.8
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
- Alignment No. 14140
- gi No. 1172817
- % Identity 97.9
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
- Alignment No. 14141
- gi No. 1172952
- % Identity 84.2
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
- Alignment No. 14142
- gi No. 1172954
- % Identity 78.9
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158

- Alignment No. 14143
- gi No. 1172969
- % Identity 97.9
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158

- Alignment No. 14144
- gi No. 1173055
- % Identity 100
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158

- Alignment No. 14145
- gi No. 1246369
- % Identity 74.5
- Alignment Length 94
- Location of Alignment in SEQ ID NO 2153: from 65 to 158

- Alignment No. 14146
- gi No. 132649
- % Identity 85.3
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158

- Alignment No. 14147
- gi No. 132777
- % Identity 74.7
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158

- Alignment No. 14148
- gi No. 132951
- % Identity 83.2
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158

- Alignment No. 14149
- gi No. 132992
- % Identity 77.8
- Alignment Length 63
- Location of Alignment in SEQ ID NO 2153: from 65 to 127

- Alignment No. 14150
- gi No. 1350658
- % Identity 83.2
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158

- Alignment No. 14151
- gi No. 1350659
- % Identity 77.9
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158

- Alignment No. 14152
- gi No. 1710480
- % Identity 75.8
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158

- Alignment No. 14153

- gi No. 1710494
- % Identity 87.4
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158

- Alignment No. 14154
- gi No. 2500240
- % Identity 84
- Alignment Length 94
- Location of Alignment in SEQ ID NO 2153: from 65 to 158

- Alignment No. 14155
- gi No. 2500241
- % Identity 81.3
- Alignment Length 91
- Location of Alignment in SEQ ID NO 2153: from 65 to 155

- Alignment No. 14156
- gi No. 2570507
- % Identity 89.5
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158

- Alignment No. 14157
- gi No. 3914659
- % Identity 84.2
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158

- Alignment No. 14158
- gi No. 4322
- % Identity 82.1
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158

- Alignment No. 14159
- gi No. 4432750
- % Identity 96
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2153: from 65 to 89

- Alignment No. 14160
- gi No. 4506595
- % Identity 81.1
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158

- Alignment No. 14161
- gi No. 4512679
- % Identity 88.6
- Alignment Length 105
- Location of Alignment in SEQ ID NO 2153: from 65 to 158

- Alignment No. 14162
- gi No. 4586222
- % Identity 85.3
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158

- Alignment No. 14163
- gi No. 71107

- % Identity 83.2
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2154
- Ceres seq_id 1502389
- Location of start within SEQ ID NO 2152: at 117 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14164
- gi No. 1172816
- % Identity 85.7
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2154: from 1 to 28

- Alignment No. 14165
- gi No. 1172817
- % Identity 85.2
- Alignment Length 27
- Location of Alignment in SEQ ID NO 2154: from 2 to 28

- Alignment No. 14166
- gi No. 1172969
- % Identity 85.7
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2154: from 1 to 28

- Alignment No. 14167
- gi No. 1173055
- % Identity 89.3
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2154: from 1 to 28

- Alignment No. 14168
- gi No. 2570507
- % Identity 89.3
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2154: from 1 to 28

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2155
- Ceres seq_id 1502390
- Location of start within SEQ ID NO 2152: at 147 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14169
- gi No. 1172816
- % Identity 85.7
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2155: from 1 to 18

- Alignment No. 14170
- gi No. 1172817
- % Identity 85.2
- Alignment Length 27
- Location of Alignment in SEQ ID NO 2155: from 1 to 18

- Alignment No. 14171
- gi No. 1172969
- % Identity 85.7
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2155: from 1 to 18

- Alignment No. 14172
- gi No. 1173055
- % Identity 89.3
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2155: from 1 to 18

- Alignment No. 14173
- gi No. 2570507
- % Identity 89.3
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2155: from 1 to 18

Maximum Length Sequence corresponding to clone ID 311538

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2156
- Ceres seq_id 1502407

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2157
- Ceres seq_id 1502408
- Location of start within SEQ ID NO 2156: at 72 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14174
- Peroxidase
- Location within SEQ ID NO 2157: from 61 to 134 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2158
- Ceres seq_id 1502409
- Location of start within SEQ ID NO 2156: at 210 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14175
- Peroxidase
- Location within SEQ ID NO 2158: from 15 to 88 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 311554

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2159
- Ceres seq_id 1502420

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2160
- Ceres seq_id 1502421
- Location of start within SEQ ID NO 2159: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14176

- Ribosomal protein S12
- Location within SEQ ID NO 2160: from 58 to 144 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14177
- gi No. 1173187
- % Identity 97.7
- Alignment Length 88
- Location of Alignment in SEQ ID NO 2160: from 58 to 144
- Alignment No. 14178
- gi No. 1350965
- % Identity 97.7
- Alignment Length 86
- Location of Alignment in SEQ ID NO 2160: from 58 to 143
- Alignment No. 14179
- gi No. 1850766
- % Identity 74.2
- Alignment Length 89
- Location of Alignment in SEQ ID NO 2160: from 58 to 144
- Alignment No. 14180
- gi No. 2500455
- % Identity 74.2
- Alignment Length 89
- Location of Alignment in SEQ ID NO 2160: from 58 to 144
- Alignment No. 14181
- gi No. 2829742
- % Identity 81.8
- Alignment Length 88
- Location of Alignment in SEQ ID NO 2160: from 59 to 144
- Alignment No. 14182
- gi No. 2833303
- % Identity 79.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 2160: from 59 to 144
- Alignment No. 14183
- gi No. 3088342
- % Identity 92.9
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2160: from 118 to 144
- Alignment No. 14184
- gi No. 417716
- % Identity 75.3
- Alignment Length 89
- Location of Alignment in SEQ ID NO 2160: from 58 to 144
- Alignment No. 14185
- gi No. 4493905
- % Identity 75.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 2160: from 54 to 144
- Alignment No. 14186
- gi No. 4506701
- % Identity 81.8

- Alignment Length 88
- Location of Alignment in SEQ ID NO 2160: from 59 to 144

Maximum Length Sequence corresponding to clone ID 311571

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2161
- Ceres seq_id 1502422

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2162
- Ceres seq_id 1502423
- Location of start within SEQ ID NO 2161: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

- Alignment No. 14187
- AhpC/TSA family
- Location within SEQ ID NO 2162: from 11 to 67 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14188
- gi No. 5441879
- % Identity 80
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2162: from 28 to 67

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2163
- Ceres seq_id 1502424
- Location of start within SEQ ID NO 2161: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

- Alignment No. 14189
- AhpC/TSA family
- Location within SEQ ID NO 2163: from 66 to 142 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14190
- gi No. 5441879
- % Identity 72.2
- Alignment Length 97
- Location of Alignment in SEQ ID NO 2163: from 65 to 159

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2164
- Ceres seq_id 1502425
- Location of start within SEQ ID NO 2161: at 68 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 311596

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2165
- Ceres seq_id 1502429

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2166
- Ceres seq_id 1502430
- Location of start within SEQ ID NO 2165: at 167 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14191
- gi No. 417298
- % Identity 74.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2166: from 1 to 75

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2167
- Ceres seq_id 1502431
- Location of start within SEQ ID NO 2165: at 185 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14192
- gi No. 417298
- % Identity 74.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2167: from 1 to 69

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2168
- Ceres seq_id 1502432
- Location of start within SEQ ID NO 2165: at 188 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14193
- gi No. 417298
- % Identity 74.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2168: from 1 to 68

Maximum Length Sequence corresponding to clone ID 311614

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2169
- Ceres seq_id 1502441

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2170
- Ceres seq_id 1502442
- Location of start within SEQ ID NO 2169: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14194
- gi No. 3335351
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2170: from 41 to 51

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2171
- Ceres seq_id 1502443
- Location of start within SEQ ID NO 2169: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14195
- gi No. 2924785
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2171: from 12 to 29

Maximum Length Sequence corresponding to clone ID 311726

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2172
- Ceres seq_id 1502461

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2173
- Ceres seq_id 1502462
- Location of start within SEQ ID NO 2172: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14196
- gi No. 4028260
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2173: from 38 to 48

Maximum Length Sequence corresponding to clone ID 311791

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2174
- Ceres seq_id 1502479

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2175
- Ceres seq_id 1502480
- Location of start within SEQ ID NO 2174: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2176
- Ceres seq_id 1502481
- Location of start within SEQ ID NO 2174: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14197
- Elongation factor 1 gamma, conserved domain.
- Location within SEQ ID NO 2176: from 29 to 81 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14198
- gi No. 2160158
- % Identity 75.9
- Alignment Length 79
- Location of Alignment in SEQ ID NO 2176: from 1 to 73
- Alignment No. 14199
- gi No. 3868758
- % Identity 87.8

- Alignment Length 74
- Location of Alignment in SEQ ID NO 2176: from 1 to 73

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2177
- Ceres seq_id 1502482
- Location of start within SEQ ID NO 2174: at 7 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 311814

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2178
- Ceres seq_id 1502487

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2179
- Ceres seq_id 1502488
- Location of start within SEQ ID NO 2178: at 102 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14200
- G-protein alpha subunit
- Location within SEQ ID NO 2179: from 46 to 112 aa.

- Alignment No. 14201
- ADP-ribosylation factor family
- Location within SEQ ID NO 2179: from 1 to 117 aa.

- Alignment No. 14202
- Ras family
- Location within SEQ ID NO 2179: from 18 to 92 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14203
- gi No. 4309728
- % Identity 91.5
- Alignment Length 118
- Location of Alignment in SEQ ID NO 2179: from 1 to 117

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2180
- Ceres seq_id 1502489
- Location of start within SEQ ID NO 2178: at 150 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14204
- G-protein alpha subunit
- Location within SEQ ID NO 2180: from 30 to 96 aa.

- Alignment No. 14205
- ADP-ribosylation factor family
- Location within SEQ ID NO 2180: from 1 to 101 aa.

- Alignment No. 14206
- Ras family
- Location within SEQ ID NO 2180: from 2 to 76 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14207
- gi No. 4309728
- % Identity 91.5
- Alignment Length 118
- Location of Alignment in SEQ ID NO 2180: from 1 to 101

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2181
- Ceres seq_id 1502490
- Location of start within SEQ ID NO 2178: at 162 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14208
- G-protein alpha subunit
- Location within SEQ ID NO 2181: from 26 to 92 aa.
- Alignment No. 14209
- ADP-ribosylation factor family
- Location within SEQ ID NO 2181: from 1 to 97 aa.
- Alignment No. 14210
- Ras family
- Location within SEQ ID NO 2181: from 1 to 72 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14211
- gi No. 4309728
- % Identity 91.5
- Alignment Length 118
- Location of Alignment in SEQ ID NO 2181: from 1 to 97

Maximum Length Sequence corresponding to clone ID 311865

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2182
- Ceres seq_id 1502514

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2183
- Ceres seq_id 1502515
- Location of start within SEQ ID NO 2182: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2184
- Ceres seq_id 1502516
- Location of start within SEQ ID NO 2182: at 89 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14212
- Ribosomal L29 protein
- Location within SEQ ID NO 2184: from 6 to 69 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14213
- gi No. 3355468
- % Identity 85.2

- Alignment Length 122
- Location of Alignment in SEQ ID NO 2184: from 1 to 122

Maximum Length Sequence corresponding to clone ID 311870

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2185
- Ceres seq_id 1502517

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2186
- Ceres seq_id 1502518
- Location of start within SEQ ID NO 2185: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14214
- Protein-tyrosine phosphatase
- Location within SEQ ID NO 2186: from 1 to 60 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14215
- gi No. 3413473
- % Identity 71.7
- Alignment Length 60
- Location of Alignment in SEQ ID NO 2186: from 1 to 60

- Alignment No. 14216
- gi No. 3413500
- % Identity 73.3
- Alignment Length 60
- Location of Alignment in SEQ ID NO 2186: from 1 to 60

- Alignment No. 14217
- gi No. 348540
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2186: from 1 to 14

- Alignment No. 14218
- gi No. 464498
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2186: from 1 to 14

Maximum Length Sequence corresponding to clone ID 311889

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2187
- Ceres seq_id 1502519

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2188
- Ceres seq_id 1502520
- Location of start within SEQ ID NO 2187: at 147 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2189
- Ceres seq_id 1502521
- Location of start within SEQ ID NO 2187: at 197 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14219
- gi No. 1769895
- % Identity 72.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 2189: from 1 to 76

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2190
- Ceres seq_id 1502522
- Location of start within SEQ ID NO 2187: at 218 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14220
- gi No. 1769895
- % Identity 72.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 2190: from 1 to 69

Maximum Length Sequence corresponding to clone ID 311911

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2191
- Ceres seq_id 1502527

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2192
- Ceres seq_id 1502528
- Location of start within SEQ ID NO 2191: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14221
- ATPases associated with various cellular activities (AAA)
- Location within SEQ ID NO 2192: from 1 to 62 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14222
- gi No. 1078797
- % Identity 80.2
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96

- Alignment No. 14223
- gi No. 1170767
- % Identity 75
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96

- Alignment No. 14224
- gi No. 1262435
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96

- Alignment No. 14225
- gi No. 1346812
- % Identity 81.3
- Alignment Length 96

- Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14226
 - gi No. 1709799
 - % Identity 81.3
 - Alignment Length 96
 - Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14227
 - gi No. 1709800
 - % Identity 81.3
 - Alignment Length 96
 - Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14228
 - gi No. 228885
 - % Identity 70.3
 - Alignment Length 91
 - Location of Alignment in SEQ ID NO 2192: from 1 to 91
- Alignment No. 14229
 - gi No. 2492521
 - % Identity 76
 - Alignment Length 96
 - Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14230
 - gi No. 2564007
 - % Identity 81.3
 - Alignment Length 96
 - Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14231
 - gi No. 2661071
 - % Identity 81.3
 - Alignment Length 96
 - Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14232
 - gi No. 2815905
 - % Identity 81.3
 - Alignment Length 96
 - Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14233
 - gi No. 2982331
 - % Identity 94.8
 - Alignment Length 96
 - Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14234
 - gi No. 3041724
 - % Identity 81.3
 - Alignment Length 96
 - Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14235
 - gi No. 3122626
 - % Identity 81.3
 - Alignment Length 96
 - Location of Alignment in SEQ ID NO 2192: from 1 to 96

- Alignment No. 14236
- gi No. 3790757
- % Identity 77.1
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14237
- gi No. 3979998
- % Identity 78.1
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14238
- gi No. 4506213
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14239
- gi No. 464863
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2193
- Ceres seq_id 1502529
- Location of start within SEQ ID NO 2191: at 76 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14240
- gi No. 1078797
- % Identity 80.2
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14241
- gi No. 1170767
- % Identity 75
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14242
- gi No. 1262435
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14243
- gi No. 1346812
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14244
- gi No. 1709799
- % Identity 81.3
- Alignment Length 96

- Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14245
 - gi No. 1709800
 - % Identity 81.3
 - Alignment Length 96
 - Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14246
 - gi No. 228885
 - % Identity 70.3
 - Alignment Length 91
 - Location of Alignment in SEQ ID NO 2193: from 1 to 66
- Alignment No. 14247
 - gi No. 2492521
 - % Identity 76
 - Alignment Length 96
 - Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14248
 - gi No. 2564007
 - % Identity 81.3
 - Alignment Length 96
 - Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14249
 - gi No. 2661071
 - % Identity 81.3
 - Alignment Length 96
 - Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14250
 - gi No. 2815905
 - % Identity 81.3
 - Alignment Length 96
 - Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14251
 - gi No. 2982331
 - % Identity 94.8
 - Alignment Length 96
 - Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14252
 - gi No. 3041724
 - % Identity 81.3
 - Alignment Length 96
 - Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14253
 - gi No. 3122626
 - % Identity 81.3
 - Alignment Length 96
 - Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14254
 - gi No. 3790757
 - % Identity 77.1
 - Alignment Length 96
 - Location of Alignment in SEQ ID NO 2193: from 1 to 71

- Alignment No. 14255
- gi No. 3979998
- % Identity 78.1
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71

- Alignment No. 14256
- gi No. 4506213
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71

- Alignment No. 14257
- gi No. 464863
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2194
- Ceres seq_id 1502530
- Location of start within SEQ ID NO 2191: at 85 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14258
- gi No. 1078797
- % Identity 80.2
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68

- Alignment No. 14259
- gi No. 1170767
- % Identity 75
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68

- Alignment No. 14260
- gi No. 1262435
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68

- Alignment No. 14261
- gi No. 1346812
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68

- Alignment No. 14262
- gi No. 1709799
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68

- Alignment No. 14263
- gi No. 1709800
- % Identity 81.3
- Alignment Length 96

- Location of Alignment in SEQ ID NO 2194: from 1 to 68
- Alignment No. 14264
- gi No. 228885
- % Identity 70.3
- Alignment Length 91
- Location of Alignment in SEQ ID NO 2194: from 1 to 63
- Alignment No. 14265
- gi No. 2492521
- % Identity 76
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68
- Alignment No. 14266
- gi No. 2564007
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68
- Alignment No. 14267
- gi No. 2661071
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68
- Alignment No. 14268
- gi No. 2815905
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68
- Alignment No. 14269
- gi No. 2982331
- % Identity 94.8
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68
- Alignment No. 14270
- gi No. 3041724
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68
- Alignment No. 14271
- gi No. 3122626
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68
- Alignment No. 14272
- gi No. 3790757
- % Identity 77.1
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68
- Alignment No. 14273
- gi No. 3979998
- % Identity 78.1
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68

- Alignment No. 14274
- gi No. 4506213
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68

- Alignment No. 14275
- gi No. 464863
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68

Maximum Length Sequence corresponding to clone ID 311937

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2195
- Ceres seq_id 1502542

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2196
- Ceres seq_id 1502543
- Location of start within SEQ ID NO 2195: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14276
- Ras family
- Location within SEQ ID NO 2196: from 69 to 147 aa.

- Alignment No. 14277
- ADP-ribosylation factor family
- Location within SEQ ID NO 2196: from 52 to 169 aa.

- Alignment No. 14278
- G-protein alpha subunit
- Location within SEQ ID NO 2196: from 94 to 169 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14279
- gi No. 1065361
- % Identity 90.8
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2196: from 52 to 169

- Alignment No. 14280
- gi No. 114121
- % Identity 79
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2196: from 51 to 169

- Alignment No. 14281
- gi No. 114122
- % Identity 91.7
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169

- Alignment No. 14282
- gi No. 114124
- % Identity 78.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169

- Alignment No. 14283
- gi No. 114128
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2196: from 56 to 169

- Alignment No. 14284
- gi No. 114131
- % Identity 74.4
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2196: from 51 to 169

- Alignment No. 14285
- gi No. 1168489
- % Identity 85
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169

- Alignment No. 14286
- gi No. 1351973
- % Identity 86.7
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169

- Alignment No. 14287
- gi No. 1351974
- % Identity 97.5
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169

- Alignment No. 14288
- gi No. 1703373
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169

- Alignment No. 14289
- gi No. 1703374
- % Identity 95.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169

- Alignment No. 14290
- gi No. 1703375
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169

- Alignment No. 14291
- gi No. 1703376
- % Identity 93.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169

- Alignment No. 14292
- gi No. 1703377
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169

- Alignment No. 14293

- gi No. 1703378
- % Identity 88.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14294
- gi No. 1703379
- % Identity 75.7
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2196: from 56 to 169
- Alignment No. 14295
- gi No. 1703380
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14296
- gi No. 2129946
- % Identity 97.7
- Alignment Length 87
- Location of Alignment in SEQ ID NO 2196: from 51 to 137
- Alignment No. 14297
- gi No. 2293566
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14298
- gi No. 2462736
- % Identity 97.6
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2196: from 51 to 92
- Alignment No. 14299
- gi No. 2492925
- % Identity 80
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14300
- gi No. 2689631
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14301
- gi No. 283391
- % Identity 85
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14302
- gi No. 2852443
- % Identity 95
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14303
- gi No. 2854182

- % Identity 87.4
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2196: from 51 to 169

- Alignment No. 14304
- gi No. 3182915
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169

- Alignment No. 14305
- gi No. 3182916
- % Identity 80.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169

- Alignment No. 14306
- gi No. 3182917
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169

- Alignment No. 14307
- gi No. 3182919
- % Identity 95.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169

- Alignment No. 14308
- gi No. 3252999
- % Identity 94.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 2196: from 68 to 160

- Alignment No. 14309
- gi No. 3746799
- % Identity 87.3
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2196: from 69 to 169

- Alignment No. 14310
- gi No. 3746801
- % Identity 86.3
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2196: from 69 to 169

- Alignment No. 14311
- gi No. 4056469
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169

- Alignment No. 14312
- gi No. 4102193
- % Identity 77.3
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2196: from 51 to 116

- Alignment No. 14313
- gi No. 4324967
- % Identity 98.3

- Alignment Length 117
- Location of Alignment in SEQ ID NO 2196: from 54 to 169
- Alignment No. 14314
- gi No. 4502201
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14315
- gi No. 4502203
- % Identity 90
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14316
- gi No. 4502205
- % Identity 85.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14317
- gi No. 4502209
- % Identity 88.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14318
- gi No. 4502211
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2196: from 56 to 169
- Alignment No. 14319
- gi No. 461532
- % Identity 89.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14320
- gi No. 461533
- % Identity 89.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14321
- gi No. 4662630
- % Identity 70.6
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14322
- gi No. 543841
- % Identity 99.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14323
- gi No. 543842
- % Identity 90
- Alignment Length 120

- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14324
- gi No. 543843
- % Identity 88.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14325
- gi No. 543844
- % Identity 85.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14326
- gi No. 5579053
- % Identity 70.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2196: from 48 to 169
- Alignment No. 14327
- gi No. 728881
- % Identity 85.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14328
- gi No. 728883
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2196: from 56 to 169
- Alignment No. 14329
- gi No. 83900
- % Identity 85
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2197
- Ceres seq_id 1502544
- Location of start within SEQ ID NO 2195: at 151 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14330
- Ras family
- Location within SEQ ID NO 2197: from 19 to 97 aa.
- Alignment No. 14331
- ADP-ribosylation factor family
- Location within SEQ ID NO 2197: from 2 to 119 aa.
- Alignment No. 14332
- G-protein alpha subunit
- Location within SEQ ID NO 2197: from 44 to 119 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14333
- gi No. 1065361
- % Identity 90.8

- Alignment Length 119
- Location of Alignment in SEQ ID NO 2197: from 2 to 119
- Alignment No. 14334
- gi No. 114121
- % Identity 79
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14335
- gi No. 114122
- % Identity 91.7
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14336
- gi No. 114124
- % Identity 78.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14337
- gi No. 114128
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2197: from 6 to 119
- Alignment No. 14338
- gi No. 114131
- % Identity 74.4
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14339
- gi No. 1168489
- % Identity 85
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14340
- gi No. 1351973
- % Identity 86.7
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14341
- gi No. 1351974
- % Identity 97.5
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14342
- gi No. 1703373
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14343
- gi No. 1703374
- % Identity 95.8
- Alignment Length 120

- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14344
- gi No. 1703375
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14345
- gi No. 1703376
- % Identity 93.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14346
- gi No. 1703377
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14347
- gi No. 1703378
- % Identity 88.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14348
- gi No. 1703379
- % Identity 75.7
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2197: from 6 to 119
- Alignment No. 14349
- gi No. 1703380
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14350
- gi No. 2129946
- % Identity 97.7
- Alignment Length 87
- Location of Alignment in SEQ ID NO 2197: from 1 to 87
- Alignment No. 14351
- gi No. 2293566
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14352
- gi No. 2462736
- % Identity 97.6
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2197: from 1 to 42
- Alignment No. 14353
- gi No. 2492925
- % Identity 80
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14354
- gi No. 2689631
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14355
- gi No. 283391
- % Identity 85
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14356
- gi No. 2852443
- % Identity 95
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14357
- gi No. 2854182
- % Identity 87.4
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14358
- gi No. 3182915
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14359
- gi No. 3182916
- % Identity 80.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14360
- gi No. 3182917
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14361
- gi No. 3182919
- % Identity 95.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14362
- gi No. 3252999
- % Identity 94.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 2197: from 18 to 110

- Alignment No. 14363
- gi No. 3746799
- % Identity 87.3
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2197: from 19 to 119

- Alignment No. 14364
- gi No. 3746801
- % Identity 86.3
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2197: from 19 to 119
- Alignment No. 14365
- gi No. 4056469
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14366
- gi No. 4102193
- % Identity 77.3
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2197: from 1 to 66
- Alignment No. 14367
- gi No. 4324967
- % Identity 98.3
- Alignment Length 117
- Location of Alignment in SEQ ID NO 2197: from 4 to 119
- Alignment No. 14368
- gi No. 4502201
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14369
- gi No. 4502203
- % Identity 90
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14370
- gi No. 4502205
- % Identity 85.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14371
- gi No. 4502209
- % Identity 88.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14372
- gi No. 4502211
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2197: from 6 to 119
- Alignment No. 14373
- gi No. 461532
- % Identity 89.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14374

- gi No. 461533
- % Identity 89.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14375
- gi No. 4662630
- % Identity 70.6
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14376
- gi No. 543841
- % Identity 99.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14377
- gi No. 543842
- % Identity 90
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14378
- gi No. 543843
- % Identity 88.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14379
- gi No. 543844
- % Identity 85.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14380
- gi No. 5579053
- % Identity 70.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14381
- gi No. 728881
- % Identity 85.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119
- Alignment No. 14382
- gi No. 728883
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2197: from 6 to 119
- Alignment No. 14383
- gi No. 83900
- % Identity 85
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2198

- Ceres seq_id 1502545
- Location of start within SEQ ID NO 2195: at 202 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14384
- Ras family
- Location within SEQ ID NO 2198: from 2 to 80 aa.
- Alignment No. 14385
- ADP-ribosylation factor family
- Location within SEQ ID NO 2198: from 1 to 102 aa.
- Alignment No. 14386
- G-protein alpha subunit
- Location within SEQ ID NO 2198: from 27 to 102 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14387
- gi No. 1065361
- % Identity 90.8
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14388
- gi No. 114121
- % Identity 79
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14389
- gi No. 114122
- % Identity 91.7
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14390
- gi No. 114124
- % Identity 78.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14391
- gi No. 114128
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14392
- gi No. 114131
- % Identity 74.4
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14393
- gi No. 1168489
- % Identity 85
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14394

- gi No. 1351973
- % Identity 86.7
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102

- Alignment No. 14395
- gi No. 1351974
- % Identity 97.5
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102

- Alignment No. 14396
- gi No. 1703373
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102

- Alignment No. 14397
- gi No. 1703374
- % Identity 95.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102

- Alignment No. 14398
- gi No. 1703375
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102

- Alignment No. 14399
- gi No. 1703376
- % Identity 93.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102

- Alignment No. 14400
- gi No. 1703377
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102

- Alignment No. 14401
- gi No. 1703378
- % Identity 88.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102

- Alignment No. 14402
- gi No. 1703379
- % Identity 75.7
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2198: from 1 to 102

- Alignment No. 14403
- gi No. 1703380
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102

- Alignment No. 14404
- gi No. 2129946

- % Identity 97.7
- Alignment Length 87
- Location of Alignment in SEQ ID NO 2198: from 1 to 70

- Alignment No. 14405
- gi No. 2293566
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102

- Alignment No. 14406
- gi No. 2462736
- % Identity 97.6
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2198: from 1 to 25

- Alignment No. 14407
- gi No. 2492925
- % Identity 80
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102

- Alignment No. 14408
- gi No. 2689631
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102

- Alignment No. 14409
- gi No. 283391
- % Identity 85
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102

- Alignment No. 14410
- gi No. 2852443
- % Identity 95
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102

- Alignment No. 14411
- gi No. 2854182
- % Identity 87.4
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2198: from 1 to 102

- Alignment No. 14412
- gi No. 3182915
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102

- Alignment No. 14413
- gi No. 3182916
- % Identity 80.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102

- Alignment No. 14414
- gi No. 3182917
- % Identity 90.8

- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14415
- gi No. 3182919
- % Identity 95.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14416
- gi No. 3252999
- % Identity 94.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 2198: from 1 to 93
- Alignment No. 14417
- gi No. 3746799
- % Identity 87.3
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2198: from 2 to 102
- Alignment No. 14418
- gi No. 3746801
- % Identity 86.3
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2198: from 2 to 102
- Alignment No. 14419
- gi No. 4056469
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14420
- gi No. 4102193
- % Identity 77.3
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2198: from 1 to 49
- Alignment No. 14421
- gi No. 4324967
- % Identity 98.3
- Alignment Length 117
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14422
- gi No. 4502201
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14423
- gi No. 4502203
- % Identity 90
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14424
- gi No. 4502205
- % Identity 85.8
- Alignment Length 120

- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14425
- gi No. 4502209
- % Identity 88.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14426
- gi No. 4502211
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14427
- gi No. 461532
- % Identity 89.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14428
- gi No. 461533
- % Identity 89.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14429
- gi No. 4662630
- % Identity 70.6
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14430
- gi No. 543841
- % Identity 99.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14431
- gi No. 543842
- % Identity 90
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14432
- gi No. 543843
- % Identity 88.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14433
- gi No. 543844
- % Identity 85.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14434
- gi No. 5579053
- % Identity 70.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2198: from 1 to 102

- Alignment No. 14435
- gi No. 728881
- % Identity 85.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14436
- gi No. 728883
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14437
- gi No. 83900
- % Identity 85
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102

Maximum Length Sequence corresponding to clone ID 312050

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2199
- Ceres seq_id 1502573

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2200
- Ceres seq_id 1502574
- Location of start within SEQ ID NO 2199: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14438
- gi No. 3935181
- % Identity 82.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2200: from 9 to 83

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2201
- Ceres seq_id 1502575
- Location of start within SEQ ID NO 2199: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2202
- Ceres seq_id 1502576
- Location of start within SEQ ID NO 2199: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14439
- gi No. 3935181
- % Identity 71.7
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2202: from 50 to 161

Maximum Length Sequence corresponding to clone ID 312126

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 2203
- Ceres seq_id 1502613
(B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 2204
- Ceres seq_id 1502614
- Location of start within SEQ ID NO 2203: at 1 nt.
(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 2205
- Ceres seq_id 1502615
- Location of start within SEQ ID NO 2203: at 2 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
(D) Related Amino Acid Sequences
- Alignment No. 14440
- gi No. 3023243
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2205: from 48 to 61

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 2206
- Ceres seq_id 1502616
- Location of start within SEQ ID NO 2203: at 68 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
(D) Related Amino Acid Sequences
- Alignment No. 14441
- gi No. 3023243
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2206: from 26 to 39

Maximum Length Sequence corresponding to clone ID 312149

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 2207
- Ceres seq_id 1502621
(B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 2208
- Ceres seq_id 1502622
- Location of start within SEQ ID NO 2207: at 1 nt.
(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
(D) Related Amino Acid Sequences
- Alignment No. 14442
- gi No. 330442
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2208: from 4 to 15

- Alignment No. 14443
- gi No. 3925252
- % Identity 72.7

- Alignment Length 11
- Location of Alignment in SEQ ID NO 2208: from 35 to 45
- Alignment No. 14444
- gi No. 423830
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2208: from 4 to 15
- Alignment No. 14445
- gi No. 4504731
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2208: from 37 to 47
- Alignment No. 14446
- gi No. 4511969
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2208: from 37 to 47
- Alignment No. 14447
- gi No. 4838513
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2208: from 38 to 49
- Alignment No. 14448
- gi No. 4838515
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2208: from 38 to 49
- Alignment No. 14449
- gi No. 5305335
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2208: from 34 to 45

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2209
- Ceres seq_id 1502623
- Location of start within SEQ ID NO 2207: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14450
- gi No. 1722778
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2209: from 19 to 30
- Alignment No. 14451
- gi No. 5257260
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2209: from 21 to 35

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2210

- Ceres seq_id 1502624
- Location of start within SEQ ID NO 2207: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14452
- gi No. 102425
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2210: from 28 to 39
- Alignment No. 14453
- gi No. 102426
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2210: from 28 to 43
- Alignment No. 14454
- gi No. 1161370
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2210: from 26 to 36
- Alignment No. 14455
- gi No. 134950
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2210: from 23 to 35
- Alignment No. 14456
- gi No. 1353462
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2210: from 26 to 36
- Alignment No. 14457
- gi No. 1644455
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2210: from 28 to 41
- Alignment No. 14458
- gi No. 1644457
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2210: from 28 to 41
- Alignment No. 14459
- gi No. 1644459
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2210: from 28 to 41
- Alignment No. 14460
- gi No. 1644461
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2210: from 28 to 41
- Alignment No. 14461

- gi No. 2108256
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2210: from 28 to 43

- Alignment No. 14462
- gi No. 2143272
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2210: from 28 to 40

- Alignment No. 14463
- gi No. 2257986
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2210: from 26 to 37

- Alignment No. 14464
- gi No. 2384847
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2210: from 22 to 33

- Alignment No. 14465
- gi No. 2384847
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2210: from 23 to 34

- Alignment No. 14466
- gi No. 2501953
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2210: from 28 to 40

- Alignment No. 14467
- gi No. 2950355
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2210: from 21 to 35

- Alignment No. 14468
- gi No. 310574
- % Identity 90.9
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2210: from 27 to 37

- Alignment No. 14469
- gi No. 310574
- % Identity 90.9
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2210: from 27 to 37

- Alignment No. 14470
- gi No. 3874146
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2210: from 27 to 37

- Alignment No. 14471
- gi No. 4885040

- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2210: from 28 to 39

- Alignment No. 14472
- gi No. 539033
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2210: from 28 to 42

- Alignment No. 14473
- gi No. 5689489
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2210: from 28 to 38

- Alignment No. 14474
- gi No. 871830
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2210: from 28 to 39

- Alignment No. 14475
- gi No. 91094
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2210: from 21 to 34

Maximum Length Sequence corresponding to clone ID 312179

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2211
- Ceres seq_id 1502635

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2212
- Ceres seq_id 1502636
- Location of start within SEQ ID NO 2211: at 88 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14476
- Ribosomal protein S28e
- Location within SEQ ID NO 2212: from 1 to 65 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14477
- gi No. 1173237
- % Identity 92.3
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2212: from 1 to 65

- Alignment No. 14478
- gi No. 1313916
- % Identity 71.7
- Alignment Length 60
- Location of Alignment in SEQ ID NO 2212: from 6 to 65

- Alignment No. 14479
- gi No. 2739219
- % Identity 92.3
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2212: from 1 to 65

- Alignment No. 14480
- gi No. 2995699
- % Identity 71.2
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2212: from 1 to 65

- Alignment No. 14481
- gi No. 3947719
- % Identity 87.7
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2212: from 1 to 65

- Alignment No. 14482
- gi No. 3947725
- % Identity 86.2
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2212: from 1 to 65

- Alignment No. 14483
- gi No. 464714
- % Identity 70.1
- Alignment Length 67
- Location of Alignment in SEQ ID NO 2212: from 1 to 65

- Alignment No. 14484
- gi No. 464715
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 2212: from 3 to 65

- Alignment No. 14485
- gi No. 464720
- % Identity 80
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2212: from 1 to 65

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2213
- Ceres seq_id 1502637
- Location of start within SEQ ID NO 2211: at 127 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14486
- Ribosomal protein S28e
- Location within SEQ ID NO 2213: from 1 to 52 aa.

- (D) Related Amino Acid Sequences
- Alignment No. 14487
- gi No. 1173237
- % Identity 92.3
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2213: from 1 to 52

- Alignment No. 14488
- gi No. 1313916
- % Identity 71.7
- Alignment Length 60
- Location of Alignment in SEQ ID NO 2213: from 1 to 52

- Alignment No. 14489
- gi No. 2739219
- % Identity 92.3
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2213: from 1 to 52

- Alignment No. 14490
- gi No. 2995699
- % Identity 71.2
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2213: from 1 to 52

- Alignment No. 14491
- gi No. 3947719
- % Identity 87.7
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2213: from 1 to 52

- Alignment No. 14492
- gi No. 3947725
- % Identity 86.2
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2213: from 1 to 52

- Alignment No. 14493
- gi No. 464714
- % Identity 70.1
- Alignment Length 67
- Location of Alignment in SEQ ID NO 2213: from 1 to 52

- Alignment No. 14494
- gi No. 464715
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 2213: from 1 to 52

- Alignment No. 14495
- gi No. 464720
- % Identity 80
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2213: from 1 to 52

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2214
- Ceres seq_id 1502638
- Location of start within SEQ ID NO 2211: at 209 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 312184

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2215
- Ceres seq_id 1502643

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2216
- Ceres seq_id 1502644
- Location of start within SEQ ID NO 2215: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14496
- Zinc finger, C2H2 type
- Location within SEQ ID NO 2216: from 60 to 82 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14497
- gi No. 1362015
- % Identity 74.3
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2216: from 57 to 91

- Alignment No. 14498
- gi No. 1362020
- % Identity 75
- Alignment Length 32
- Location of Alignment in SEQ ID NO 2216: from 60 to 91

- Alignment No. 14499
- gi No. 1362021
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2216: from 57 to 91

- Alignment No. 14500
- gi No. 1871188
- % Identity 75
- Alignment Length 32
- Location of Alignment in SEQ ID NO 2216: from 60 to 91

- Alignment No. 14501
- gi No. 790687
- % Identity 75
- Alignment Length 32
- Location of Alignment in SEQ ID NO 2216: from 60 to 91

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2217
- Ceres seq_id 1502645
- Location of start within SEQ ID NO 2215: at 110 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14502
- Zinc finger, C2H2 type
- Location within SEQ ID NO 2217: from 24 to 46 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14503
- gi No. 1362015
- % Identity 74.3
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2217: from 21 to 55

- Alignment No. 14504
- gi No. 1362020
- % Identity 75
- Alignment Length 32
- Location of Alignment in SEQ ID NO 2217: from 24 to 55

- Alignment No. 14505
- gi No. 1362021
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2217: from 21 to 55
- Alignment No. 14506
- gi No. 1871188
- % Identity 75
- Alignment Length 32
- Location of Alignment in SEQ ID NO 2217: from 24 to 55
- Alignment No. 14507
- gi No. 790687
- % Identity 75
- Alignment Length 32
- Location of Alignment in SEQ ID NO 2217: from 24 to 55

Maximum Length Sequence corresponding to clone ID 312187

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2218
- Ceres seq_id 1502649

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2219
- Ceres seq_id 1502650
- Location of start within SEQ ID NO 2218: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14508
- gi No. 1945621
- % Identity 100
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2219: from 68 to 79
- Alignment No. 14509
- gi No. 1945621
- % Identity 100
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2219: from 68 to 79
- Alignment No. 14510
- gi No. 1945621
- % Identity 100
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2219: from 68 to 79
- Alignment No. 14511
- gi No. 1945621
- % Identity 100
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2219: from 68 to 79
- Alignment No. 14512
- gi No. 1945621
- % Identity 100
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2219: from 68 to 79
- Alignment No. 14513

- gi No. 2947081
- % Identity 90.9
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2219: from 69 to 79

- Alignment No. 14514
- gi No. 2947081
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2219: from 68 to 81

- Alignment No. 14515
- gi No. 4097820
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2219: from 68 to 79

- Alignment No. 14516
- gi No. 4097820
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2219: from 68 to 81

- Alignment No. 14517
- gi No. 4097820
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2219: from 67 to 80

- Alignment No. 14518
- gi No. 539415
- % Identity 100
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2219: from 68 to 78

- Alignment No. 14519
- gi No. 539415
- % Identity 91.7
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2219: from 68 to 79

- Alignment No. 14520
- gi No. 539415
- % Identity 91.7
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2219: from 68 to 79

- Alignment No. 14521
- gi No. 539415
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2219: from 68 to 79

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2220
- Ceres seq_id 1502651
- Location of start within SEQ ID NO 2218: at 126 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2221
 - Ceres seq_id 1502652
 - Location of start within SEQ ID NO 2218: at 144 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 312195

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2222
 - Ceres seq_id 1502653
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2223
 - Ceres seq_id 1502654
 - Location of start within SEQ ID NO 2222: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 14522
 - gi No. 2894228
 - % Identity 73.3
 - Alignment Length 15
 - Location of Alignment in SEQ ID NO 2223: from 9 to 23
 - Alignment No. 14523
 - gi No. 3378540
 - % Identity 71.4
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2223: from 4 to 24
 - Alignment No. 14524
 - gi No. 3660471
 - % Identity 87.5
 - Alignment Length 24
 - Location of Alignment in SEQ ID NO 2223: from 1 to 24
 - Alignment No. 14525
 - gi No. 4309723
 - % Identity 79.2
 - Alignment Length 24
 - Location of Alignment in SEQ ID NO 2223: from 1 to 24

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2224
 - Ceres seq_id 1502655
 - Location of start within SEQ ID NO 2222: at 250 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 14526
 - gi No. 3660471
 - % Identity 72.2
 - Alignment Length 18
 - Location of Alignment in SEQ ID NO 2224: from 29 to 46
 - Alignment No. 14527

- gi No. 4309723
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2224: from 29 to 46

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2225
- Ceres seq_id 1502656
- Location of start within SEQ ID NO 2222: at 256 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14528
- gi No. 3660471
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2225: from 27 to 44
- Alignment No. 14529
- gi No. 4309723
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2225: from 27 to 44

Maximum Length Sequence corresponding to clone ID 312268

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2226
- Ceres seq_id 1502682

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2227
- Ceres seq_id 1502683
- Location of start within SEQ ID NO 2226: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2228
- Ceres seq_id 1502684
- Location of start within SEQ ID NO 2226: at 117 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14530
- gi No. 462569
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2228: from 65 to 75

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2229
- Ceres seq_id 1502685
- Location of start within SEQ ID NO 2226: at 159 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14531

- gi No. 462569
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2229: from 51 to 61

Maximum Length Sequence corresponding to clone ID 312393

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2230
- Ceres seq_id 1502713

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2231
- Ceres seq_id 1502714
- Location of start within SEQ ID NO 2230: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14532
- Asparagine synthase
- Location within SEQ ID NO 2231: from 1 to 104 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14533
- gi No. 114260
- % Identity 70.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2231: from 1 to 145

- Alignment No. 14534
- gi No. 114261
- % Identity 81.3
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2231: from 1 to 123

- Alignment No. 14535
- gi No. 1184265
- % Identity 71.6
- Alignment Length 134
- Location of Alignment in SEQ ID NO 2231: from 1 to 134

- Alignment No. 14536
- gi No. 1305549
- % Identity 80.2
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2231: from 1 to 121

- Alignment No. 14537
- gi No. 1351983
- % Identity 79.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2231: from 1 to 123

- Alignment No. 14538
- gi No. 1351985
- % Identity 78
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2231: from 1 to 123

- Alignment No. 14539
- gi No. 1351987
- % Identity 80.3
- Alignment Length 122

- Location of Alignment in SEQ ID NO 2231: from 1 to 122
- Alignment No. 14540
- gi No. 1351988
- % Identity 73.5
- Alignment Length 132
- Location of Alignment in SEQ ID NO 2231: from 1 to 132
- Alignment No. 14541
- gi No. 1617002
- % Identity 81.1
- Alignment Length 122
- Location of Alignment in SEQ ID NO 2231: from 1 to 122
- Alignment No. 14542
- gi No. 1771880
- % Identity 70.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2231: from 1 to 145
- Alignment No. 14543
- gi No. 1778370
- % Identity 78
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2231: from 1 to 123
- Alignment No. 14544
- gi No. 1778372
- % Identity 78.5
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2231: from 1 to 121
- Alignment No. 14545
- gi No. 2429280
- % Identity 83.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2231: from 1 to 123
- Alignment No. 14546
- gi No. 2522320
- % Identity 71.6
- Alignment Length 134
- Location of Alignment in SEQ ID NO 2231: from 1 to 134
- Alignment No. 14547
- gi No. 3132675
- % Identity 79.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2231: from 1 to 123
- Alignment No. 14548
- gi No. 3182921
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2231: from 1 to 146
- Alignment No. 14549
- gi No. 3821280
- % Identity 80.5
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2231: from 1 to 123

- Alignment No. 14550
- gi No. 3859534
- % Identity 77.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2231: from 1 to 144
- Alignment No. 14551
- gi No. 3859536
- % Identity 76.4
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2231: from 1 to 139
- Alignment No. 14552
- gi No. 3913098
- % Identity 80
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2231: from 1 to 75
- Alignment No. 14553
- gi No. 399064
- % Identity 81.1
- Alignment Length 122
- Location of Alignment in SEQ ID NO 2231: from 1 to 122
- Alignment No. 14554
- gi No. 478402
- % Identity 81.1
- Alignment Length 122
- Location of Alignment in SEQ ID NO 2231: from 1 to 122

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2232
- Ceres seq_id 1502715
- Location of start within SEQ ID NO 2230: at 132 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14555
- Asparagine synthase
- Location within SEQ ID NO 2232: from 1 to 61 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14556
- gi No. 114260
- % Identity 70.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2232: from 1 to 102
- Alignment No. 14557
- gi No. 114261
- % Identity 81.3
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2232: from 1 to 80
- Alignment No. 14558
- gi No. 1184265
- % Identity 71.6
- Alignment Length 134
- Location of Alignment in SEQ ID NO 2232: from 1 to 91

- Alignment No. 14559
- gi No. 1305549
- % Identity 80.2
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2232: from 1 to 78
- Alignment No. 14560
- gi No. 1351983
- % Identity 79.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2232: from 1 to 80
- Alignment No. 14561
- gi No. 1351985
- % Identity 78
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2232: from 1 to 80
- Alignment No. 14562
- gi No. 1351987
- % Identity 80.3
- Alignment Length 122
- Location of Alignment in SEQ ID NO 2232: from 1 to 79
- Alignment No. 14563
- gi No. 1351988
- % Identity 73.5
- Alignment Length 132
- Location of Alignment in SEQ ID NO 2232: from 1 to 89
- Alignment No. 14564
- gi No. 1617002
- % Identity 81.1
- Alignment Length 122
- Location of Alignment in SEQ ID NO 2232: from 1 to 79
- Alignment No. 14565
- gi No. 1771880
- % Identity 70.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2232: from 1 to 102
- Alignment No. 14566
- gi No. 1778370
- % Identity 78
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2232: from 1 to 80
- Alignment No. 14567
- gi No. 1778372
- % Identity 78.5
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2232: from 1 to 78
- Alignment No. 14568
- gi No. 2429280
- % Identity 83.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2232: from 1 to 80
- Alignment No. 14569

- gi No. 2522320
- % Identity 71.6
- Alignment Length 134
- Location of Alignment in SEQ ID NO 2232: from 1 to 91
- Alignment No. 14570
- gi No. 3132675
- % Identity 79.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2232: from 1 to 80
- Alignment No. 14571
- gi No. 3182921
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2232: from 1 to 103
- Alignment No. 14572
- gi No. 3821280
- % Identity 80.5
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2232: from 1 to 80
- Alignment No. 14573
- gi No. 3859534
- % Identity 77.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2232: from 1 to 101
- Alignment No. 14574
- gi No. 3859536
- % Identity 76.4
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2232: from 1 to 96
- Alignment No. 14575
- gi No. 3913098
- % Identity 80
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2232: from 1 to 32
- Alignment No. 14576
- gi No. 399064
- % Identity 81.1
- Alignment Length 122
- Location of Alignment in SEQ ID NO 2232: from 1 to 79
- Alignment No. 14577
- gi No. 478402
- % Identity 81.1
- Alignment Length 122
- Location of Alignment in SEQ ID NO 2232: from 1 to 79

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2233
- Ceres seq_id 1502716
- Location of start within SEQ ID NO 2230: at 135 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14578

- Asparagine synthase
- Location within SEQ ID NO 2233: from 1 to 60 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14579
- gi No. 114260
- % Identity 70.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2233: from 1 to 101
- Alignment No. 14580
- gi No. 114261
- % Identity 81.3
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2233: from 1 to 79
- Alignment No. 14581
- gi No. 1184265
- % Identity 71.6
- Alignment Length 134
- Location of Alignment in SEQ ID NO 2233: from 1 to 90
- Alignment No. 14582
- gi No. 1305549
- % Identity 80.2
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2233: from 1 to 77
- Alignment No. 14583
- gi No. 1351983
- % Identity 79.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2233: from 1 to 79
- Alignment No. 14584
- gi No. 1351985
- % Identity 78
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2233: from 1 to 79
- Alignment No. 14585
- gi No. 1351987
- % Identity 80.3
- Alignment Length 122
- Location of Alignment in SEQ ID NO 2233: from 1 to 78
- Alignment No. 14586
- gi No. 1351988
- % Identity 73.5
- Alignment Length 132
- Location of Alignment in SEQ ID NO 2233: from 1 to 88
- Alignment No. 14587
- gi No. 1617002
- % Identity 81.1
- Alignment Length 122
- Location of Alignment in SEQ ID NO 2233: from 1 to 78
- Alignment No. 14588
- gi No. 1771880
- % Identity 70.3

- Alignment Length 145
- Location of Alignment in SEQ ID NO 2233: from 1 to 101
- Alignment No. 14589
- gi No. 1778370
- % Identity 78
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2233: from 1 to 79
- Alignment No. 14590
- gi No. 1778372
- % Identity 78.5
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2233: from 1 to 77
- Alignment No. 14591
- gi No. 2429280
- % Identity 83.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2233: from 1 to 79
- Alignment No. 14592
- gi No. 2522320
- % Identity 71.6
- Alignment Length 134
- Location of Alignment in SEQ ID NO 2233: from 1 to 90
- Alignment No. 14593
- gi No. 3132675
- % Identity 79.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2233: from 1 to 79
- Alignment No. 14594
- gi No. 3182921
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2233: from 1 to 102
- Alignment No. 14595
- gi No. 3821280
- % Identity 80.5
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2233: from 1 to 79
- Alignment No. 14596
- gi No. 3859534
- % Identity 77.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2233: from 1 to 100
- Alignment No. 14597
- gi No. 3859536
- % Identity 76.4
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2233: from 1 to 95
- Alignment No. 14598
- gi No. 3913098
- % Identity 80
- Alignment Length 75

- Location of Alignment in SEQ ID NO 2233: from 1 to 31
- Alignment No. 14599
- gi No. 399064
- % Identity 81.1
- Alignment Length 122
- Location of Alignment in SEQ ID NO 2233: from 1 to 78
- Alignment No. 14600
- gi No. 478402
- % Identity 81.1
- Alignment Length 122
- Location of Alignment in SEQ ID NO 2233: from 1 to 78

Maximum Length Sequence corresponding to clone ID 312402

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2234
- Ceres seq_id 1502717

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2235
- Ceres seq_id 1502718
- Location of start within SEQ ID NO 2234: at 136 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14601
- gi No. 1778093
- % Identity 73.5
- Alignment Length 34
- Location of Alignment in SEQ ID NO 2235: from 1 to 19
- Alignment No. 14602
- gi No. 1778095
- % Identity 73.5
- Alignment Length 34
- Location of Alignment in SEQ ID NO 2235: from 1 to 19
- Alignment No. 14603
- gi No. 4678208
- % Identity 71
- Alignment Length 31
- Location of Alignment in SEQ ID NO 2235: from 1 to 19

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2236
- Ceres seq_id 1502719
- Location of start within SEQ ID NO 2234: at 172 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2237
- Ceres seq_id 1502720
- Location of start within SEQ ID NO 2234: at 194 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 312407

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2238
- Ceres seq_id 1502721

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2239
- Ceres seq_id 1502722
- Location of start within SEQ ID NO 2238: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14604
- gi No. 1705677
- % Identity 76.1
- Alignment Length 109
- Location of Alignment in SEQ ID NO 2239: from 1 to 108
- Alignment No. 14605
- gi No. 1705678
- % Identity 75.9
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2239: from 1 to 108
- Alignment No. 14606
- gi No. 2492504
- % Identity 77.8
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2239: from 1 to 108

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2240
- Ceres seq_id 1502723
- Location of start within SEQ ID NO 2238: at 70 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14607
- gi No. 1705677
- % Identity 76.1
- Alignment Length 109
- Location of Alignment in SEQ ID NO 2240: from 1 to 85
- Alignment No. 14608
- gi No. 1705678
- % Identity 75.9
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2240: from 1 to 85
- Alignment No. 14609
- gi No. 2492504
- % Identity 77.8
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2240: from 1 to 85

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2241
- Ceres seq_id 1502724
- Location of start within SEQ ID NO 2238: at 137 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)
(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 312409

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2242
- Ceres seq_id 1502726

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2243
- Ceres seq_id 1502727
- Location of start within SEQ ID NO 2242: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2244
- Ceres seq_id 1502728
- Location of start within SEQ ID NO 2242: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 14610
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2244: from 21 to 78 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2245
- Ceres seq_id 1502729
- Location of start within SEQ ID NO 2242: at 20 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 312432

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2246
- Ceres seq_id 1502730

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2247
- Ceres seq_id 1502731
- Location of start within SEQ ID NO 2246: at 114 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14611
- gi No. 2500047
- % Identity 87.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2247: from 15 to 54
- Alignment No. 14612
- gi No. 3510259
- % Identity 73.2

- Alignment Length 56
- Location of Alignment in SEQ ID NO 2247: from 1 to 54
- Alignment No. 14613
- gi No. 4033417
- % Identity 77.2
- Alignment Length 57
- Location of Alignment in SEQ ID NO 2247: from 1 to 54
- Alignment No. 14614
- gi No. 4033424
- % Identity 100
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2247: from 1 to 54

Maximum Length Sequence corresponding to clone ID 312476

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2248
- Ceres seq_id 1502755

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2249
- Ceres seq_id 1502756
- Location of start within SEQ ID NO 2248: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2250
- Ceres seq_id 1502757
- Location of start within SEQ ID NO 2248: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14615
- gi No. 2129800
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2250: from 68 to 87
- Alignment No. 14616
- gi No. 2129804
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2250: from 68 to 87
- Alignment No. 14617
- gi No. 2129805
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2250: from 68 to 87
- Alignment No. 14618
- gi No. 2317758
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2250: from 68 to 87
- Alignment No. 14619

- gi No. 2317758
- % Identity 72
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2250: from 65 to 87
- Alignment No. 14620
- gi No. 5391446
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2250: from 68 to 87

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2251
- Ceres seq_id 1502758
- Location of start within SEQ ID NO 2248: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 312486

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2252
- Ceres seq_id 1502759

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2253
- Ceres seq_id 1502760
- Location of start within SEQ ID NO 2252: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2254
- Ceres seq_id 1502761
- Location of start within SEQ ID NO 2252: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14621
- gi No. 2781345
- % Identity 79.3
- Alignment Length 58
- Location of Alignment in SEQ ID NO 2254: from 1 to 58
- Alignment No. 14622
- gi No. 3157933
- % Identity 76.1
- Alignment Length 71
- Location of Alignment in SEQ ID NO 2254: from 1 to 71

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2255
- Ceres seq_id 1502762
- Location of start within SEQ ID NO 2252: at 320 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 312499

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2256
- Ceres seq_id 1502763

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2257
- Ceres seq_id 1502764
- Location of start within SEQ ID NO 2256: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14623
- gi No. 4512216
- % Identity 80.5
- Alignment Length 41
- Location of Alignment in SEQ ID NO 2257: from 114 to 154
- Alignment No. 14624
- gi No. 5689236
- % Identity 75.6
- Alignment Length 41
- Location of Alignment in SEQ ID NO 2257: from 114 to 154

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2258
- Ceres seq_id 1502765
- Location of start within SEQ ID NO 2256: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2259
- Ceres seq_id 1502766
- Location of start within SEQ ID NO 2256: at 8 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 312502

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2260
- Ceres seq_id 1502767

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2261
- Ceres seq_id 1502768
- Location of start within SEQ ID NO 2260: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2262
- Ceres seq_id 1502769
- Location of start within SEQ ID NO 2260: at 135 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2263
- Ceres seq_id 1502770
- Location of start within SEQ ID NO 2260: at 250 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14625
- gi No. 5262791
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2263: from 57 to 69

Maximum Length Sequence corresponding to clone ID 312503

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2264
- Ceres seq_id 1502771

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2265
- Ceres seq_id 1502772
- Location of start within SEQ ID NO 2264: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14626
- gi No. 2149640
- % Identity 81.2
- Alignment Length 101
- Location of Alignment in SEQ ID NO 2265: from 1 to 99
- Alignment No. 14627
- gi No. 2959781
- % Identity 70.7
- Alignment Length 101
- Location of Alignment in SEQ ID NO 2265: from 1 to 99
- Alignment No. 14628
- gi No. 5107374
- % Identity 70.7
- Alignment Length 101
- Location of Alignment in SEQ ID NO 2265: from 1 to 99

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2266
- Ceres seq_id 1502773
- Location of start within SEQ ID NO 2264: at 146 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14629
- gi No. 2149640
- % Identity 81.2
- Alignment Length 101
- Location of Alignment in SEQ ID NO 2266: from 1 to 51

- Alignment No. 14630
- gi No. 2959781
- % Identity 70.7
- Alignment Length 101
- Location of Alignment in SEQ ID NO 2266: from 1 to 51

- Alignment No. 14631
- gi No. 5107374
- % Identity 70.7
- Alignment Length 101
- Location of Alignment in SEQ ID NO 2266: from 1 to 51

Maximum Length Sequence corresponding to clone ID 312523

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2267
- Ceres seq_id 1502781

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2268
- Ceres seq_id 1502782
- Location of start within SEQ ID NO 2267: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2269
- Ceres seq_id 1502783
- Location of start within SEQ ID NO 2267: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14632
- gi No. 3264598
- % Identity 76
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2269: from 19 to 39

Maximum Length Sequence corresponding to clone ID 312525

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2270
- Ceres seq_id 1502784

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2271
- Ceres seq_id 1502785
- Location of start within SEQ ID NO 2270: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2272
- Ceres seq_id 1502786
- Location of start within SEQ ID NO 2270: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2273
- Ceres seq_id 1502787
- Location of start within SEQ ID NO 2270: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14633
- gi No. 102706
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2273: from 4 to 19
- Alignment No. 14634
- gi No. 1042189
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2273: from 5 to 19
- Alignment No. 14635
- gi No. 1168711
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2273: from 5 to 18
- Alignment No. 14636
- gi No. 131044
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2273: from 4 to 19
- Alignment No. 14637
- gi No. 1362586
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2273: from 4 to 19
- Alignment No. 14638
- gi No. 1362587
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2273: from 5 to 19
- Alignment No. 14639
- gi No. 1362587
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2273: from 5 to 19

Maximum Length Sequence corresponding to clone ID 312595

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2274
- Ceres seq_id 1502805

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2275
- Ceres seq_id 1502806
- Location of start within SEQ ID NO 2274: at 123 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14640
- Macrophage migration inhibitory factor (MIF)
- Location within SEQ ID NO 2275: from 2 to 104 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2276
- Ceres seq_id 1502807
- Location of start within SEQ ID NO 2274: at 240 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14641
- Macrophage migration inhibitory factor (MIF)
- Location within SEQ ID NO 2276: from 1 to 65 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2277
- Ceres seq_id 1502808
- Location of start within SEQ ID NO 2274: at 267 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14642
- Macrophage migration inhibitory factor (MIF)
- Location within SEQ ID NO 2277: from 1 to 56 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 312598

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2278
- Ceres seq_id 1502809

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2279
- Ceres seq_id 1502810
- Location of start within SEQ ID NO 2278: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2280
- Ceres seq_id 1502811
- Location of start within SEQ ID NO 2278: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14643
- gi No. 4115377
- % Identity 82.8
- Alignment Length 58
- Location of Alignment in SEQ ID NO 2280: from 58 to 115

Maximum Length Sequence corresponding to clone ID 312622

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2281
- Ceres seq_id 1502820

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2282
- Ceres seq_id 1502821
- Location of start within SEQ ID NO 2281: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2283
- Ceres seq_id 1502822
- Location of start within SEQ ID NO 2281: at 101 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14644
- Ribosomal protein S11
- Location within SEQ ID NO 2283: from 28 to 105 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14645
- gi No. 1173200
- % Identity 82.1
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2283: from 67 to 105
- Alignment No. 14646
- gi No. 1173201
- % Identity 82.2
- Alignment Length 101
- Location of Alignment in SEQ ID NO 2283: from 5 to 105
- Alignment No. 14647
- gi No. 131772
- % Identity 92.4
- Alignment Length 105
- Location of Alignment in SEQ ID NO 2283: from 1 to 105
- Alignment No. 14648
- gi No. 131773
- % Identity 89.3
- Alignment Length 103
- Location of Alignment in SEQ ID NO 2283: from 3 to 105
- Alignment No. 14649
- gi No. 133771
- % Identity 74.5
- Alignment Length 106
- Location of Alignment in SEQ ID NO 2283: from 1 to 105
- Alignment No. 14650
- gi No. 133777
- % Identity 77.6
- Alignment Length 85
- Location of Alignment in SEQ ID NO 2283: from 21 to 105

- Alignment No. 14651
- gi No. 133782
- % Identity 72.9
- Alignment Length 107
- Location of Alignment in SEQ ID NO 2283: from 1 to 105
- Alignment No. 14652
- gi No. 133785
- % Identity 78.3
- Alignment Length 106
- Location of Alignment in SEQ ID NO 2283: from 1 to 105
- Alignment No. 14653
- gi No. 1346941
- % Identity 74.1
- Alignment Length 85
- Location of Alignment in SEQ ID NO 2283: from 21 to 105
- Alignment No. 14654
- gi No. 1350935
- % Identity 74.8
- Alignment Length 107
- Location of Alignment in SEQ ID NO 2283: from 1 to 105
- Alignment No. 14655
- gi No. 2350992
- % Identity 77
- Alignment Length 74
- Location of Alignment in SEQ ID NO 2283: from 27 to 100
- Alignment No. 14656
- gi No. 2414647
- % Identity 80.5
- Alignment Length 87
- Location of Alignment in SEQ ID NO 2283: from 16 to 102
- Alignment No. 14657
- gi No. 2500442
- % Identity 70.5
- Alignment Length 78
- Location of Alignment in SEQ ID NO 2283: from 4 to 80
- Alignment No. 14658
- gi No. 2500443
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2283: from 85 to 105
- Alignment No. 14659
- gi No. 3097244
- % Identity 80.2
- Alignment Length 106
- Location of Alignment in SEQ ID NO 2283: from 1 to 105
- Alignment No. 14660
- gi No. 3122785
- % Identity 84.8
- Alignment Length 105
- Location of Alignment in SEQ ID NO 2283: from 1 to 105
- Alignment No. 14661

- gi No. 4574240
- % Identity 77.6
- Alignment Length 85
- Location of Alignment in SEQ ID NO 2283: from 21 to 105

- Alignment No. 14662
- gi No. 4588920
- % Identity 74.5
- Alignment Length 106
- Location of Alignment in SEQ ID NO 2283: from 1 to 105

- Alignment No. 14663
- gi No. 4678226
- % Identity 84.8
- Alignment Length 105
- Location of Alignment in SEQ ID NO 2283: from 1 to 105

- Alignment No. 14664
- gi No. 4886269
- % Identity 85.7
- Alignment Length 105
- Location of Alignment in SEQ ID NO 2283: from 1 to 105

- Alignment No. 14665
- gi No. 5032051
- % Identity 79.2
- Alignment Length 106
- Location of Alignment in SEQ ID NO 2283: from 1 to 105

- Alignment No. 14666
- gi No. 5441523
- % Identity 88.2
- Alignment Length 34
- Location of Alignment in SEQ ID NO 2283: from 72 to 105

- Alignment No. 14667
- gi No. 547604
- % Identity 75.3
- Alignment Length 85
- Location of Alignment in SEQ ID NO 2283: from 21 to 105

- Alignment No. 14668
- gi No. 70946
- % Identity 74.1
- Alignment Length 85
- Location of Alignment in SEQ ID NO 2283: from 21 to 105

- Alignment No. 14669
- gi No. 730453
- % Identity 75.3
- Alignment Length 85
- Location of Alignment in SEQ ID NO 2283: from 21 to 105

- Alignment No. 14670
- gi No. 730633
- % Identity 76.4
- Alignment Length 106
- Location of Alignment in SEQ ID NO 2283: from 1 to 105

- Alignment No. 14671
- gi No. 83794

- % Identity 74.3
- Alignment Length 105
- Location of Alignment in SEQ ID NO 2283: from 1 to 105

Maximum Length Sequence corresponding to clone ID 312649

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2284
- Ceres seq_id 1502834

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2285
- Ceres seq_id 1502835
- Location of start within SEQ ID NO 2284: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14672
- Forkhead-associated (FHA) domain
- Location within SEQ ID NO 2285: from 92 to 145 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2286
- Ceres seq_id 1502836
- Location of start within SEQ ID NO 2284: at 57 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14673
- Forkhead-associated (FHA) domain
- Location within SEQ ID NO 2286: from 74 to 127 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 312672

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2287
- Ceres seq_id 1502844

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2288
- Ceres seq_id 1502845
- Location of start within SEQ ID NO 2287: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14674
- DnaJ domain
- Location within SEQ ID NO 2288: from 1 to 29 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 312697

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2289
- Ceres seq_id 1502850

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2290
- Ceres seq_id 1502851
- Location of start within SEQ ID NO 2289: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2291
- Ceres seq_id 1502852
- Location of start within SEQ ID NO 2289: at 144 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2292
- Ceres seq_id 1502853
- Location of start within SEQ ID NO 2289: at 217 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14675
- gi No. 4220472
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 2292: from 1 to 19

Maximum Length Sequence corresponding to clone ID 312744

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2293
- Ceres seq_id 1502860

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2294
- Ceres seq_id 1502861
- Location of start within SEQ ID NO 2293: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2295
- Ceres seq_id 1502862
- Location of start within SEQ ID NO 2293: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 14676
- Plant lipid transfer protein family
- Location within SEQ ID NO 2295: from 75 to 153 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14677
- gi No. 1084462
- % Identity 70
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2295: from 75 to 152
- Alignment No. 14678
- gi No. 2226329
- % Identity 93.8

- Alignment Length 80
- Location of Alignment in SEQ ID NO 2295: from 75 to 154
- Alignment No. 14679
- gi No. 399204
- % Identity 92.5
- Alignment Length 80
- Location of Alignment in SEQ ID NO 2295: from 75 to 154

Maximum Length Sequence corresponding to clone ID 312842

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2296
- Ceres seq_id 1502896

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2297
- Ceres seq_id 1502897
- Location of start within SEQ ID NO 2296: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14680
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 2297: from 1 to 101 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14681
- gi No. 100610
- % Identity 80.2
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
- Alignment No. 14682
- gi No. 100611
- % Identity 78.4
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
- Alignment No. 14683
- gi No. 1076633
- % Identity 88.3
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
- Alignment No. 14684
- gi No. 1082205
- % Identity 72.2
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2297: from 2 to 109
- Alignment No. 14685
- gi No. 1216280
- % Identity 89.2
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
- Alignment No. 14686
- gi No. 1216285
- % Identity 89.2
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110

- Alignment No. 14687
- gi No. 134588
- % Identity 72.5
- Alignment Length 109
- Location of Alignment in SEQ ID NO 2297: from 1 to 109
- Alignment No. 14688
- gi No. 1362153
- % Identity 100
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2297: from 1 to 28
- Alignment No. 14689
- gi No. 1362154
- % Identity 100
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2297: from 1 to 28
- Alignment No. 14690
- gi No. 1362155
- % Identity 96.4
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2297: from 1 to 28
- Alignment No. 14691
- gi No. 1477684
- % Identity 94.6
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
- Alignment No. 14692
- gi No. 1703034
- % Identity 72.2
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2297: from 2 to 109
- Alignment No. 14693
- gi No. 1729444
- % Identity 91
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
- Alignment No. 14694
- gi No. 1742967
- % Identity 91
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
- Alignment No. 14695
- gi No. 1743009
- % Identity 91
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
- Alignment No. 14696
- gi No. 1935916
- % Identity 89.2
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
- Alignment No. 14697

- gi No. 2130048
- % Identity 96.4
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110

- Alignment No. 14698
- gi No. 2136044
- % Identity 75
- Alignment Length 32
- Location of Alignment in SEQ ID NO 2297: from 3 to 34

- Alignment No. 14699
- gi No. 2137442
- % Identity 94.1
- Alignment Length 34
- Location of Alignment in SEQ ID NO 2297: from 1 to 34

- Alignment No. 14700
- gi No. 2146759
- % Identity 100
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2297: from 1 to 28

- Alignment No. 14701
- gi No. 2146812
- % Identity 78.4
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110

- Alignment No. 14702
- gi No. 2274869
- % Identity 97.2
- Alignment Length 36
- Location of Alignment in SEQ ID NO 2297: from 5 to 40

- Alignment No. 14703
- gi No. 2499626
- % Identity 72.5
- Alignment Length 109
- Location of Alignment in SEQ ID NO 2297: from 1 to 109

- Alignment No. 14704
- gi No. 2507201
- % Identity 71.8
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2297: from 1 to 109

- Alignment No. 14705
- gi No. 3023235
- % Identity 86.7
- Alignment Length 30
- Location of Alignment in SEQ ID NO 2297: from 2 to 31

- Alignment No. 14706
- gi No. 322596
- % Identity 92.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110

- Alignment No. 14707
- gi No. 3341452

- % Identity 79.3
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110

- Alignment No. 14708
- gi No. 400982
- % Identity 82.9
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110

- Alignment No. 14709
- gi No. 4091885
- % Identity 93.7
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110

- Alignment No. 14710
- gi No. 4099088
- % Identity 78.4
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110

- Alignment No. 14711
- gi No. 4107001
- % Identity 96.4
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110

- Alignment No. 14712
- gi No. 4107003
- % Identity 96.4
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110

- Alignment No. 14713
- gi No. 4107005
- % Identity 96.4
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110

- Alignment No. 14714
- gi No. 4107009
- % Identity 95.5
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110

- Alignment No. 14715
- gi No. 4432983
- % Identity 70
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2297: from 8 to 47

- Alignment No. 14716
- gi No. 4520332
- % Identity 74.3
- Alignment Length 109
- Location of Alignment in SEQ ID NO 2297: from 1 to 109

- Alignment No. 14717
- gi No. 4567091
- % Identity 92.8

- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110

- Alignment No. 14718
- gi No. 4982468
- % Identity 75.2
- Alignment Length 109
- Location of Alignment in SEQ ID NO 2297: from 2 to 110

- Alignment No. 14719
- gi No. 5410312
- % Identity 72.2
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2297: from 2 to 109

- Alignment No. 14720
- gi No. 5442424
- % Identity 72.5
- Alignment Length 109
- Location of Alignment in SEQ ID NO 2297: from 1 to 109

- Alignment No. 14721
- gi No. 5453964
- % Identity 71.3
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2297: from 2 to 109

- Alignment No. 14722
- gi No. 5453966
- % Identity 71.3
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2297: from 2 to 109

- Alignment No. 14723
- gi No. 575292
- % Identity 96.4
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110

- Alignment No. 14724
- gi No. 728758
- % Identity 72.2
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2297: from 2 to 109

- Alignment No. 14725
- gi No. 862473
- % Identity 72.2
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2297: from 2 to 109

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2298
- Ceres seq_id 1502898
- Location of start within SEQ ID NO 2296: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 312860

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2299
- Ceres seq_id 1502902

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2300
- Ceres seq_id 1502903
- Location of start within SEQ ID NO 2299: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14726
- gi No. 2160438
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2300: from 66 to 76
- Alignment No. 14727
- gi No. 286238
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2300: from 66 to 76
- Alignment No. 14728
- gi No. 348497
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2300: from 66 to 76
- Alignment No. 14729
- gi No. 548375
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2300: from 66 to 76

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2301
- Ceres seq_id 1502904
- Location of start within SEQ ID NO 2299: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14730
- gi No. 3413810
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2301: from 26 to 37

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2302
- Ceres seq_id 1502905
- Location of start within SEQ ID NO 2299: at 46 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14731
- gi No. 2160438
- % Identity 72.7
- Alignment Length 11

- Location of Alignment in SEQ ID NO 2302: from 51 to 61
- Alignment No. 14732
- gi No. 286238
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2302: from 51 to 61
- Alignment No. 14733
- gi No. 348497
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2302: from 51 to 61
- Alignment No. 14734
- gi No. 548375
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2302: from 51 to 61

Maximum Length Sequence corresponding to clone ID 312920

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2303
- Ceres seq_id 1502937

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2304
- Ceres seq_id 1502938
- Location of start within SEQ ID NO 2303: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14735
- gi No. 3367741
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2304: from 85 to 96

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2305
- Ceres seq_id 1502939
- Location of start within SEQ ID NO 2303: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14736
- Nuclear transition protein 2
- Location within SEQ ID NO 2305: from 7 to 72 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2306
- Ceres seq_id 1502940
- Location of start within SEQ ID NO 2303: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 313030

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2307
- Ceres seq_id 1502981

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2308
- Ceres seq_id 1502982
- Location of start within SEQ ID NO 2307: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14737
- gi No. 465445
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2308: from 107 to 119

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2309
- Ceres seq_id 1502983
- Location of start within SEQ ID NO 2307: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2310
- Ceres seq_id 1502984
- Location of start within SEQ ID NO 2307: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14738
- gi No. 102706
- % Identity 92.3
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2310: from 106 to 118

- Alignment No. 14739
- gi No. 102706
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2310: from 106 to 119

- Alignment No. 14740
- gi No. 102706
- % Identity 86.7
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2310: from 106 to 119

- Alignment No. 14741
- gi No. 102706
- % Identity 76.5
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2310: from 106 to 119

- Alignment No. 14742
- gi No. 102707
- % Identity 92.3

- Alignment Length 13
- Location of Alignment in SEQ ID NO 2310: from 107 to 119
- Alignment No. 14743
- gi No. 1170389
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2310: from 106 to 119
- Alignment No. 14744
- gi No. 1170392
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2310: from 106 to 119
- Alignment No. 14745
- gi No. 1170396
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2310: from 106 to 119
- Alignment No. 14746
- gi No. 1170397
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2310: from 106 to 119
- Alignment No. 14747
- gi No. 1170398
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2310: from 106 to 119
- Alignment No. 14748
- gi No. 1170401
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2310: from 108 to 119
- Alignment No. 14749
- gi No. 1170405
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2310: from 106 to 119
- Alignment No. 14750
- gi No. 1170406
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2310: from 106 to 119
- Alignment No. 14751
- gi No. 123689
- % Identity 92.9
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2310: from 106 to 119
- Alignment No. 14752
- gi No. 123689
- % Identity 82.4
- Alignment Length 17

- Location of Alignment in SEQ ID NO 2310: from 106 to 122
- Alignment No. 14753
- gi No. 123695
- % Identity 92.3
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2310: from 107 to 119
- Alignment No. 14754
- gi No. 131040
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2310: from 107 to 117
- Alignment No. 14755
- gi No. 131040
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2310: from 108 to 118
- Alignment No. 14756
- gi No. 131044
- % Identity 92.3
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2310: from 106 to 118
- Alignment No. 14757
- gi No. 131044
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2310: from 106 to 119
- Alignment No. 14758
- gi No. 131044
- % Identity 86.7
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2310: from 106 to 119
- Alignment No. 14759
- gi No. 131044
- % Identity 76.5
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2310: from 106 to 119
- Alignment No. 14760
- gi No. 163635
- % Identity 92.9
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2310: from 106 to 119
- Alignment No. 14761
- gi No. 163635
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2310: from 106 to 119
- Alignment No. 14762
- gi No. 163635
- % Identity 82.4
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2310: from 106 to 122

- Alignment No. 14763
- gi No. 2134213
- % Identity 92.3
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2310: from 107 to 119

- Alignment No. 14764
- gi No. 2134213
- % Identity 92.9
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2310: from 106 to 119

- Alignment No. 14765
- gi No. 225057
- % Identity 92.9
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2310: from 106 to 119

- Alignment No. 14766
- gi No. 225057
- % Identity 82.4
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2310: from 106 to 122

- Alignment No. 14767
- gi No. 357984
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2310: from 108 to 118

- Alignment No. 14768
- gi No. 5456964
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2310: from 106 to 118

- Alignment No. 14769
- gi No. 85630
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2310: from 107 to 117

- Alignment No. 14770
- gi No. 85630
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2310: from 108 to 118

Maximum Length Sequence corresponding to clone ID 313054

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2311
- Ceres seq_id 1502985

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2312
- Ceres seq_id 1502986
- Location of start within SEQ ID NO 2311: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14771

- Assemblin (Peptidase family S21)
- Location within SEQ ID NO 2312: from 21 to 102 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2313
- Ceres seq_id 1502987
- Location of start within SEQ ID NO 2311: at 167 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 313104

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2314
- Ceres seq_id 1503000

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2315
- Ceres seq_id 1503001
- Location of start within SEQ ID NO 2314: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2316
- Ceres seq_id 1503002
- Location of start within SEQ ID NO 2314: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14772
- CRAL/TRIO domain.
- Location within SEQ ID NO 2316: from 7 to 80 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 313149

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2317
- Ceres seq_id 1503010

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2318
- Ceres seq_id 1503011
- Location of start within SEQ ID NO 2317: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14773
- Zinc finger, C3HC4 type (RING finger)
- Location within SEQ ID NO 2318: from 58 to 106 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2319
- Ceres seq_id 1503012
- Location of start within SEQ ID NO 2317: at 77 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14774
- Zinc finger, C3HC4 type (RING finger)
- Location within SEQ ID NO 2319: from 33 to 81 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 313273

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2320
- Ceres seq_id 1503042

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2321
- Ceres seq_id 1503043
- Location of start within SEQ ID NO 2320: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14775
- gi No. 2529670
- % Identity 81.3
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2321: from 24 to 39

- Alignment No. 14776
- gi No. 3021348
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2321: from 26 to 40

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2322
- Ceres seq_id 1503044
- Location of start within SEQ ID NO 2320: at 67 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14777
- gi No. 2529670
- % Identity 81.3
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2322: from 2 to 17

- Alignment No. 14778
- gi No. 3021348
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2322: from 4 to 18

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2323
- Ceres seq_id 1503045
- Location of start within SEQ ID NO 2320: at 225 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14779

- Eukaryotic ribosomal protein L18
- Location within SEQ ID NO 2323: from 1 to 51 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14780
- gi No. 1172977
- % Identity 72.3
- Alignment Length 83
- Location of Alignment in SEQ ID NO 2323: from 1 to 49
- Alignment No. 14781
- gi No. 2529670
- % Identity 73.1
- Alignment Length 78
- Location of Alignment in SEQ ID NO 2323: from 1 to 44

Maximum Length Sequence corresponding to clone ID 313280

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2324
- Ceres seq_id 1503048

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2325
- Ceres seq_id 1503049
- Location of start within SEQ ID NO 2324: at 85 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14782
- gi No. 1171036
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
- Alignment No. 14783
- gi No. 1480016
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
- Alignment No. 14784
- gi No. 2407331
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
- Alignment No. 14785
- gi No. 2497887
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2325: from 1 to 18
- Alignment No. 14786
- gi No. 2497888
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2325: from 1 to 18
- Alignment No. 14787
- gi No. 2497890
- % Identity 77.8

- Alignment Length 18
- Location of Alignment in SEQ ID NO 2325: from 1 to 18

- Alignment No. 14788
- gi No. 2497892
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20

- Alignment No. 14789
- gi No. 2497893
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20

- Alignment No. 14790
- gi No. 2497895
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20

- Alignment No. 14791
- gi No. 2497901
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20

- Alignment No. 14792
- gi No. 2497903
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20

- Alignment No. 14793
- gi No. 2497904
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20

- Alignment No. 14794
- gi No. 2507587
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20

- Alignment No. 14795
- gi No. 266579
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20

- Alignment No. 14796
- gi No. 3694984
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20

- Alignment No. 14797
- gi No. 3900980
- % Identity 70
- Alignment Length 20

- Location of Alignment in SEQ ID NO 2325: from 1 to 20
- Alignment No. 14798
- gi No. 3901014
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
- Alignment No. 14799
- gi No. 4877893
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
- Alignment No. 14800
- gi No. 72178
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20

Maximum Length Sequence corresponding to clone ID 313319

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2326
- Ceres seq_id 1503064

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2327
- Ceres seq_id 1503065
- Location of start within SEQ ID NO 2326: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14801
- Fatty acid desaturase
- Location within SEQ ID NO 2327: from 37 to 128 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14802
- gi No. 4104056
- % Identity 71.7
- Alignment Length 166
- Location of Alignment in SEQ ID NO 2327: from 5 to 169

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2328
- Ceres seq_id 1503066
- Location of start within SEQ ID NO 2326: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14803
- gi No. 100214
- % Identity 71.4
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2328: from 2 to 15
- Alignment No. 14804
- gi No. 100214
- % Identity 71.4
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2328: from 2 to 15

- Alignment No. 14805
- gi No. 100214
- % Identity 71.4
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2328: from 2 to 15

- Alignment No. 14806
- gi No. 1185397
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2328: from 4 to 15

- Alignment No. 14807
- gi No. 1185397
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2328: from 3 to 15

- Alignment No. 14808
- gi No. 1185397
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2328: from 3 to 15

- Alignment No. 14809
- gi No. 168237
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2328: from 2 to 15

- Alignment No. 14810
- gi No. 2429362
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2328: from 5 to 15

- Alignment No. 14811
- gi No. 4096360
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2328: from 4 to 15

- Alignment No. 14812
- gi No. 4096360
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2328: from 3 to 15

- Alignment No. 14813
- gi No. 4096360
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2328: from 3 to 15

- Alignment No. 14814
- gi No. 5430752
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2328: from 2 to 15

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2329
 - Ceres seq_id 1503067
 - Location of start within SEQ ID NO 2326: at 115 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14815
- Fatty acid desaturase
- Location within SEQ ID NO 2329: from 1 to 90 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14816
- gi No. 4104056
- % Identity 71.7
- Alignment Length 166
- Location of Alignment in SEQ ID NO 2329: from 1 to 131

Maximum Length Sequence corresponding to clone ID 313321

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2330
- Ceres seq_id 1503071

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2331
- Ceres seq_id 1503072
- Location of start within SEQ ID NO 2330: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14817
- gi No. 3850569
- % Identity 73.1
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2331: from 16 to 41

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2332
- Ceres seq_id 1503073
- Location of start within SEQ ID NO 2330: at 147 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 313406

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2333
- Ceres seq_id 1503104

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2334
- Ceres seq_id 1503105
- Location of start within SEQ ID NO 2333: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14818
- gi No. 2564066
- % Identity 78.5
- Alignment Length 65

- Location of Alignment in SEQ ID NO 2334: from 38 to 102
- Alignment No. 14819
- gi No. 5031275
- % Identity 70.8
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2334: from 38 to 102

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2335
- Ceres seq_id 1503106
- Location of start within SEQ ID NO 2333: at 112 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14820
- gi No. 2564066
- % Identity 78.5
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2335: from 1 to 65
- Alignment No. 14821
- gi No. 5031275
- % Identity 70.8
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2335: from 1 to 65

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2336
- Ceres seq_id 1503107
- Location of start within SEQ ID NO 2333: at 222 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14822
- gi No. 2464905
- % Identity 77.8
- Alignment Length 36
- Location of Alignment in SEQ ID NO 2336: from 29 to 63
- Alignment No. 14823
- gi No. 2564066
- % Identity 83.8
- Alignment Length 37
- Location of Alignment in SEQ ID NO 2336: from 28 to 63
- Alignment No. 14824
- gi No. 3269288
- % Identity 86.5
- Alignment Length 37
- Location of Alignment in SEQ ID NO 2336: from 28 to 63
- Alignment No. 14825
- gi No. 5031275
- % Identity 83.8
- Alignment Length 37
- Location of Alignment in SEQ ID NO 2336: from 28 to 63

Maximum Length Sequence corresponding to clone ID 313421

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2337
- Ceres seq_id 1503108

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2338
- Ceres seq_id 1503109
- Location of start within SEQ ID NO 2337: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14826
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 2338: from 38 to 145 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14827
- gi No. 1161254
- % Identity 83.6
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2338: from 36 to 145
- Alignment No. 14828
- gi No. 1168529
- % Identity 80.9
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2338: from 36 to 145
- Alignment No. 14829
- gi No. 1168530
- % Identity 77.3
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2338: from 36 to 145
- Alignment No. 14830
- gi No. 1362002
- % Identity 77.6
- Alignment Length 116
- Location of Alignment in SEQ ID NO 2338: from 31 to 145
- Alignment No. 14831
- gi No. 1362026
- % Identity 80
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2338: from 36 to 145
- Alignment No. 14832
- gi No. 1362050
- % Identity 83
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2338: from 34 to 145
- Alignment No. 14833
- gi No. 1362051
- % Identity 84.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2338: from 36 to 145
- Alignment No. 14834
- gi No. 1669573
- % Identity 93.8
- Alignment Length 112

- Location of Alignment in SEQ ID NO 2338: from 34 to 145
- Alignment No. 14835
- gi No. 1944000
- % Identity 93.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2338: from 34 to 145
- Alignment No. 14836
- gi No. 2055374
- % Identity 76.4
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2338: from 36 to 145
- Alignment No. 14837
- gi No. 2129803
- % Identity 81.8
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2338: from 36 to 145
- Alignment No. 14838
- gi No. 2146746
- % Identity 77.6
- Alignment Length 116
- Location of Alignment in SEQ ID NO 2338: from 31 to 145
- Alignment No. 14839
- gi No. 3046731
- % Identity 81.8
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2338: from 36 to 145
- Alignment No. 14840
- gi No. 310580
- % Identity 82.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2338: from 34 to 145
- Alignment No. 14841
- gi No. 3169176
- % Identity 75.2
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2338: from 36 to 148
- Alignment No. 14842
- gi No. 3297819
- % Identity 78.4
- Alignment Length 116
- Location of Alignment in SEQ ID NO 2338: from 31 to 145
- Alignment No. 14843
- gi No. 3811293
- % Identity 84.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2338: from 34 to 145
- Alignment No. 14844
- gi No. 4098174
- % Identity 85.7
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2338: from 34 to 145

- Alignment No. 14845
- gi No. 416564
- % Identity 80.2
- Alignment Length 101
- Location of Alignment in SEQ ID NO 2338: from 45 to 145

- Alignment No. 14846
- gi No. 4490752
- % Identity 76.4
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2338: from 36 to 145

- Alignment No. 14847
- gi No. 481002
- % Identity 74.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2338: from 36 to 145

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2339
- Ceres seq_id 1503110
- Location of start within SEQ ID NO 2337: at 102 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14848
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 2339: from 5 to 112 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14849
- gi No. 1161254
- % Identity 83.6
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2339: from 3 to 112

- Alignment No. 14850
- gi No. 1168529
- % Identity 80.9
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2339: from 3 to 112

- Alignment No. 14851
- gi No. 1168530
- % Identity 77.3
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2339: from 3 to 112

- Alignment No. 14852
- gi No. 1362002
- % Identity 77.6
- Alignment Length 116
- Location of Alignment in SEQ ID NO 2339: from 1 to 112

- Alignment No. 14853
- gi No. 1362026
- % Identity 80
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2339: from 3 to 112

- Alignment No. 14854
- gi No. 1362050
- % Identity 83
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2339: from 1 to 112

- Alignment No. 14855
- gi No. 1362051
- % Identity 84.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2339: from 3 to 112

- Alignment No. 14856
- gi No. 1669573
- % Identity 93.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2339: from 1 to 112

- Alignment No. 14857
- gi No. 1944000
- % Identity 93.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2339: from 1 to 112

- Alignment No. 14858
- gi No. 2055374
- % Identity 76.4
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2339: from 3 to 112

- Alignment No. 14859
- gi No. 2129803
- % Identity 81.8
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2339: from 3 to 112

- Alignment No. 14860
- gi No. 2146746
- % Identity 77.6
- Alignment Length 116
- Location of Alignment in SEQ ID NO 2339: from 1 to 112

- Alignment No. 14861
- gi No. 3046731
- % Identity 81.8
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2339: from 3 to 112

- Alignment No. 14862
- gi No. 310580
- % Identity 82.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2339: from 1 to 112

- Alignment No. 14863
- gi No. 3169176
- % Identity 75.2
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2339: from 3 to 115

- Alignment No. 14864

- gi No. 3297819
- % Identity 78.4
- Alignment Length 116
- Location of Alignment in SEQ ID NO 2339: from 1 to 112

- Alignment No. 14865
- gi No. 3811293
- % Identity 84.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2339: from 1 to 112

- Alignment No. 14866
- gi No. 4098174
- % Identity 85.7
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2339: from 1 to 112

- Alignment No. 14867
- gi No. 416564
- % Identity 80.2
- Alignment Length 101
- Location of Alignment in SEQ ID NO 2339: from 12 to 112

- Alignment No. 14868
- gi No. 4490752
- % Identity 76.4
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2339: from 3 to 112

- Alignment No. 14869
- gi No. 481002
- % Identity 74.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2339: from 3 to 112

Maximum Length Sequence corresponding to clone ID 313476

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2340
- Ceres seq_id 1503132

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2341
- Ceres seq_id 1503133
- Location of start within SEQ ID NO 2340: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2342
- Ceres seq_id 1503134
- Location of start within SEQ ID NO 2340: at 80 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14870
- gi No. 547305
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2342: from 32 to 51

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2343
- Ceres seq_id 1503135
- Location of start within SEQ ID NO 2340: at 122 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14871
- gi No. 547305
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2343: from 18 to 37

Maximum Length Sequence corresponding to clone ID 313477

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2344
- Ceres seq_id 1503136

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2345
- Ceres seq_id 1503137
- Location of start within SEQ ID NO 2344: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14872
- gi No. 103026
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2345: from 4 to 14

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2346
- Ceres seq_id 1503138
- Location of start within SEQ ID NO 2344: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14873
- gi No. 1869859
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2346: from 64 to 75

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2347
- Ceres seq_id 1503139
- Location of start within SEQ ID NO 2344: at 42 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14874
- gi No. 1869859
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2347: from 51 to 62

Maximum Length Sequence corresponding to clone ID 313513

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2348
- Ceres seq_id 1503144

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2349
- Ceres seq_id 1503145
- Location of start within SEQ ID NO 2348: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14875
- gi No. 3426262
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2349: from 28 to 108

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2350
- Ceres seq_id 1503146
- Location of start within SEQ ID NO 2348: at 20 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14876
- gi No. 3426262
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2350: from 22 to 102

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2351
- Ceres seq_id 1503147
- Location of start within SEQ ID NO 2348: at 137 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14877
- gi No. 3426262
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2351: from 1 to 63

Maximum Length Sequence corresponding to clone ID 313560

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2352
- Ceres seq_id 1503148

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2353
- Ceres seq_id 1503149
- Location of start within SEQ ID NO 2352: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14878
- gi No. 1351999
- % Identity 81

- Alignment Length 21
- Location of Alignment in SEQ ID NO 2353: from 1 to 21

- Alignment No. 14879
- gi No. 2129613
- % Identity 78.3
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2353: from 1 to 23

- Alignment No. 14880
- gi No. 3096930
- % Identity 89.5
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2353: from 1 to 19

- Alignment No. 14881
- gi No. 4510417
- % Identity 77.3
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2353: from 1 to 22

- Alignment No. 14882
- gi No. 4544389
- % Identity 94.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2353: from 1 to 19

- Alignment No. 14883
- gi No. 5678605
- % Identity 76
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2353: from 1 to 25

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2354
- Ceres seq_id 1503150
- Location of start within SEQ ID NO 2352: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 313561

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2355
- Ceres seq_id 1503151

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2356
- Ceres seq_id 1503152
- Location of start within SEQ ID NO 2355: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2357
- Ceres seq_id 1503153
- Location of start within SEQ ID NO 2355: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2358
- Ceres seq_id 1503154
- Location of start within SEQ ID NO 2355: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 14884
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2358: from 5 to 95 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 313590

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2359
- Ceres seq_id 1503160

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2360
- Ceres seq_id 1503161
- Location of start within SEQ ID NO 2359: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14885
- gi No. 5689238
- % Identity 75
- Alignment Length 44
- Location of Alignment in SEQ ID NO 2360: from 108 to 150

Maximum Length Sequence corresponding to clone ID 313616

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2361
- Ceres seq_id 1503170

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2362
- Ceres seq_id 1503171
- Location of start within SEQ ID NO 2361: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 14886
- Integrase
- Location within SEQ ID NO 2362: from 58 to 125 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2363
- Ceres seq_id 1503172
- Location of start within SEQ ID NO 2361: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 14887
- Integrase

- Location within SEQ ID NO 2363: from 58 to 125 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 313650

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2364
- Ceres seq_id 1503191

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2365
- Ceres seq_id 1503192
- Location of start within SEQ ID NO 2364: at 37 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14888
- gi No. 102707
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2365: from 115 to 126
- Alignment No. 14889
- gi No. 3153821
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2365: from 13 to 26
- Alignment No. 14890
- gi No. 5032119
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2365: from 13 to 26

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2366
- Ceres seq_id 1503193
- Location of start within SEQ ID NO 2364: at 134 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 313677

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2367
- Ceres seq_id 1503200

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2368
- Ceres seq_id 1503201
- Location of start within SEQ ID NO 2367: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14891
- DEAD/DEAH box helicase
- Location within SEQ ID NO 2368: from 73 to 151 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2369
- Ceres seq_id 1503202
- Location of start within SEQ ID NO 2367: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14892
- DEAD/DEAH box helicase
- Location within SEQ ID NO 2369: from 73 to 151 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2370
- Ceres seq_id 1503203
- Location of start within SEQ ID NO 2367: at 106 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14893
- DEAD/DEAH box helicase
- Location within SEQ ID NO 2370: from 38 to 116 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 313754

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2371
- Ceres seq_id 1503237

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2372
- Ceres seq_id 1503238
- Location of start within SEQ ID NO 2371: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14894
- gi No. 1710490
- % Identity 78.9
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2372: from 22 to 40
- Alignment No. 14895
- gi No. 2245098
- % Identity 94.1
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2372: from 24 to 40
- Alignment No. 14896
- gi No. 2982249
- % Identity 78.9
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2372: from 22 to 40
- Alignment No. 14897
- gi No. 2982318
- % Identity 78.9
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2372: from 22 to 40

- Alignment No. 14898
- gi No. 3122673
- % Identity 94.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2372: from 22 to 40

- Alignment No. 14899
- gi No. 3608479
- % Identity 89.5
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2372: from 22 to 40

- Alignment No. 14900
- gi No. 4506593
- % Identity 84.2
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2372: from 22 to 40

- Alignment No. 14901
- gi No. 730532
- % Identity 84.2
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2372: from 22 to 40

- Alignment No. 14902
- gi No. 730533
- % Identity 84.2
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2372: from 22 to 40

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2373
- Ceres seq_id 1503239
- Location of start within SEQ ID NO 2371: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2374
- Ceres seq_id 1503240
- Location of start within SEQ ID NO 2371: at 64 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14903
- gi No. 1710490
- % Identity 78.9
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2374: from 1 to 19

- Alignment No. 14904
- gi No. 2245098
- % Identity 94.1
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2374: from 3 to 19

- Alignment No. 14905
- gi No. 2982249

- % Identity 78.9
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2374: from 1 to 19

- Alignment No. 14906
- gi No. 2982318
- % Identity 78.9
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2374: from 1 to 19

- Alignment No. 14907
- gi No. 3122673
- % Identity 94.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2374: from 1 to 19

- Alignment No. 14908
- gi No. 3608479
- % Identity 89.5
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2374: from 1 to 19

- Alignment No. 14909
- gi No. 4506593
- % Identity 84.2
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2374: from 1 to 19

- Alignment No. 14910
- gi No. 730532
- % Identity 84.2
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2374: from 1 to 19

- Alignment No. 14911
- gi No. 730533
- % Identity 84.2
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2374: from 1 to 19

Maximum Length Sequence corresponding to clone ID 313846

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2375
- Ceres seq_id 1503268

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2376
- Ceres seq_id 1503269
- Location of start within SEQ ID NO 2375: at 197 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14912
- gi No. 2062167
- % Identity 74.4
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2376: from 24 to 62

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2377
- Ceres seq_id 1503270

- Location of start within SEQ ID NO 2375: at 266 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14913
- gi No. 2062167
- % Identity 74.4
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2377: from 1 to 39

Maximum Length Sequence corresponding to clone ID 313854

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2378
- Ceres seq_id 1503275

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2379
- Ceres seq_id 1503276
- Location of start within SEQ ID NO 2378: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14914
- gi No. 1174492
- % Identity 76.2
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2379: from 42 to 83

- Alignment No. 14915
- gi No. 2494300
- % Identity 76.2
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2379: from 42 to 83

- Alignment No. 14916
- gi No. 2832707
- % Identity 81
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2379: from 42 to 83

- Alignment No. 14917
- gi No. 3142294
- % Identity 78.3
- Alignment Length 46
- Location of Alignment in SEQ ID NO 2379: from 39 to 83

- Alignment No. 14918
- gi No. 3790165
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2379: from 44 to 83

- Alignment No. 14919
- gi No. 3790184
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2379: from 44 to 83

- Alignment No. 14920
- gi No. 4185138

- % Identity 81
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2379: from 42 to 83
- Alignment No. 14921
- gi No. 4503507
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2379: from 44 to 83

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2380
- Ceres seq_id 1503277
- Location of start within SEQ ID NO 2378: at 115 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14922
- gi No. 1174492
- % Identity 76.2
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2380: from 4 to 45
- Alignment No. 14923
- gi No. 2494300
- % Identity 76.2
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2380: from 4 to 45
- Alignment No. 14924
- gi No. 2832707
- % Identity 81
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2380: from 4 to 45
- Alignment No. 14925
- gi No. 3142294
- % Identity 78.3
- Alignment Length 46
- Location of Alignment in SEQ ID NO 2380: from 1 to 45
- Alignment No. 14926
- gi No. 3790165
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2380: from 6 to 45
- Alignment No. 14927
- gi No. 3790184
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2380: from 6 to 45
- Alignment No. 14928
- gi No. 4185138
- % Identity 81
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2380: from 4 to 45
- Alignment No. 14929

- gi No. 4503507
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2380: from 6 to 45

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2381
- Ceres seq_id 1503278
- Location of start within SEQ ID NO 2378: at 233 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14930
- Elongation factor Tu family
- Location within SEQ ID NO 2381: from 4 to 76 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14931
- gi No. 1174492
- % Identity 82.1
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2381: from 4 to 42
- Alignment No. 14932
- gi No. 2494300
- % Identity 76.6
- Alignment Length 64
- Location of Alignment in SEQ ID NO 2381: from 4 to 67
- Alignment No. 14933
- gi No. 2494301
- % Identity 77.3
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2381: from 4 to 69
- Alignment No. 14934
- gi No. 2832707
- % Identity 89.2
- Alignment Length 74
- Location of Alignment in SEQ ID NO 2381: from 4 to 76
- Alignment No. 14935
- gi No. 3142294
- % Identity 90.5
- Alignment Length 74
- Location of Alignment in SEQ ID NO 2381: from 4 to 76
- Alignment No. 14936
- gi No. 3790165
- % Identity 70.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2381: from 4 to 76
- Alignment No. 14937
- gi No. 3790184
- % Identity 75
- Alignment Length 68
- Location of Alignment in SEQ ID NO 2381: from 4 to 71
- Alignment No. 14938
- gi No. 417179

- % Identity 73.5
- Alignment Length 68
- Location of Alignment in SEQ ID NO 2381: from 4 to 71

- Alignment No. 14939
- gi No. 4185138
- % Identity 73
- Alignment Length 74
- Location of Alignment in SEQ ID NO 2381: from 4 to 76

- Alignment No. 14940
- gi No. 4503507
- % Identity 75
- Alignment Length 68
- Location of Alignment in SEQ ID NO 2381: from 4 to 71

Maximum Length Sequence corresponding to clone ID 313864

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2382
- Ceres seq_id 1503279

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2383
- Ceres seq_id 1503280
- Location of start within SEQ ID NO 2382: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14941
- gi No. 4512664
- % Identity 93.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2383: from 1 to 15

- Alignment No. 14942
- gi No. 4874278
- % Identity 93.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2383: from 1 to 15

- Alignment No. 14943
- gi No. 4902470
- % Identity 93.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2383: from 1 to 15

- Alignment No. 14944
- gi No. 4902877
- % Identity 93.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2383: from 1 to 15

- Alignment No. 14945
- gi No. 4902879
- % Identity 93.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2383: from 1 to 15

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2384
- Ceres seq_id 1503281

- Location of start within SEQ ID NO 2382: at 98 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2385
- Ceres seq_id 1503282
- Location of start within SEQ ID NO 2382: at 133 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14946
- gi No. 4512664
- % Identity 70.6
- Alignment Length 85
- Location of Alignment in SEQ ID NO 2385: from 1 to 49

Maximum Length Sequence corresponding to clone ID 313894

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2386
- Ceres seq_id 1503297

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2387
- Ceres seq_id 1503298
- Location of start within SEQ ID NO 2386: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14947
- C2 domain
- Location within SEQ ID NO 2387: from 27 to 84 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 313912

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2388
- Ceres seq_id 1503299

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2389
- Ceres seq_id 1503300
- Location of start within SEQ ID NO 2388: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14948
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 2389: from 1 to 54 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14949
- gi No. 2191149
- % Identity 74
- Alignment Length 50
- Location of Alignment in SEQ ID NO 2389: from 1 to 50
- Alignment No. 14950
- gi No. 2505874

- % Identity 74
- Alignment Length 50
- Location of Alignment in SEQ ID NO 2389: from 1 to 50

- Alignment No. 14951
- gi No. 3482919
- % Identity 70.4
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2389: from 1 to 54

- Alignment No. 14952
- gi No. 4204849
- % Identity 70
- Alignment Length 50
- Location of Alignment in SEQ ID NO 2389: from 1 to 50

- Alignment No. 14953
- gi No. 4263791
- % Identity 74.7
- Alignment Length 79
- Location of Alignment in SEQ ID NO 2389: from 1 to 79

- Alignment No. 14954
- gi No. 4512659
- % Identity 70.4
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2389: from 1 to 54

- Alignment No. 14955
- gi No. 4836880
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2389: from 1 to 56

- Alignment No. 14956
- gi No. 5042449
- % Identity 75
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2389: from 1 to 56

Maximum Length Sequence corresponding to clone ID 313922

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2390
- Ceres seq_id 1503305

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2391
- Ceres seq_id 1503306
- Location of start within SEQ ID NO 2390: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2392
- Ceres seq_id 1503307
- Location of start within SEQ ID NO 2390: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14957

- Major intrinsic protein
- Location within SEQ ID NO 2392: from 35 to 135 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14958
- gi No. 1076687
- % Identity 80.2
- Alignment Length 106
- Location of Alignment in SEQ ID NO 2392: from 30 to 135

- Alignment No. 14959
- gi No. 1212915
- % Identity 71.7
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2392: from 25 to 137

- Alignment No. 14960
- gi No. 1212921
- % Identity 75.2
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2392: from 25 to 137

- Alignment No. 14961
- gi No. 1212923
- % Identity 72.6
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2392: from 25 to 137

- Alignment No. 14962
- gi No. 126959
- % Identity 77.5
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2392: from 25 to 135

- Alignment No. 14963
- gi No. 1518057
- % Identity 78.4
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2392: from 25 to 135

- Alignment No. 14964
- gi No. 1743369
- % Identity 74.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2392: from 25 to 135

- Alignment No. 14965
- gi No. 1794147
- % Identity 76.6
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2392: from 25 to 135

- Alignment No. 14966
- gi No. 2058706
- % Identity 80.2
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2392: from 25 to 135

- Alignment No. 14967
- gi No. 2245093
- % Identity 74.3

- Alignment Length 113
- Location of Alignment in SEQ ID NO 2392: from 25 to 137
- Alignment No. 14968
- gi No. 257238
- % Identity 73
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2392: from 25 to 135
- Alignment No. 14969
- gi No. 267135
- % Identity 77.5
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2392: from 25 to 135
- Alignment No. 14970
- gi No. 3264596
- % Identity 80.2
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2392: from 25 to 135
- Alignment No. 14971
- gi No. 3298458
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2392: from 103 to 137
- Alignment No. 14972
- gi No. 461929
- % Identity 80.2
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2392: from 25 to 135
- Alignment No. 14973
- gi No. 4884870
- % Identity 75.4
- Alignment Length 69
- Location of Alignment in SEQ ID NO 2392: from 69 to 137

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2393
- Ceres seq_id 1503308
- Location of start within SEQ ID NO 2390: at 75 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14974
- Major intrinsic protein
- Location within SEQ ID NO 2393: from 11 to 111 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14975
- gi No. 1076687
- % Identity 80.2
- Alignment Length 106
- Location of Alignment in SEQ ID NO 2393: from 6 to 111
- Alignment No. 14976
- gi No. 1212915
- % Identity 71.7
- Alignment Length 113

- Location of Alignment in SEQ ID NO 2393: from 1 to 113
- Alignment No. 14977
- gi No. 1212921
- % Identity 75.2
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2393: from 1 to 113
- Alignment No. 14978
- gi No. 1212923
- % Identity 72.6
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2393: from 1 to 113
- Alignment No. 14979
- gi No. 126959
- % Identity 77.5
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2393: from 1 to 111
- Alignment No. 14980
- gi No. 1518057
- % Identity 78.4
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2393: from 1 to 111
- Alignment No. 14981
- gi No. 1743369
- % Identity 74.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2393: from 1 to 111
- Alignment No. 14982
- gi No. 1794147
- % Identity 76.6
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2393: from 1 to 111
- Alignment No. 14983
- gi No. 2058706
- % Identity 80.2
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2393: from 1 to 111
- Alignment No. 14984
- gi No. 2245093
- % Identity 74.3
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2393: from 1 to 113
- Alignment No. 14985
- gi No. 257238
- % Identity 73
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2393: from 1 to 111
- Alignment No. 14986
- gi No. 267135
- % Identity 77.5
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2393: from 1 to 111

- Alignment No. 14987
- gi No. 3264596
- % Identity 80.2
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2393: from 1 to 111

- Alignment No. 14988
- gi No. 3298458
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2393: from 79 to 113

- Alignment No. 14989
- gi No. 461929
- % Identity 80.2
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2393: from 1 to 111

- Alignment No. 14990
- gi No. 4884870
- % Identity 75.4
- Alignment Length 69
- Location of Alignment in SEQ ID NO 2393: from 45 to 113

Maximum Length Sequence corresponding to clone ID 314003

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2394
- Ceres seq_id 1503322

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2395
- Ceres seq_id 1503323
- Location of start within SEQ ID NO 2394: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2396
- Ceres seq_id 1503324
- Location of start within SEQ ID NO 2394: at 156 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 14991
- short chain dehydrogenase
- Location within SEQ ID NO 2396: from 7 to 102 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2397
- Ceres seq_id 1503325
- Location of start within SEQ ID NO 2394: at 174 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 14992
- short chain dehydrogenase
- Location within SEQ ID NO 2397: from 1 to 96 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 314019

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2398
- Ceres seq_id 1503330

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2399
- Ceres seq_id 1503331
- Location of start within SEQ ID NO 2398: at 42 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14993
- gi No. 4680192
- % Identity 87.4
- Alignment Length 143
- Location of Alignment in SEQ ID NO 2399: from 6 to 148

Maximum Length Sequence corresponding to clone ID 314030

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2400
- Ceres seq_id 1503332

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2401
- Ceres seq_id 1503333
- Location of start within SEQ ID NO 2400: at 132 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14994
- gi No. 2997589
- % Identity 98.2
- Alignment Length 109
- Location of Alignment in SEQ ID NO 2401: from 1 to 105
- Alignment No. 14995
- gi No. 2997591
- % Identity 84.3
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2401: from 1 to 105
- Alignment No. 14996
- gi No. 2997593
- % Identity 77.8
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2401: from 1 to 105
- Alignment No. 14997
- gi No. 3367515
- % Identity 86.1
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2401: from 1 to 105

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2402
- Ceres seq_id 1503334
- Location of start within SEQ ID NO 2400: at 156 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14998
- gi No. 2997589
- % Identity 98.2
- Alignment Length 109
- Location of Alignment in SEQ ID NO 2402: from 1 to 97

- Alignment No. 14999
- gi No. 2997591
- % Identity 84.3
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2402: from 1 to 97

- Alignment No. 15000
- gi No. 2997593
- % Identity 77.8
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2402: from 1 to 97

- Alignment No. 15001
- gi No. 3367515
- % Identity 86.1
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2402: from 1 to 97

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2403
- Ceres seq_id 1503335
- Location of start within SEQ ID NO 2400: at 183 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15002
- gi No. 2997589
- % Identity 98.2
- Alignment Length 109
- Location of Alignment in SEQ ID NO 2403: from 1 to 88

- Alignment No. 15003
- gi No. 2997591
- % Identity 84.3
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2403: from 1 to 88

- Alignment No. 15004
- gi No. 2997593
- % Identity 77.8
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2403: from 1 to 88

- Alignment No. 15005
- gi No. 3367515
- % Identity 86.1
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2403: from 1 to 88

Maximum Length Sequence corresponding to clone ID 314034

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 2404
- Ceres seq_id 1503336
(B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 2405
- Ceres seq_id 1503337
- Location of start within SEQ ID NO 2404: at 133 nt.
(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
(D) Related Amino Acid Sequences
- Alignment No. 15006
- gi No. 4006906
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2405: from 2 to 13

Maximum Length Sequence corresponding to clone ID 314077

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 2406
- Ceres seq_id 1503342
(B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 2407
- Ceres seq_id 1503343
- Location of start within SEQ ID NO 2406: at 2 nt.
(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
(D) Related Amino Acid Sequences
- Alignment No. 15007
- gi No. 3786009
- % Identity 87.3
- Alignment Length 157
- Location of Alignment in SEQ ID NO 2407: from 1 to 157
(B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 2408
- Ceres seq_id 1503344
- Location of start within SEQ ID NO 2406: at 179 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
(D) Related Amino Acid Sequences
- Alignment No. 15008
- gi No. 3786009
- % Identity 87.3
- Alignment Length 157
- Location of Alignment in SEQ ID NO 2408: from 1 to 98

Maximum Length Sequence corresponding to clone ID 314080

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 2409
- Ceres seq_id 1503345
(B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 2410
- Ceres seq_id 1503346
- Location of start within SEQ ID NO 2409: at 2 nt.
(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2411
- Ceres seq_id 1503347
- Location of start within SEQ ID NO 2409: at 39 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15009
- gi No. 2150000
- % Identity 71.7
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2411: from 1 to 53

Maximum Length Sequence corresponding to clone ID 314106

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2412
- Ceres seq_id 1503351

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2413
- Ceres seq_id 1503352
- Location of start within SEQ ID NO 2412: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15010
- gi No. 1185397
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15011
- gi No. 1644455
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15012
- gi No. 1644455
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15013
- gi No. 1644457
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15014
- gi No. 1644457
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15015
- gi No. 1644457
- % Identity 72.7
- Alignment Length 11

- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15016
 - gi No. 1644457
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15017
 - gi No. 1644459
 - % Identity 81.8
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15018
 - gi No. 1644459
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15019
 - gi No. 1644459
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15020
 - gi No. 1644459
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15021
 - gi No. 1644461
 - % Identity 81.8
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15022
 - gi No. 1644461
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15023
 - gi No. 1644461
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15024
 - gi No. 1644461
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15025
 - gi No. 178014
 - % Identity 75
 - Alignment Length 13
 - Location of Alignment in SEQ ID NO 2413: from 13 to 24

- Alignment No. 15026
- gi No. 1914853
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15027
- gi No. 19923
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15028
- gi No. 2244878
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15029
- gi No. 2462823
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15030
- gi No. 322755
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 15 to 25
- Alignment No. 15031
- gi No. 322755
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 15 to 25
- Alignment No. 15032
- gi No. 322755
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2413: from 14 to 27
- Alignment No. 15033
- gi No. 322757
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15034
- gi No. 3551531
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15035
- gi No. 5306259
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24

- (B) Polypeptide Sequence.
 - Pat. Appln. SEQ ID NO 2414
 - Ceres seq_id 1503353
 - Location of start within SEQ ID NO 2412: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 314122

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2415
- Ceres seq_id 1503354

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2416
- Ceres seq_id 1503355
- Location of start within SEQ ID NO 2415: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2417
- Ceres seq_id 1503356
- Location of start within SEQ ID NO 2415: at 9 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2418
- Ceres seq_id 1503357
- Location of start within SEQ ID NO 2415: at 103 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15036
- DnaJ domain
- Location within SEQ ID NO 2418: from 24 to 75 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 314197

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2419
- Ceres seq_id 1503378

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2420
- Ceres seq_id 1503379
- Location of start within SEQ ID NO 2419: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15037
- Protein phosphatase 2C
- Location within SEQ ID NO 2420: from 3 to 84 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 314305

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2421
- Ceres seq_id 1503400

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2422
- Ceres seq_id 1503401
- Location of start within SEQ ID NO 2421: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15038
- gi No. 445612
- % Identity 72.1
- Alignment Length 43
- Location of Alignment in SEQ ID NO 2422: from 39 to 81

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2423
- Ceres seq_id 1503402
- Location of start within SEQ ID NO 2421: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2424
- Ceres seq_id 1503403
- Location of start within SEQ ID NO 2421: at 101 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15039
- gi No. 445612
- % Identity 72.1
- Alignment Length 43
- Location of Alignment in SEQ ID NO 2424: from 6 to 48

Maximum Length Sequence corresponding to clone ID 314409

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2425
- Ceres seq_id 1503422

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2426
- Ceres seq_id 1503423
- Location of start within SEQ ID NO 2425: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15040
- gi No. 1743388
- % Identity 94.2
- Alignment Length 86
- Location of Alignment in SEQ ID NO 2426: from 77 to 161

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2427

- Ceres seq_id 1503424
- Location of start within SEQ ID NO 2425: at 133 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 15041
 - gi No. 1743388
 - % Identity 94.2
 - Alignment Length 86
 - Location of Alignment in SEQ ID NO 2427: from 33 to 117

Maximum Length Sequence corresponding to clone ID 314420

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2428
- Ceres seq_id 1503429

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2429
- Ceres seq_id 1503430
- Location of start within SEQ ID NO 2428: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 15042
 - gi No. 2914700
 - % Identity 86.7
 - Alignment Length 30
 - Location of Alignment in SEQ ID NO 2429: from 2 to 31

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2430
- Ceres seq_id 1503431
- Location of start within SEQ ID NO 2428: at 183 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2431
- Ceres seq_id 1503432
- Location of start within SEQ ID NO 2428: at 269 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 314461

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2432
- Ceres seq_id 1503443

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2433
- Ceres seq_id 1503444
- Location of start within SEQ ID NO 2432: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 2434
 - Ceres seq_id 1503445
 - Location of start within SEQ ID NO 2432: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 15043
 - gi No. 119111
 - % Identity 78.6
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 2434: from 38 to 51
 - Alignment No. 15044
 - gi No. 4008584
 - % Identity 75
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 2434: from 41 to 51
 - Alignment No. 15045
 - gi No. 4008584
 - % Identity 73.3
 - Alignment Length 15
 - Location of Alignment in SEQ ID NO 2434: from 37 to 51
 - Alignment No. 15046
 - gi No. 628112
 - % Identity 78.6
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 2434: from 38 to 51
 - Alignment No. 15047
 - gi No. 628185
 - % Identity 78.6
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 2434: from 38 to 51
 - Alignment No. 15048
 - gi No. 688080
 - % Identity 75
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 2434: from 42 to 52

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 2435
 - Ceres seq_id 1503446
 - Location of start within SEQ ID NO 2432: at 101 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 15049
 - gi No. 119111
 - % Identity 78.6
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 2435: from 5 to 18
 - Alignment No. 15050
 - gi No. 4008584
 - % Identity 75

- Alignment Length 12
- Location of Alignment in SEQ ID NO 2435: from 8 to 18

- Alignment No. 15051
- gi No. 4008584
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2435: from 4 to 18

- Alignment No. 15052
- gi No. 628112
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2435: from 5 to 18

- Alignment No. 15053
- gi No. 628185
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2435: from 5 to 18

- Alignment No. 15054
- gi No. 688080
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2435: from 9 to 19

Maximum Length Sequence corresponding to clone ID 314605

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2436
- Ceres seq_id 1503476

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2437
- Ceres seq_id 1503477
- Location of start within SEQ ID NO 2436: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2438
- Ceres seq_id 1503478
- Location of start within SEQ ID NO 2436: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15055
- Chitin recognition protein
- Location within SEQ ID NO 2438: from 44 to 77 aa.

- Alignment No. 15056
- Chitinases class I
- Location within SEQ ID NO 2438: from 90 to 146 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15057
- gi No. 299189
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2438: from 49 to 69

- Alignment No. 15058
- gi No. 299190
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2438: from 49 to 69

- Alignment No. 15059
- gi No. 994881
- % Identity 75.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 2438: from 112 to 144

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2439
- Ceres seq_id 1503479
- Location of start within SEQ ID NO 2436: at 60 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15060
- Chitin recognition protein
- Location within SEQ ID NO 2439: from 25 to 58 aa.

- Alignment No. 15061
- Chitinases class I
- Location within SEQ ID NO 2439: from 71 to 127 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15062
- gi No. 299189
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2439: from 30 to 50

- Alignment No. 15063
- gi No. 299190
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2439: from 30 to 50

- Alignment No. 15064
- gi No. 994881
- % Identity 75.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 2439: from 93 to 125

Maximum Length Sequence corresponding to clone ID 314613

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2440
- Ceres seq_id 1503480

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2441
- Ceres seq_id 1503481
- Location of start within SEQ ID NO 2440: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15065
- chorismate binding enzyme
- Location within SEQ ID NO 2441: from 4 to 147 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15066
- gi No. 320552
- % Identity 82.6
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2441: from 4 to 147
- Alignment No. 15067
- gi No. 320553
- % Identity 79.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2441: from 2 to 147
- Alignment No. 15068
- gi No. 3348124
- % Identity 76.8
- Alignment Length 155
- Location of Alignment in SEQ ID NO 2441: from 2 to 155
- Alignment No. 15069
- gi No. 418133
- % Identity 82.6
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2441: from 4 to 147
- Alignment No. 15070
- gi No. 418134
- % Identity 79.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2441: from 2 to 147
- Alignment No. 15071
- gi No. 5360657
- % Identity 78.5
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2441: from 4 to 147
- Alignment No. 15072
- gi No. 5360659
- % Identity 95.2
- Alignment Length 147
- Location of Alignment in SEQ ID NO 2441: from 1 to 147
- Alignment No. 15073
- gi No. 960289
- % Identity 83.3
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2441: from 4 to 147
- Alignment No. 15074
- gi No. 960291
- % Identity 80.3
- Alignment Length 147
- Location of Alignment in SEQ ID NO 2441: from 1 to 147

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2442
- Ceres seq_id 1503482
- Location of start within SEQ ID NO 2440: at 4 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15075
- chorismate binding enzyme
- Location within SEQ ID NO 2442: from 3 to 146 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15076
- gi No. 320552
- % Identity 82.6
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2442: from 3 to 146
- Alignment No. 15077
- gi No. 320553
- % Identity 79.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2442: from 1 to 146
- Alignment No. 15078
- gi No. 3348124
- % Identity 76.8
- Alignment Length 155
- Location of Alignment in SEQ ID NO 2442: from 1 to 154
- Alignment No. 15079
- gi No. 418133
- % Identity 82.6
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2442: from 3 to 146
- Alignment No. 15080
- gi No. 418134
- % Identity 79.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2442: from 1 to 146
- Alignment No. 15081
- gi No. 5360657
- % Identity 78.5
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2442: from 3 to 146
- Alignment No. 15082
- gi No. 5360659
- % Identity 95.2
- Alignment Length 147
- Location of Alignment in SEQ ID NO 2442: from 1 to 146
- Alignment No. 15083
- gi No. 960289
- % Identity 83.3
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2442: from 3 to 146
- Alignment No. 15084
- gi No. 960291
- % Identity 80.3
- Alignment Length 147
- Location of Alignment in SEQ ID NO 2442: from 1 to 146

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2443
- Ceres seq_id 1503483
- Location of start within SEQ ID NO 2440: at 55 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15085
- chorismate binding enzyme
- Location within SEQ ID NO 2443: from 1 to 129 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15086
- gi No. 320552
- % Identity 82.6
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2443: from 1 to 129
- Alignment No. 15087
- gi No. 320553
- % Identity 79.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2443: from 1 to 129
- Alignment No. 15088
- gi No. 3348124
- % Identity 76.8
- Alignment Length 155
- Location of Alignment in SEQ ID NO 2443: from 1 to 137
- Alignment No. 15089
- gi No. 418133
- % Identity 82.6
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2443: from 1 to 129
- Alignment No. 15090
- gi No. 418134
- % Identity 79.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2443: from 1 to 129
- Alignment No. 15091
- gi No. 5360657
- % Identity 78.5
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2443: from 1 to 129
- Alignment No. 15092
- gi No. 5360659
- % Identity 95.2
- Alignment Length 147
- Location of Alignment in SEQ ID NO 2443: from 1 to 129
- Alignment No. 15093
- gi No. 960289
- % Identity 83.3
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2443: from 1 to 129
- Alignment No. 15094

- gi No. 960291
- % Identity 80.3
- Alignment Length 147
- Location of Alignment in SEQ ID NO 2443: from 1 to 129

Maximum Length Sequence corresponding to clone ID 314618

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2444
- Ceres seq_id 1503484

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2445
- Ceres seq_id 1503485
- Location of start within SEQ ID NO 2444: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15095
- Thioredoxin
- Location within SEQ ID NO 2445: from 22 to 128 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15096
- gi No. 3915131
- % Identity 70.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2445: from 16 to 138

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2446
- Ceres seq_id 1503486
- Location of start within SEQ ID NO 2444: at 46 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15097
- Thioredoxin
- Location within SEQ ID NO 2446: from 7 to 113 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15098
- gi No. 3915131
- % Identity 70.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2446: from 1 to 123

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2447
- Ceres seq_id 1503487
- Location of start within SEQ ID NO 2444: at 109 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15099
- Thioredoxin
- Location within SEQ ID NO 2447: from 1 to 92 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15100
- gi No. 3915131
- % Identity 70.7
- Alignment Length 123

- Location of Alignment in SEQ ID NO 2447: from 1 to 102

Maximum Length Sequence corresponding to clone ID 314637

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2448
- Ceres seq_id 1503492

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2449
- Ceres seq_id 1503493
- Location of start within SEQ ID NO 2448: at 201 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15101
- Chalcone and stilbene synthases
- Location within SEQ ID NO 2449: from 12 to 62 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15102
- gi No. 322636
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2449: from 41 to 62

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2450
- Ceres seq_id 1503494
- Location of start within SEQ ID NO 2448: at 228 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15103
- Chalcone and stilbene synthases
- Location within SEQ ID NO 2450: from 3 to 53 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15104
- gi No. 322636
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2450: from 32 to 53

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2451
- Ceres seq_id 1503495
- Location of start within SEQ ID NO 2448: at 261 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15105
- gi No. 322636
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2451: from 21 to 42

Maximum Length Sequence corresponding to clone ID 314643

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2452
- Ceres seq_id 1503496

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2453
- Ceres seq_id 1503497
- Location of start within SEQ ID NO 2452: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15106
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2453: from 9 to 136 aa.
- Alignment No. 15107
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2453: from 28 to 151 aa.
- Alignment No. 15108
- Assemblin (Peptidase family S21)
- Location within SEQ ID NO 2453: from 23 to 125 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2454
- Ceres seq_id 1503498
- Location of start within SEQ ID NO 2452: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15109
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2454: from 9 to 136 aa.
- Alignment No. 15110
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2454: from 28 to 151 aa.
- Alignment No. 15111
- Assemblin (Peptidase family S21)
- Location within SEQ ID NO 2454: from 23 to 125 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2455
- Ceres seq_id 1503499
- Location of start within SEQ ID NO 2452: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 314669

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2456
- Ceres seq_id 1503507

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2457
- Ceres seq_id 1503508
- Location of start within SEQ ID NO 2456: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 15112
 - gi No. 2894378
 - % Identity 82.5
 - Alignment Length 114
 - Location of Alignment in SEQ ID NO 2457: from 1 to 114

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2458
 - Ceres seq_id 1503509
 - Location of start within SEQ ID NO 2456: at 231 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 15113
 - gi No. 2894378
 - % Identity 82.5
 - Alignment Length 114
 - Location of Alignment in SEQ ID NO 2458: from 1 to 38

Maximum Length Sequence corresponding to clone ID 314683

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2459
 - Ceres seq_id 1503510
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2460
 - Ceres seq_id 1503511
 - Location of start within SEQ ID NO 2459: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 15114
 - gi No. 4091080
 - % Identity 70.7
 - Alignment Length 59
 - Location of Alignment in SEQ ID NO 2460: from 1 to 57

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2461
 - Ceres seq_id 1503512
 - Location of start within SEQ ID NO 2459: at 39 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 15115
 - gi No. 4091080
 - % Identity 70.7
 - Alignment Length 59
 - Location of Alignment in SEQ ID NO 2461: from 1 to 45

Maximum Length Sequence corresponding to clone ID 314729

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2462
 - Ceres seq_id 1503522
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2463
 - Ceres seq_id 1503523
 - Location of start within SEQ ID NO 2462: at 87 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15116
- gi No. 1173045
- % Identity 87
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2463: from 1 to 23

- Alignment No. 15117
- gi No. 1346945
- % Identity 78.3
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2463: from 1 to 23

- Alignment No. 15118
- gi No. 2281793
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2463: from 12 to 28

- Alignment No. 15119
- gi No. 2565332
- % Identity 73.1
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2463: from 3 to 28

- Alignment No. 15120
- gi No. 2996185
- % Identity 91.3
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2463: from 1 to 23

- Alignment No. 15121
- gi No. 3098458
- % Identity 75
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2463: from 1 to 28

- Alignment No. 15122
- gi No. 3845189
- % Identity 73.9
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2463: from 1 to 23

- Alignment No. 15123
- gi No. 400996
- % Identity 91.3
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2463: from 1 to 23

- Alignment No. 15124
- gi No. 4090257
- % Identity 100
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2463: from 1 to 23

- Alignment No. 15125
- gi No. 4455775
- % Identity 71.4

- Alignment Length 28
- Location of Alignment in SEQ ID NO 2463: from 1 to 28
- Alignment No. 15126
- gi No. 4506643
- % Identity 91.3
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2463: from 1 to 23
- Alignment No. 15127
- gi No. 4741896
- % Identity 100
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2463: from 1 to 23
- Alignment No. 15128
- gi No. 5007072
- % Identity 100
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2463: from 9 to 23

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2464
- Ceres seq_id 1503524
- Location of start within SEQ ID NO 2462: at 127 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2465
- Ceres seq_id 1503525
- Location of start within SEQ ID NO 2462: at 139 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 314734

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2466
- Ceres seq_id 1503526

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2467
- Ceres seq_id 1503527
- Location of start within SEQ ID NO 2466: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2468
- Ceres seq_id 1503528
- Location of start within SEQ ID NO 2466: at 162 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15129
- Ribosomal protein L13

- Location within SEQ ID NO 2468: from 29 to 85 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2469
- Ceres seq_id 1503529
- Location of start within SEQ ID NO 2466: at 352 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 314824

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2470
- Ceres seq_id 1503550

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2471
- Ceres seq_id 1503551
- Location of start within SEQ ID NO 2470: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15130
- gi No. 3935157
- % Identity 71.5
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2471: from 28 to 150

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2472
- Ceres seq_id 1503552
- Location of start within SEQ ID NO 2470: at 42 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2473
- Ceres seq_id 1503553
- Location of start within SEQ ID NO 2470: at 73 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15131
- gi No. 3935157
- % Identity 71.5
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2473: from 4 to 126

Maximum Length Sequence corresponding to clone ID 314826

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2474
- Ceres seq_id 1503554

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2475
- Ceres seq_id 1503555

- Location of start within SEQ ID NO 2474: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15132
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 2475: from 2 to 94 aa.
- Alignment No. 15133
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 2475: from 9 to 133 aa.
- Alignment No. 15134
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 2475: from 11 to 138 aa.
- Alignment No. 15135
 - Assemblin (Peptidase family S21)
 - Location within SEQ ID NO 2475: from 3 to 114 aa.
- Alignment No. 15136
 - Assemblin (Peptidase family S21)
 - Location within SEQ ID NO 2475: from 4 to 138 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15137
 - gi No. 2281102
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2475: from 128 to 138

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2476
- Ceres seq_id 1503556
- Location of start within SEQ ID NO 2474: at 60 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15138
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 2476: from 1 to 75 aa.
- Alignment No. 15139
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 2476: from 1 to 114 aa.
- Alignment No. 15140
 - 7 transmembrane receptor (rhodopsin family)
 - Location within SEQ ID NO 2476: from 1 to 119 aa.
- Alignment No. 15141
 - Assemblin (Peptidase family S21)
 - Location within SEQ ID NO 2476: from 1 to 95 aa.
- Alignment No. 15142
 - Assemblin (Peptidase family S21)
 - Location within SEQ ID NO 2476: from 1 to 119 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15143
 - gi No. 2281102

- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2476: from 109 to 119

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2477
- Ceres seq_id 1503557
- Location of start within SEQ ID NO 2474: at 118 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15144
- gi No. 109944
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2477: from 74 to 87

- Alignment No. 15145
- gi No. 1350911
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2477: from 74 to 87

- Alignment No. 15146
- gi No. 1350912
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2477: from 74 to 87

- Alignment No. 15147
- gi No. 200880
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2477: from 74 to 87

- Alignment No. 15148
- gi No. 2564955
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2477: from 76 to 86

- Alignment No. 15149
- gi No. 337720
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2477: from 74 to 87

- Alignment No. 15150
- gi No. 483195
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2477: from 74 to 87

- Alignment No. 15151
- gi No. 542994
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2477: from 74 to 87

Maximum Length Sequence corresponding to clone ID 314875

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2478
- Ceres seq_id 1503569

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2479
- Ceres seq_id 1503570
- Location of start within SEQ ID NO 2478: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15152
- gi No. 4455361
- % Identity 72.2
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2479: from 34 to 87

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2480
- Ceres seq_id 1503571
- Location of start within SEQ ID NO 2478: at 100 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15153
- gi No. 4455361
- % Identity 72.2
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2480: from 1 to 54

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2481
- Ceres seq_id 1503572
- Location of start within SEQ ID NO 2478: at 142 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15154
- gi No. 4455361
- % Identity 72.2
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2481: from 1 to 40

Maximum Length Sequence corresponding to clone ID 314917

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2482
- Ceres seq_id 1503585

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2483
- Ceres seq_id 1503586
- Location of start within SEQ ID NO 2482: at 87 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15155
- WD domain, G-beta repeat
- Location within SEQ ID NO 2483: from 20 to 58 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15156
- gi No. 1143814
- % Identity 74.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2483: from 1 to 108

- Alignment No. 15157
- gi No. 1346106
- % Identity 74.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2483: from 1 to 108

- Alignment No. 15158
- gi No. 1346107
- % Identity 99.1
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2483: from 1 to 108

- Alignment No. 15159
- gi No. 2935698
- % Identity 91.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2483: from 1 to 108

- Alignment No. 15160
- gi No. 3023832
- % Identity 73.9
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2483: from 1 to 108

- Alignment No. 15161
- gi No. 3023839
- % Identity 74.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2483: from 1 to 108

- Alignment No. 15162
- gi No. 3023841
- % Identity 73
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2483: from 1 to 108

- Alignment No. 15163
- gi No. 3023842
- % Identity 75.7
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2483: from 1 to 108

- Alignment No. 15164
- gi No. 3023843
- % Identity 92.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2483: from 1 to 108

- Alignment No. 15165
- gi No. 3023859
- % Identity 74.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2483: from 1 to 108

- Alignment No. 15166

- gi No. 4929352
- % Identity 76.6
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2483: from 1 to 108

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2484
- Ceres seq_id 1503587
- Location of start within SEQ ID NO 2482: at 261 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15167
- gi No. 1143814
- % Identity 74.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2484: from 1 to 50

- Alignment No. 15168
- gi No. 1346106
- % Identity 74.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2484: from 1 to 50

- Alignment No. 15169
- gi No. 1346107
- % Identity 99.1
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2484: from 1 to 50

- Alignment No. 15170
- gi No. 2935698
- % Identity 91.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2484: from 1 to 50

- Alignment No. 15171
- gi No. 3023832
- % Identity 73.9
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2484: from 1 to 50

- Alignment No. 15172
- gi No. 3023839
- % Identity 74.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2484: from 1 to 50

- Alignment No. 15173
- gi No. 3023841
- % Identity 73
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2484: from 1 to 50

- Alignment No. 15174
- gi No. 3023842
- % Identity 75.7
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2484: from 1 to 50

- Alignment No. 15175
- gi No. 3023843
- % Identity 92.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2484: from 1 to 50
- Alignment No. 15176
- gi No. 3023859
- % Identity 74.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2484: from 1 to 50
- Alignment No. 15177
- gi No. 4929352
- % Identity 76.6
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2484: from 1 to 50

Maximum Length Sequence corresponding to clone ID 314924

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2485
- Ceres seq_id 1503588

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2486
- Ceres seq_id 1503589
- Location of start within SEQ ID NO 2485: at 184 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15178
- Ubiquitin-conjugating enzyme
- Location within SEQ ID NO 2486: from 1 to 100 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15179
- gi No. 1142614
- % Identity 85.2
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15180
- gi No. 1174848
- % Identity 76.1
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2486: from 1 to 98
- Alignment No. 15181
- gi No. 1174849
- % Identity 79.6
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15182
- gi No. 136643
- % Identity 77.4
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15183
- gi No. 136645
- % Identity 75.7

- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15184
- gi No. 136646
- % Identity 76.5
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15185
- gi No. 2130087
- % Identity 81.4
- Alignment Length 118
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15186
- gi No. 2130088
- % Identity 80.5
- Alignment Length 118
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15187
- gi No. 2136339
- % Identity 78.3
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15188
- gi No. 2501431
- % Identity 75.2
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15189
- gi No. 2612962
- % Identity 75.3
- Alignment Length 89
- Location of Alignment in SEQ ID NO 2486: from 1 to 74
- Alignment No. 15190
- gi No. 2668744
- % Identity 90.3
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15191
- gi No. 3043432
- % Identity 95.2
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2486: from 59 to 100
- Alignment No. 15192
- gi No. 3323498
- % Identity 77.4
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15193
- gi No. 3915190
- % Identity 93.3
- Alignment Length 105

- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15194
 - gi No. 4097684
 - % Identity 82
 - Alignment Length 89
- Location of Alignment in SEQ ID NO 2486: from 12 to 100
- Alignment No. 15195
 - gi No. 4100646
 - % Identity 81.7
 - Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15196
 - gi No. 441457
 - % Identity 88.5
 - Alignment Length 113
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15197
 - gi No. 4433363
 - % Identity 94.2
 - Alignment Length 69
- Location of Alignment in SEQ ID NO 2486: from 32 to 100
- Alignment No. 15198
 - gi No. 4507773
 - % Identity 74.8
 - Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15199
 - gi No. 4507775
 - % Identity 78.3
 - Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15200
 - gi No. 4507777
 - % Identity 78.3
 - Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15201
 - gi No. 456568
 - % Identity 88.5
 - Alignment Length 113
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15202
 - gi No. 4581117
 - % Identity 85.2
 - Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15203
 - gi No. 4583656
 - % Identity 73.9
 - Alignment Length 111
- Location of Alignment in SEQ ID NO 2486: from 1 to 98

- Alignment No. 15204
- gi No. 464979
- % Identity 76.5
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100

- Alignment No. 15205
- gi No. 464981
- % Identity 89.4
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2486: from 1 to 100

- Alignment No. 15206
- gi No. 464985
- % Identity 87.6
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2486: from 1 to 100

- Alignment No. 15207
- gi No. 464986
- % Identity 89.4
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2486: from 1 to 100

- Alignment No. 15208
- gi No. 464987
- % Identity 89.4
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2486: from 1 to 100

- Alignment No. 15209
- gi No. 464988
- % Identity 91.9
- Alignment Length 99
- Location of Alignment in SEQ ID NO 2486: from 2 to 100

- Alignment No. 15210
- gi No. 477134
- % Identity 76.5
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100

- Alignment No. 15211
- gi No. 4868140
- % Identity 78.3
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100

- Alignment No. 15212
- gi No. 4868141
- % Identity 79.8
- Alignment Length 89
- Location of Alignment in SEQ ID NO 2486: from 12 to 100

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2487
- Ceres seq_id 1503590
- Location of start within SEQ ID NO 2485: at 208 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15213
- Ubiquitin-conjugating enzyme
- Location within SEQ ID NO 2487: from 1 to 92 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15214
- gi No. 1142614
- % Identity 85.2
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15215
- gi No. 1174848
- % Identity 76.1
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2487: from 1 to 90
- Alignment No. 15216
- gi No. 1174849
- % Identity 79.6
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15217
- gi No. 136643
- % Identity 77.4
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15218
- gi No. 136645
- % Identity 75.7
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15219
- gi No. 136646
- % Identity 76.5
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15220
- gi No. 2130087
- % Identity 81.4
- Alignment Length 118
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15221
- gi No. 2130088
- % Identity 80.5
- Alignment Length 118
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15222
- gi No. 2136339
- % Identity 78.3
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92

- Alignment No. 15223
- gi No. 2501431
- % Identity 75.2
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2487: from 1 to 92

- Alignment No. 15224
- gi No. 2612962
- % Identity 75.3
- Alignment Length 89
- Location of Alignment in SEQ ID NO 2487: from 1 to 66

- Alignment No. 15225
- gi No. 2668744
- % Identity 90.3
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2487: from 1 to 92

- Alignment No. 15226
- gi No. 3043432
- % Identity 95.2
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2487: from 51 to 92

- Alignment No. 15227
- gi No. 3323498
- % Identity 77.4
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92

- Alignment No. 15228
- gi No. 3915190
- % Identity 93.3
- Alignment Length 105
- Location of Alignment in SEQ ID NO 2487: from 1 to 92

- Alignment No. 15229
- gi No. 4097684
- % Identity 82
- Alignment Length 89
- Location of Alignment in SEQ ID NO 2487: from 4 to 92

- Alignment No. 15230
- gi No. 4100646
- % Identity 81.7
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92

- Alignment No. 15231
- gi No. 441457
- % Identity 88.5
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2487: from 1 to 92

- Alignment No. 15232
- gi No. 4433363
- % Identity 94.2
- Alignment Length 69
- Location of Alignment in SEQ ID NO 2487: from 24 to 92

- Alignment No. 15233

- gi No. 4507773
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92

- Alignment No. 15234
- gi No. 4507775
- % Identity 78.3
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92

- Alignment No. 15235
- gi No. 4507777
- % Identity 78.3
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92

- Alignment No. 15236
- gi No. 456568
- % Identity 88.5
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2487: from 1 to 92

- Alignment No. 15237
- gi No. 4581117
- % Identity 85.2
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92

- Alignment No. 15238
- gi No. 4583656
- % Identity 73.9
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2487: from 1 to 90

- Alignment No. 15239
- gi No. 464979
- % Identity 76.5
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92

- Alignment No. 15240
- gi No. 464981
- % Identity 89.4
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2487: from 1 to 92

- Alignment No. 15241
- gi No. 464985
- % Identity 87.6
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2487: from 1 to 92

- Alignment No. 15242
- gi No. 464986
- % Identity 89.4
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2487: from 1 to 92

- Alignment No. 15243
- gi No. 464987

- % Identity 89.4
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2487: from 1 to 92

- Alignment No. 15244
- gi No. 464988
- % Identity 91.9
- Alignment Length 99
- Location of Alignment in SEQ ID NO 2487: from 1 to 92

- Alignment No. 15245
- gi No. 477134
- % Identity 76.5
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92

- Alignment No. 15246
- gi No. 4868140
- % Identity 78.3
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92

- Alignment No. 15247
- gi No. 4868141
- % Identity 79.8
- Alignment Length 89
- Location of Alignment in SEQ ID NO 2487: from 4 to 92

Maximum Length Sequence corresponding to clone ID 314967

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2488
- Ceres seq_id 1503591

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2489
- Ceres seq_id 1503592
- Location of start within SEQ ID NO 2488: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 15248
- Glycosyl hydrolases family 16
- Location within SEQ ID NO 2489: from 1 to 115 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15249
- gi No. 2129770
- % Identity 70.9
- Alignment Length 127
- Location of Alignment in SEQ ID NO 2489: from 1 to 126

- Alignment No. 15250
- gi No. 2154609
- % Identity 70.9
- Alignment Length 127
- Location of Alignment in SEQ ID NO 2489: from 1 to 126

- Alignment No. 15251
- gi No. 5533313
- % Identity 70.9
- Alignment Length 127
- Location of Alignment in SEQ ID NO 2489: from 1 to 126

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 2490
 - Ceres seq_id 1503593
 - Location of start within SEQ ID NO 2488: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15252
- Mucin-like glycoprotein
- Location within SEQ ID NO 2490: from 1 to 126 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 314971

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2491
- Ceres seq_id 1503594

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2492
- Ceres seq_id 1503595
- Location of start within SEQ ID NO 2491: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15253
- Ubiquitin-conjugating enzyme
- Location within SEQ ID NO 2492: from 1 to 59 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15254
- gi No. 4006890
- % Identity 84.7
- Alignment Length 59
- Location of Alignment in SEQ ID NO 2492: from 1 to 59
- Alignment No. 15255
- gi No. 4217999
- % Identity 84.7
- Alignment Length 59
- Location of Alignment in SEQ ID NO 2492: from 1 to 59

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2493
- Ceres seq_id 1503596
- Location of start within SEQ ID NO 2491: at 224 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2494
- Ceres seq_id 1503597
- Location of start within SEQ ID NO 2491: at 246 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 314996

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2495
- Ceres seq_id 1503600

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2496
- Ceres seq_id 1503601
- Location of start within SEQ ID NO 2495: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15256
- gi No. 1173018
- % Identity 100
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2496: from 35 to 49
- Alignment No. 15257
- gi No. 132849
- % Identity 100
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2496: from 35 to 49
- Alignment No. 15258
- gi No. 266944
- % Identity 100
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2496: from 35 to 49
- Alignment No. 15259
- gi No. 2961372
- % Identity 100
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2496: from 35 to 49
- Alignment No. 15260
- gi No. 3088346
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2496: from 35 to 49
- Alignment No. 15261
- gi No. 4406816
- % Identity 100
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2496: from 35 to 49

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2497
- Ceres seq_id 1503602
- Location of start within SEQ ID NO 2495: at 79 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15262
- Ribosomal Proteins L2
- Location within SEQ ID NO 2497: from 25 to 110 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15263
- gi No. 132849

- % Identity 75.9
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2497: from 1 to 110

- Alignment No. 15264
- gi No. 266944
- % Identity 77.7
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2497: from 1 to 110

- Alignment No. 15265
- gi No. 2961372
- % Identity 74.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2497: from 1 to 110

- Alignment No. 15266
- gi No. 4406816
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2497: from 1 to 110

Maximum Length Sequence corresponding to clone ID 315057

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2498
- Ceres seq_id 1503615

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2499
- Ceres seq_id 1503616
- Location of start within SEQ ID NO 2498: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15267
- gi No. 481728
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2499: from 76 to 86

- Alignment No. 15268
- gi No. 481728
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2499: from 76 to 86

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2500
- Ceres seq_id 1503617
- Location of start within SEQ ID NO 2498: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15269
- gi No. 3941736
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2500: from 93 to 104

- Alignment No. 15270

- gi No. 4337109
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2500: from 93 to 104

- Alignment No. 15271
- gi No. 4758110
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2500: from 93 to 104

- Alignment No. 15272
- gi No. 5668598
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2500: from 93 to 104

- Alignment No. 15273
- gi No. 5668598
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2500: from 95 to 106

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2501
- Ceres seq_id 1503618
- Location of start within SEQ ID NO 2498: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 315079

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2502
- Ceres seq_id 1503621

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2503
- Ceres seq_id 1503622
- Location of start within SEQ ID NO 2502: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15274
- Putative GTP-ase activating protein for Arf
- Location within SEQ ID NO 2503: from 74 to 132 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15275
- gi No. 3236238
- % Identity 83.1
- Alignment Length 59
- Location of Alignment in SEQ ID NO 2503: from 74 to 132

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2504
- Ceres seq_id 1503623
- Location of start within SEQ ID NO 2502: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2505
- Ceres seq_id 1503624
- Location of start within SEQ ID NO 2502: at 140 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 315215

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2506
- Ceres seq_id 1503662

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2507
- Ceres seq_id 1503663
- Location of start within SEQ ID NO 2506: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15276
- gi No. 3123264
- % Identity 75.5
- Alignment Length 49
- Location of Alignment in SEQ ID NO 2507: from 81 to 128

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2508
- Ceres seq_id 1503664
- Location of start within SEQ ID NO 2506: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15277
- gi No. 3123264
- % Identity 70.5
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2508: from 26 to 86

- Alignment No. 15278
- gi No. 498906
- % Identity 70.5
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2508: from 26 to 86

- Alignment No. 15279
- gi No. 730547
- % Identity 75.4
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2508: from 26 to 86

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2509
- Ceres seq_id 1503665
- Location of start within SEQ ID NO 2506: at 78 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15280
- gi No. 3123264
- % Identity 70.5
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2509: from 1 to 61

- Alignment No. 15281
- gi No. 498906
- % Identity 70.5
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2509: from 1 to 61

- Alignment No. 15282
- gi No. 730547
- % Identity 75.4
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2509: from 1 to 61

Maximum Length Sequence corresponding to clone ID 315227

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2510
- Ceres seq_id 1503670

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2511
- Ceres seq_id 1503671
- Location of start within SEQ ID NO 2510: at 104 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15283
- gi No. 1170395
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2511: from 29 to 43

- Alignment No. 15284
- gi No. 1170396
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2511: from 29 to 43

- Alignment No. 15285
- gi No. 1170396
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2511: from 29 to 45

- Alignment No. 15286
- gi No. 1170397
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2511: from 29 to 43

- Alignment No. 15287
- gi No. 1170397
- % Identity 70.6
- Alignment Length 17

- Location of Alignment in SEQ ID NO 2511: from 29 to 45
- Alignment No. 15288
- gi No. 1170398
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2511: from 29 to 43
- Alignment No. 15289
- gi No. 1170398
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2511: from 29 to 45

Maximum Length Sequence corresponding to clone ID 315373

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2512
- Ceres seq_id 1503697

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2513
- Ceres seq_id 1503698
- Location of start within SEQ ID NO 2512: at 73 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15290
- Copper amine oxidase
- Location within SEQ ID NO 2513: from 1 to 123 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15291
- gi No. 4559342
- % Identity 93.1
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2513: from 1 to 122
- Alignment No. 15292
- gi No. 4567319
- % Identity 93.1
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2513: from 1 to 122
- Alignment No. 15293
- gi No. 5230728
- % Identity 90.8
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2513: from 1 to 122

Maximum Length Sequence corresponding to clone ID 315404

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2514
- Ceres seq_id 1503703

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2515
- Ceres seq_id 1503704
- Location of start within SEQ ID NO 2514: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2516
- Ceres seq_id 1503705
- Location of start within SEQ ID NO 2514: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15294
 - gi No. 4512664
 - % Identity 77.8
 - Alignment Length 45
 - Location of Alignment in SEQ ID NO 2516: from 35 to 79
- Alignment No. 15295
 - gi No. 4874278
 - % Identity 74
 - Alignment Length 77
 - Location of Alignment in SEQ ID NO 2516: from 75 to 151
- Alignment No. 15296
 - gi No. 4902470
 - % Identity 74
 - Alignment Length 77
 - Location of Alignment in SEQ ID NO 2516: from 75 to 151
- Alignment No. 15297
 - gi No. 4902877
 - % Identity 72.7
 - Alignment Length 77
 - Location of Alignment in SEQ ID NO 2516: from 75 to 151
- Alignment No. 15298
 - gi No. 4902879
 - % Identity 72.7
 - Alignment Length 44
 - Location of Alignment in SEQ ID NO 2516: from 36 to 79

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2517
- Ceres seq_id 1503706
- Location of start within SEQ ID NO 2514: at 72 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15299
 - gi No. 4512664
 - % Identity 77.8
 - Alignment Length 45
 - Location of Alignment in SEQ ID NO 2517: from 12 to 56
- Alignment No. 15300
 - gi No. 4874278
 - % Identity 74
 - Alignment Length 77
 - Location of Alignment in SEQ ID NO 2517: from 52 to 128
- Alignment No. 15301
 - gi No. 4902470
 - % Identity 74

- Alignment Length 77
- Location of Alignment in SEQ ID NO 2517: from 52 to 128
- Alignment No. 15302
- gi No. 4902877
- % Identity 72.7
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2517: from 52 to 128
- Alignment No. 15303
- gi No. 4902879
- % Identity 72.7
- Alignment Length 44
- Location of Alignment in SEQ ID NO 2517: from 13 to 56

Maximum Length Sequence corresponding to clone ID 315430

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2518
- Ceres seq_id 1503714

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2519
- Ceres seq_id 1503715
- Location of start within SEQ ID NO 2518: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15304
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2519: from 36 to 129 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15305
- gi No. 141279
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2519: from 46 to 62
- Alignment No. 15306
- gi No. 1914851
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2519: from 46 to 61
- Alignment No. 15307
- gi No. 2224619
- % Identity 70
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2519: from 49 to 68
- Alignment No. 15308
- gi No. 539033
- % Identity 72
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2519: from 46 to 70
- Alignment No. 15309
- gi No. 688080
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2519: from 48 to 60

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2520
 - Ceres seq_id 1503716
 - Location of start within SEQ ID NO 2518: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2521
 - Ceres seq_id 1503717
 - Location of start within SEQ ID NO 2518: at 65 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 315437

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2522
 - Ceres seq_id 1503718

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2523
 - Ceres seq_id 1503719
 - Location of start within SEQ ID NO 2522: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15310
- Cystatin domain
- Location within SEQ ID NO 2523: from 77 to 132 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 315445

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2524
 - Ceres seq_id 1503720

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2525
 - Ceres seq_id 1503721
 - Location of start within SEQ ID NO 2524: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2526
 - Ceres seq_id 1503722
 - Location of start within SEQ ID NO 2524: at 49 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2527
 - Ceres seq_id 1503723
 - Location of start within SEQ ID NO 2524: at 200 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15311
- Armadillo/beta-catenin-like repeats
- Location within SEQ ID NO 2527: from 21 to 62 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15312
- gi No. 2950210
- % Identity 73
- Alignment Length 74
- Location of Alignment in SEQ ID NO 2527: from 21 to 93
- Alignment No. 15313
- gi No. 3091280
- % Identity 70.2
- Alignment Length 57
- Location of Alignment in SEQ ID NO 2527: from 22 to 77
- Alignment No. 15314
- gi No. 3122278
- % Identity 71.9
- Alignment Length 57
- Location of Alignment in SEQ ID NO 2527: from 22 to 77
- Alignment No. 15315
- gi No. 3273243
- % Identity 71.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 2527: from 21 to 93

Maximum Length Sequence corresponding to clone ID 315466

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2528
- Ceres seq_id 1503728

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2529
- Ceres seq_id 1503729
- Location of start within SEQ ID NO 2528: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15316
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 2529: from 4 to 108 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 315475

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2530
- Ceres seq_id 1503734

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2531
- Ceres seq_id 1503735
- Location of start within SEQ ID NO 2530: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15317

- Multicopper oxidase
- Location within SEQ ID NO 2531: from 22 to 84 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15318
- gi No. 4454012
- % Identity 71.6
- Alignment Length 88
- Location of Alignment in SEQ ID NO 2531: from 23 to 110
- Alignment No. 15319
- gi No. 4725941
- % Identity 71.9
- Alignment Length 89
- Location of Alignment in SEQ ID NO 2531: from 22 to 110

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2532
- Ceres seq_id 1503736
- Location of start within SEQ ID NO 2530: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2533
- Ceres seq_id 1503737
- Location of start within SEQ ID NO 2530: at 49 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15320
- Multicopper oxidase
- Location within SEQ ID NO 2533: from 6 to 68 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15321
- gi No. 4454012
- % Identity 71.6
- Alignment Length 88
- Location of Alignment in SEQ ID NO 2533: from 7 to 94
- Alignment No. 15322
- gi No. 4725941
- % Identity 71.9
- Alignment Length 89
- Location of Alignment in SEQ ID NO 2533: from 6 to 94

Maximum Length Sequence corresponding to clone ID 315510

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2534
- Ceres seq_id 1503743

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2535
- Ceres seq_id 1503744
- Location of start within SEQ ID NO 2534: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2536
- Ceres seq_id 1503745
- Location of start within SEQ ID NO 2534: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15323
- gi No. 1076556
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2536: from 20 to 31
- Alignment No. 15324
- gi No. 1655699
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2536: from 18 to 29
- Alignment No. 15325
- gi No. 1655699
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2536: from 17 to 32
- Alignment No. 15326
- gi No. 1655699
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2536: from 17 to 32
- Alignment No. 15327
- gi No. 1655699
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2536: from 17 to 32
- Alignment No. 15328
- gi No. 1655699
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2536: from 17 to 32
- Alignment No. 15329
- gi No. 1655699
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2536: from 17 to 32
- Alignment No. 15330
- gi No. 1655699
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2536: from 17 to 32
- Alignment No. 15331
- gi No. 1655699
- % Identity 70.6
- Alignment Length 17

- Location of Alignment in SEQ ID NO 2536: from 17 to 32
- Alignment No. 15332
- gi No. 322747
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2536: from 17 to 30
- Alignment No. 15333
- gi No. 322749
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2536: from 17 to 30

Maximum Length Sequence corresponding to clone ID 315548

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2537
- Ceres seq_id 1503746

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2538
- Ceres seq_id 1503747
- Location of start within SEQ ID NO 2537: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2539
- Ceres seq_id 1503748
- Location of start within SEQ ID NO 2537: at 68 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15334
- gi No. 112110
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 2539: from 2 to 28

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2540
- Ceres seq_id 1503749
- Location of start within SEQ ID NO 2537: at 301 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 315587

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2541
- Ceres seq_id 1503769

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2542
- Ceres seq_id 1503770
- Location of start within SEQ ID NO 2541: at 104 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15335
- Nucleoside diphosphate kinases
- Location within SEQ ID NO 2542: from 2 to 114 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15336
- gi No. 1076713
- % Identity 87
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2542: from 1 to 22

- Alignment No. 15337
- gi No. 1304478
- % Identity 73
- Alignment Length 37
- Location of Alignment in SEQ ID NO 2542: from 2 to 38

- Alignment No. 15338
- gi No. 1729427
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 2542: from 1 to 38

- Alignment No. 15339
- gi No. 2129487
- % Identity 80.2
- Alignment Length 116
- Location of Alignment in SEQ ID NO 2542: from 1 to 114

- Alignment No. 15340
- gi No. 2829275
- % Identity 88.8
- Alignment Length 116
- Location of Alignment in SEQ ID NO 2542: from 1 to 114

- Alignment No. 15341
- gi No. 4972094
- % Identity 90.5
- Alignment Length 116
- Location of Alignment in SEQ ID NO 2542: from 1 to 114

Maximum Length Sequence corresponding to clone ID 315593

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2543
- Ceres seq_id 1503775

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2544
- Ceres seq_id 1503776
- Location of start within SEQ ID NO 2543: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15342
- Elongation factor G C-terminus
- Location within SEQ ID NO 2544: from 21 to 152 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15343
- gi No. 4895248
- % Identity 83.3
- Alignment Length 156

- Location of Alignment in SEQ ID NO 2544: from 1 to 156

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2545
- Ceres seq_id 1503777
- Location of start within SEQ ID NO 2543: at 110 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15344
- Elongation factor G C-terminus
- Location within SEQ ID NO 2545: from 1 to 116 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15345
- gi No. 4895248
- % Identity 83.3
- Alignment Length 156
- Location of Alignment in SEQ ID NO 2545: from 1 to 120

Maximum Length Sequence corresponding to clone ID 315595

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2546
- Ceres seq_id 1503778

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2547
- Ceres seq_id 1503779
- Location of start within SEQ ID NO 2546: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15346
- gi No. 3786005
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2547: from 1 to 26

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2548
- Ceres seq_id 1503780
- Location of start within SEQ ID NO 2546: at 269 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2549
- Ceres seq_id 1503781
- Location of start within SEQ ID NO 2546: at 324 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 315627

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2550
- Ceres seq_id 1503796

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2551
- Ceres seq_id 1503797
- Location of start within SEQ ID NO 2550: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2552
- Ceres seq_id 1503798
- Location of start within SEQ ID NO 2550: at 153 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15347
- gi No. 2352921
- % Identity 87.1
- Alignment Length 62
- Location of Alignment in SEQ ID NO 2552: from 1 to 38

- Alignment No. 15348
- gi No. 2352923
- % Identity 82.3
- Alignment Length 62
- Location of Alignment in SEQ ID NO 2552: from 1 to 38

- Alignment No. 15349
- gi No. 3021508
- % Identity 73.1
- Alignment Length 67
- Location of Alignment in SEQ ID NO 2552: from 1 to 41

- Alignment No. 15350
- gi No. 3021510
- % Identity 76.1
- Alignment Length 67
- Location of Alignment in SEQ ID NO 2552: from 1 to 41

- Alignment No. 15351
- gi No. 3023815
- % Identity 77.4
- Alignment Length 62
- Location of Alignment in SEQ ID NO 2552: from 1 to 38

- Alignment No. 15352
- gi No. 4206114
- % Identity 77.6
- Alignment Length 67
- Location of Alignment in SEQ ID NO 2552: from 1 to 41

- Alignment No. 15353
- gi No. 5360754
- % Identity 87.5
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2552: from 1 to 41

- Alignment No. 15354
- gi No. 585165
- % Identity 76.1

- Alignment Length 67
- Location of Alignment in SEQ ID NO 2552: from 1 to 41

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2553
- Ceres seq_id 1503799
- Location of start within SEQ ID NO 2550: at 262 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15355
- Glucose-6-phosphate dehydrogenase
- Location within SEQ ID NO 2553: from 1 to 42 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15356
- gi No. 1169799
- % Identity 70.7
- Alignment Length 41
- Location of Alignment in SEQ ID NO 2553: from 3 to 43
- Alignment No. 15357
- gi No. 3021508
- % Identity 81
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2553: from 3 to 43
- Alignment No. 15358
- gi No. 585165
- % Identity 75
- Alignment Length 48
- Location of Alignment in SEQ ID NO 2553: from 1 to 43

Maximum Length Sequence corresponding to clone ID 315647

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2554
- Ceres seq_id 1503810

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2555
- Ceres seq_id 1503811
- Location of start within SEQ ID NO 2554: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15359
- gi No. 1173201
- % Identity 75.7
- Alignment Length 37
- Location of Alignment in SEQ ID NO 2555: from 37 to 73
- Alignment No. 15360
- gi No. 131772
- % Identity 97.6
- Alignment Length 41
- Location of Alignment in SEQ ID NO 2555: from 33 to 73
- Alignment No. 15361
- gi No. 131773
- % Identity 89.7
- Alignment Length 39

- Location of Alignment in SEQ ID NO 2555: from 35 to 73
- Alignment No. 15362
- gi No. 133720
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2555: from 60 to 73
- Alignment No. 15363
- gi No. 2350992
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2555: from 59 to 73
- Alignment No. 15364
- gi No. 2414647
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2555: from 48 to 73
- Alignment No. 15365
- gi No. 3097244
- % Identity 71.4
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2555: from 33 to 73
- Alignment No. 15366
- gi No. 3122785
- % Identity 78
- Alignment Length 41
- Location of Alignment in SEQ ID NO 2555: from 33 to 73
- Alignment No. 15367
- gi No. 4574240
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2555: from 53 to 73
- Alignment No. 15368
- gi No. 4678226
- % Identity 80.5
- Alignment Length 41
- Location of Alignment in SEQ ID NO 2555: from 33 to 73
- Alignment No. 15369
- gi No. 4886269
- % Identity 82.9
- Alignment Length 41
- Location of Alignment in SEQ ID NO 2555: from 33 to 73

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2556
- Ceres seq_id 1503812
- Location of start within SEQ ID NO 2554: at 99 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15370
- gi No. 1173201
- % Identity 75.7

- Alignment Length 37
- Location of Alignment in SEQ ID NO 2556: from 5 to 41
- Alignment No. 15371
- gi No. 131772
- % Identity 97.6
- Alignment Length 41
- Location of Alignment in SEQ ID NO 2556: from 1 to 41
- Alignment No. 15372
- gi No. 131773
- % Identity 89.7
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2556: from 3 to 41
- Alignment No. 15373
- gi No. 133720
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2556: from 28 to 41
- Alignment No. 15374
- gi No. 2350992
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2556: from 27 to 41
- Alignment No. 15375
- gi No. 2414647
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2556: from 16 to 41
- Alignment No. 15376
- gi No. 3097244
- % Identity 71.4
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2556: from 1 to 41
- Alignment No. 15377
- gi No. 3122785
- % Identity 78
- Alignment Length 41
- Location of Alignment in SEQ ID NO 2556: from 1 to 41
- Alignment No. 15378
- gi No. 4574240
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2556: from 21 to 41
- Alignment No. 15379
- gi No. 4678226
- % Identity 80.5
- Alignment Length 41
- Location of Alignment in SEQ ID NO 2556: from 1 to 41
- Alignment No. 15380
- gi No. 4886269
- % Identity 82.9
- Alignment Length 41

- Location of Alignment in SEQ ID NO 2556: from 1 to 41

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2557
- Ceres seq_id 1503813
- Location of start within SEQ ID NO 2554: at 295 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15381
- Ribosomal protein S11
- Location within SEQ ID NO 2557: from 3 to 68 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15382
- gi No. 1173200
- % Identity 90.2
- Alignment Length 41
- Location of Alignment in SEQ ID NO 2557: from 28 to 68

- Alignment No. 15383
- gi No. 1173201
- % Identity 89.4
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15384
- gi No. 131772
- % Identity 97
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15385
- gi No. 131773
- % Identity 95.5
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15386
- gi No. 133771
- % Identity 86.4
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15387
- gi No. 133777
- % Identity 80.3
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15388
- gi No. 133782
- % Identity 82.4
- Alignment Length 68
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15389
- gi No. 133785
- % Identity 89.4
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15390
- gi No. 133789
- % Identity 75.8
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15391
- gi No. 1346941
- % Identity 77.3
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15392
- gi No. 1350935
- % Identity 83.3
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15393
- gi No. 1350937
- % Identity 84.8
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15394
- gi No. 2350992
- % Identity 72.1
- Alignment Length 68
- Location of Alignment in SEQ ID NO 2557: from 3 to 69

- Alignment No. 15395
- gi No. 2414647
- % Identity 77.3
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15396
- gi No. 2500442
- % Identity 74.4
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2557: from 3 to 41

- Alignment No. 15397
- gi No. 2500443
- % Identity 87
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2557: from 46 to 68

- Alignment No. 15398
- gi No. 3097244
- % Identity 89.4
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15399
- gi No. 3122785
- % Identity 95.5
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15400
- gi No. 4574240
- % Identity 84.8
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15401
- gi No. 4588920
- % Identity 86.4
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15402
- gi No. 4678226
- % Identity 93.9
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15403
- gi No. 4886269
- % Identity 93.9
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15404
- gi No. 5032051
- % Identity 89.4
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15405
- gi No. 5441523
- % Identity 91.7
- Alignment Length 36
- Location of Alignment in SEQ ID NO 2557: from 33 to 68

- Alignment No. 15406
- gi No. 547604
- % Identity 78.8
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15407
- gi No. 70946
- % Identity 77.3
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15408
- gi No. 730453
- % Identity 78.8
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15409
- gi No. 730633
- % Identity 84.8
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15410

- gi No. 83794
- % Identity 84.8
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

Maximum Length Sequence corresponding to clone ID 315681

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2558
- Ceres seq_id 1503822

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2559
- Ceres seq_id 1503823
- Location of start within SEQ ID NO 2558: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15411
- 6,7-dimethyl-8-ribityllumazine synthase
- Location within SEQ ID NO 2559: from 57 to 150 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2560
- Ceres seq_id 1503824
- Location of start within SEQ ID NO 2558: at 84 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15412
- 6,7-dimethyl-8-ribityllumazine synthase
- Location within SEQ ID NO 2560: from 30 to 123 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2561
- Ceres seq_id 1503825
- Location of start within SEQ ID NO 2558: at 150 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15413
- 6,7-dimethyl-8-ribityllumazine synthase
- Location within SEQ ID NO 2561: from 8 to 101 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 315697

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2562
- Ceres seq_id 1503826

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2563
- Ceres seq_id 1503827
- Location of start within SEQ ID NO 2562: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 15414

- gi No. 1834333
- % Identity 89.5
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2563: from 99 to 117

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2564
- Ceres seq_id 1503828
- Location of start within SEQ ID NO 2562: at 22 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15415
- gi No. 1834333
- % Identity 89.5
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2564: from 92 to 110

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2565
- Ceres seq_id 1503829
- Location of start within SEQ ID NO 2562: at 61 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15416
- gi No. 1834333
- % Identity 89.5
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2565: from 79 to 97

Maximum Length Sequence corresponding to clone ID 315810

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2566
- Ceres seq_id 1503869

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2567
- Ceres seq_id 1503870
- Location of start within SEQ ID NO 2566: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2568
- Ceres seq_id 1503871
- Location of start within SEQ ID NO 2566: at 219 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15417
- gi No. 2072023
- % Identity 82.3
- Alignment Length 79
- Location of Alignment in SEQ ID NO 2568: from 3 to 81
- Alignment No. 15418

- gi No. 2245008
- % Identity 91.2
- Alignment Length 68
- Location of Alignment in SEQ ID NO 2568: from 14 to 81

- Alignment No. 15419
- gi No. 2583137
- % Identity 88
- Alignment Length 50
- Location of Alignment in SEQ ID NO 2568: from 32 to 81

- Alignment No. 15420
- gi No. 2961343
- % Identity 87.9
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2568: from 17 to 81

- Alignment No. 15421
- gi No. 3024687
- % Identity 82.3
- Alignment Length 79
- Location of Alignment in SEQ ID NO 2568: from 3 to 81

- Alignment No. 15422
- gi No. 3367536
- % Identity 78.5
- Alignment Length 93
- Location of Alignment in SEQ ID NO 2568: from 1 to 81

- Alignment No. 15423
- gi No. 3810848
- % Identity 74.7
- Alignment Length 79
- Location of Alignment in SEQ ID NO 2568: from 3 to 81

- Alignment No. 15424
- gi No. 4581162
- % Identity 87.8
- Alignment Length 82
- Location of Alignment in SEQ ID NO 2568: from 1 to 81

- Alignment No. 15425
- gi No. 4773906
- % Identity 76.8
- Alignment Length 82
- Location of Alignment in SEQ ID NO 2568: from 1 to 81

- Alignment No. 15426
- gi No. 4895235
- % Identity 82.1
- Alignment Length 78
- Location of Alignment in SEQ ID NO 2568: from 4 to 81

- Alignment No. 15427
- gi No. 586441
- % Identity 72.2
- Alignment Length 79
- Location of Alignment in SEQ ID NO 2568: from 3 to 81

Maximum Length Sequence corresponding to clone ID 315827
(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2569
- Ceres seq_id 1503873
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2570
 - Ceres seq_id 1503874
 - Location of start within SEQ ID NO 2569: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2571
 - Ceres seq_id 1503875
 - Location of start within SEQ ID NO 2569: at 8 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2572
 - Ceres seq_id 1503876
 - Location of start within SEQ ID NO 2569: at 58 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 15428
 - gi No. 4539333
 - % Identity 71.4
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 2572: from 52 to 65

Maximum Length Sequence corresponding to clone ID 315859

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2573
 - Ceres seq_id 1503886
- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2574
 - Ceres seq_id 1503887
 - Location of start within SEQ ID NO 2573: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2575
 - Ceres seq_id 1503888
 - Location of start within SEQ ID NO 2573: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2576
 - Ceres seq_id 1503889
 - Location of start within SEQ ID NO 2573: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 15429
 - gi No. 3387886
 - % Identity 83.3
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 2576: from 1 to 12
- Alignment No. 15430
- gi No. 3402680
 - % Identity 75
 - Alignment Length 12
 - Location of Alignment in SEQ ID NO 2576: from 3 to 14

Maximum Length Sequence corresponding to clone ID 315865

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2577
- Ceres seq_id 1503890

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2578
- Ceres seq_id 1503891
- Location of start within SEQ ID NO 2577: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 15431
- Peroxidase
- Location within SEQ ID NO 2578: from 48 to 111 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15432
 - gi No. 1076635
 - % Identity 86.7
 - Alignment Length 15
 - Location of Alignment in SEQ ID NO 2578: from 68 to 82
- Alignment No. 15433
- gi No. 5002334
 - % Identity 73.7
 - Alignment Length 38
 - Location of Alignment in SEQ ID NO 2578: from 74 to 111

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2579
- Ceres seq_id 1503892
- Location of start within SEQ ID NO 2577: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2580
- Ceres seq_id 1503893
- Location of start within SEQ ID NO 2577: at 22 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 15434
- Peroxidase

- Location within SEQ ID NO 2580: from 41 to 104 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15435
- gi No. 1076635
- % Identity 86.7
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2580: from 61 to 75

- Alignment No. 15436
- gi No. 5002334
- % Identity 73.7
- Alignment Length 38
- Location of Alignment in SEQ ID NO 2580: from 67 to 104

Maximum Length Sequence corresponding to clone ID 315868

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2581
- Ceres seq_id 1503894

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2582
- Ceres seq_id 1503895
- Location of start within SEQ ID NO 2581: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15437
- gi No. 1142653
- % Identity 74.7
- Alignment Length 79
- Location of Alignment in SEQ ID NO 2582: from 79 to 157

- Alignment No. 15438
- gi No. 128844
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2582: from 53 to 76

- Alignment No. 15439
- gi No. 4539408
- % Identity 70.2
- Alignment Length 125
- Location of Alignment in SEQ ID NO 2582: from 36 to 159

- Alignment No. 15440
- gi No. 5031931
- % Identity 74.7
- Alignment Length 79
- Location of Alignment in SEQ ID NO 2582: from 79 to 157

- Alignment No. 15441
- gi No. 92559
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2582: from 53 to 76

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2583
- Ceres seq_id 1503896
- Location of start within SEQ ID NO 2581: at 68 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15442
- gi No. 1142653
- % Identity 74.7
- Alignment Length 79
- Location of Alignment in SEQ ID NO 2583: from 57 to 135

- Alignment No. 15443
- gi No. 128844
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2583: from 31 to 54

- Alignment No. 15444
- gi No. 4539408
- % Identity 70.2
- Alignment Length 125
- Location of Alignment in SEQ ID NO 2583: from 14 to 137

- Alignment No. 15445
- gi No. 5031931
- % Identity 74.7
- Alignment Length 79
- Location of Alignment in SEQ ID NO 2583: from 57 to 135

- Alignment No. 15446
- gi No. 92559
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2583: from 31 to 54

Maximum Length Sequence corresponding to clone ID 315884

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2584
- Ceres seq_id 1503899

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2585
- Ceres seq_id 1503900
- Location of start within SEQ ID NO 2584: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15447
- Topoisomerase DNA binding C4 zinc finger
- Location within SEQ ID NO 2585: from 69 to 106 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2586
- Ceres seq_id 1503901
- Location of start within SEQ ID NO 2584: at 18 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15448
- Topoisomerase DNA binding C4 zinc finger
- Location within SEQ ID NO 2586: from 64 to 101 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2587
- Ceres seq_id 1503902
- Location of start within SEQ ID NO 2584: at 147 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15449
- Topoisomerase DNA binding C4 zinc finger
- Location within SEQ ID NO 2587: from 21 to 58 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 316031

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2588
- Ceres seq_id 1503924

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2589
- Ceres seq_id 1503925
- Location of start within SEQ ID NO 2588: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15450
- gi No. 3004565
- % Identity 80
- Alignment Length 80
- Location of Alignment in SEQ ID NO 2589: from 1 to 80

Maximum Length Sequence corresponding to clone ID 316062

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2590
- Ceres seq_id 1503926

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2591
- Ceres seq_id 1503927
- Location of start within SEQ ID NO 2590: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15451
- Protein phosphatase 2C
- Location within SEQ ID NO 2591: from 24 to 163 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15452
- gi No. 3927836
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2591: from 3 to 13

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2592
- Ceres seq_id 1503928
- Location of start within SEQ ID NO 2590: at 17 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15453
- Protein phosphatase 2C
- Location within SEQ ID NO 2592: from 19 to 158 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2593
- Ceres seq_id 1503929
- Location of start within SEQ ID NO 2590: at 47 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15454
- Protein phosphatase 2C
- Location within SEQ ID NO 2593: from 9 to 148 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 316101

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2594
- Ceres seq_id 1503934

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2595
- Ceres seq_id 1503935
- Location of start within SEQ ID NO 2594: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2596
- Ceres seq_id 1503936
- Location of start within SEQ ID NO 2594: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15455
- gi No. 3822340
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2596: from 37 to 48

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2597
- Ceres seq_id 1503937
- Location of start within SEQ ID NO 2594: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 316143

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2598
- Ceres seq_id 1503942

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2599
 - Ceres seq_id 1503943
 - Location of start within SEQ ID NO 2598: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 15456
 - gi No. 5441235
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2599: from 74 to 84

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2600
 - Ceres seq_id 1503944
 - Location of start within SEQ ID NO 2598: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15457
- Sperm histone P2
- Location within SEQ ID NO 2600: from 38 to 118 aa.

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2601
 - Ceres seq_id 1503945
 - Location of start within SEQ ID NO 2598: at 124 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
 - Alignment No. 15458
 - gi No. 5441235
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2601: from 33 to 43

Maximum Length Sequence corresponding to clone ID 316146

- (A) Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 2602
 - Ceres seq_id 1503946

- (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 2603
 - Ceres seq_id 1503947
 - Location of start within SEQ ID NO 2602: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15459
- Phosphoribosyl pyrophosphate synthetase
- Location within SEQ ID NO 2603: from 1 to 80 aa.

- (D) Related Amino Acid Sequences
 - Alignment No. 15460
 - gi No. 2833379
 - % Identity 87.7
 - Alignment Length 81

- Location of Alignment in SEQ ID NO 2603: from 1 to 81
- Alignment No. 15461
- gi No. 2833380
- % Identity 87.7
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2603: from 1 to 81
- Alignment No. 15462
- gi No. 2833468
- % Identity 76.3
- Alignment Length 80
- Location of Alignment in SEQ ID NO 2603: from 1 to 80
- Alignment No. 15463
- gi No. 2842627
- % Identity 77.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2603: from 1 to 81
- Alignment No. 15464
- gi No. 3128195
- % Identity 90.1
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2603: from 1 to 81
- Alignment No. 15465
- gi No. 4902849
- % Identity 96.3
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2603: from 1 to 81
- Alignment No. 15466
- gi No. 4902851
- % Identity 91.4
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2603: from 1 to 81

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2604
- Ceres seq_id 1503948
- Location of start within SEQ ID NO 2602: at 80 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15467
- Phosphoribosyl pyrophosphate synthetase
- Location within SEQ ID NO 2604: from 1 to 54 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15468
- gi No. 2833379
- % Identity 87.7
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2604: from 1 to 55
- Alignment No. 15469
- gi No. 2833380
- % Identity 87.7
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2604: from 1 to 55

- Alignment No. 15470
- gi No. 2833468
- % Identity 76.3
- Alignment Length 80
- Location of Alignment in SEQ ID NO 2604: from 1 to 54
- Alignment No. 15471
- gi No. 2842627
- % Identity 77.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2604: from 1 to 55
- Alignment No. 15472
- gi No. 3128195
- % Identity 90.1
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2604: from 1 to 55
- Alignment No. 15473
- gi No. 4902849
- % Identity 96.3
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2604: from 1 to 55
- Alignment No. 15474
- gi No. 4902851
- % Identity 91.4
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2604: from 1 to 55

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2605
- Ceres seq_id 1503949
- Location of start within SEQ ID NO 2602: at 280 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15475
- Phosphoribosyl pyrophosphate synthetase
- Location within SEQ ID NO 2605: from 1 to 70 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15476
- gi No. 4902849
- % Identity 71.6
- Alignment Length 116
- Location of Alignment in SEQ ID NO 2605: from 1 to 70

Maximum Length Sequence corresponding to clone ID 316227

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2606
- Ceres seq_id 1503969

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2607
- Ceres seq_id 1503970
- Location of start within SEQ ID NO 2606: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15477
- gi No. 4587514
- % Identity 94.9
- Alignment Length 59
- Location of Alignment in SEQ ID NO 2607: from 1 to 59

- Alignment No. 15478
- gi No. 5531833
- % Identity 71.2
- Alignment Length 59
- Location of Alignment in SEQ ID NO 2607: from 1 to 59

- Alignment No. 15479
- gi No. 5531851
- % Identity 71.2
- Alignment Length 59
- Location of Alignment in SEQ ID NO 2607: from 1 to 59

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2608
- Ceres seq_id 1503971
- Location of start within SEQ ID NO 2606: at 34 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15480
- gi No. 4587514
- % Identity 94.9
- Alignment Length 59
- Location of Alignment in SEQ ID NO 2608: from 1 to 48

- Alignment No. 15481
- gi No. 5531833
- % Identity 71.2
- Alignment Length 59
- Location of Alignment in SEQ ID NO 2608: from 1 to 48

- Alignment No. 15482
- gi No. 5531851
- % Identity 71.2
- Alignment Length 59
- Location of Alignment in SEQ ID NO 2608: from 1 to 48

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2609
- Ceres seq_id 1503972
- Location of start within SEQ ID NO 2606: at 184 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 316265

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2610
- Ceres seq_id 1503989

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2611
- Ceres seq_id 1503990
- Location of start within SEQ ID NO 2610: at 67 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15483
- EF hand
- Location within SEQ ID NO 2611: from 48 to 76 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15484
- gi No. 100665
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15485
- gi No. 1076792
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15486
- gi No. 1076793
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15487
- gi No. 1084453
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15488
- gi No. 1085679
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15489
- gi No. 115480
- % Identity 97.7
- Alignment Length 133
- Location of Alignment in SEQ ID NO 2611: from 14 to 145
- Alignment No. 15490
- gi No. 115484
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15491
- gi No. 115486
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15492
- gi No. 115489
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15493
- gi No. 115492
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15494
- gi No. 115500
- % Identity 91.9
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2611: from 12 to 145

- Alignment No. 15495
- gi No. 115503
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15496
- gi No. 115504
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15497
- gi No. 115506
- % Identity 87.5
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2611: from 3 to 145

- Alignment No. 15498
- gi No. 115508
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15499
- gi No. 115509
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15500
- gi No. 115510
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145

- Alignment No. 15501
- gi No. 115511
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15502
- gi No. 115513
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15503
- gi No. 115514
- % Identity 80
- Alignment Length 30
- Location of Alignment in SEQ ID NO 2611: from 75 to 104

- Alignment No. 15504
- gi No. 115515
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15505
- gi No. 115516
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145

- Alignment No. 15506
- gi No. 115518
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145

- Alignment No. 15507
- gi No. 115519
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15508
- gi No. 115520
- % Identity 87
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15509
- gi No. 115521
- % Identity 89.7
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145

- Alignment No. 15510
- gi No. 115522
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145

- Alignment No. 15511
- gi No. 115523
- % Identity 75.4
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2611: from 5 to 145

- Alignment No. 15512
- gi No. 115524
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15513

- gi No. 115525
- % Identity 97.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
- Alignment No. 15514
- gi No. 115526
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
- Alignment No. 15515
- gi No. 115527
- % Identity 87
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2611: from 70 to 145
- Alignment No. 15516
- gi No. 115528
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15517
- gi No. 115530
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15518
- gi No. 115531
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15519
- gi No. 115532
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
- Alignment No. 15520
- gi No. 115534
- % Identity 93.1
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2611: from 12 to 142
- Alignment No. 15521
- gi No. 115541
- % Identity 83.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15522
- gi No. 1168748
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15523
- gi No. 1168749

- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15524
- gi No. 1235664
- % Identity 85.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15525
- gi No. 1292710
- % Identity 97.3
- Alignment Length 147
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15526
- gi No. 1292853
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15527
- gi No. 1311052
- % Identity 88.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 2611: from 77 to 145

- Alignment No. 15528
- gi No. 1345451
- % Identity 94.8
- Alignment Length 58
- Location of Alignment in SEQ ID NO 2611: from 2 to 59

- Alignment No. 15529
- gi No. 1345660
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15530
- gi No. 1345661
- % Identity 87.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15531
- gi No. 1362058
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15532
- gi No. 1402947
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15533
- gi No. 1421816
- % Identity 85.5

- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
- Alignment No. 15534
- gi No. 1565285
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15535
- gi No. 162030
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15536
- gi No. 16225
- % Identity 99.3
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2611: from 12 to 145
- Alignment No. 15537
- gi No. 166655
- % Identity 98.6
- Alignment Length 140
- Location of Alignment in SEQ ID NO 2611: from 7 to 145
- Alignment No. 15538
- gi No. 167676
- % Identity 87.4
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2611: from 12 to 145
- Alignment No. 15539
- gi No. 168777
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15540
- gi No. 169406
- % Identity 88
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2611: from 41 to 115
- Alignment No. 15541
- gi No. 170076
- % Identity 79.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15542
- gi No. 170567
- % Identity 85.4
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2611: from 3 to 145
- Alignment No. 15543
- gi No. 1754997
- % Identity 98.3
- Alignment Length 121

- Location of Alignment in SEQ ID NO 2611: from 26 to 145
- Alignment No. 15544
- gi No. 1754999
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15545
- gi No. 1785953
- % Identity 84.1
- Alignment Length 63
- Location of Alignment in SEQ ID NO 2611: from 57 to 119
- Alignment No. 15546
- gi No. 1785955
- % Identity 72.5
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2611: from 16 to 145
- Alignment No. 15547
- gi No. 1785958
- % Identity 87.3
- Alignment Length 63
- Location of Alignment in SEQ ID NO 2611: from 57 to 119
- Alignment No. 15548
- gi No. 20186
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15549
- gi No. 208092
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15550
- gi No. 2119350
- % Identity 92.2
- Alignment Length 51
- Location of Alignment in SEQ ID NO 2611: from 77 to 127
- Alignment No. 15551
- gi No. 2119353
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15552
- gi No. 2119360
- % Identity 99.2
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2611: from 26 to 145
- Alignment No. 15553
- gi No. 2119361
- % Identity 94.2
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2611: from 26 to 145

- Alignment No. 15554
- gi No. 2119362
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15555
- gi No. 2119364
- % Identity 90
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2611: from 94 to 113
- Alignment No. 15556
- gi No. 2129557
- % Identity 96.8
- Alignment Length 31
- Location of Alignment in SEQ ID NO 2611: from 1 to 31
- Alignment No. 15557
- gi No. 2129558
- % Identity 93.5
- Alignment Length 31
- Location of Alignment in SEQ ID NO 2611: from 1 to 31
- Alignment No. 15558
- gi No. 2129978
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15559
- gi No. 2147165
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15560
- gi No. 2181205
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15561
- gi No. 222925
- % Identity 92.6
- Alignment Length 136
- Location of Alignment in SEQ ID NO 2611: from 8 to 143
- Alignment No. 15562
- gi No. 223036
- % Identity 88.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
- Alignment No. 15563
- gi No. 223218
- % Identity 89
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145

- Alignment No. 15564
- gi No. 223872
- % Identity 86.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
- Alignment No. 15565
- gi No. 2244820
- % Identity 75.4
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2611: from 5 to 145
- Alignment No. 15566
- gi No. 225024
- % Identity 87.5
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2611: from 3 to 145
- Alignment No. 15567
- gi No. 2267084
- % Identity 94.1
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2611: from 12 to 145
- Alignment No. 15568
- gi No. 228408
- % Identity 97.7
- Alignment Length 133
- Location of Alignment in SEQ ID NO 2611: from 14 to 145
- Alignment No. 15569
- gi No. 2291247
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15570
- gi No. 230381
- % Identity 88.2
- Alignment Length 68
- Location of Alignment in SEQ ID NO 2611: from 79 to 145
- Alignment No. 15571
- gi No. 230382
- % Identity 86.4
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2611: from 81 to 145
- Alignment No. 15572
- gi No. 2388889
- % Identity 99.2
- Alignment Length 118
- Location of Alignment in SEQ ID NO 2611: from 9 to 126
- Alignment No. 15573
- gi No. 2388891
- % Identity 95.2
- Alignment Length 104
- Location of Alignment in SEQ ID NO 2611: from 1 to 104
- Alignment No. 15574

- gi No. 2392137
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145

- Alignment No. 15575
- gi No. 2464957
- % Identity 89.5
- Alignment Length 86
- Location of Alignment in SEQ ID NO 2611: from 61 to 145

- Alignment No. 15576
- gi No. 249170
- % Identity 92.3
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2611: from 32 to 70

- Alignment No. 15577
- gi No. 249171
- % Identity 75.4
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2611: from 77 to 133

- Alignment No. 15578
- gi No. 254773
- % Identity 100
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2611: from 108 to 127

- Alignment No. 15579
- gi No. 2554673
- % Identity 93.3
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2611: from 2 to 76

- Alignment No. 15580
- gi No. 2623680
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15581
- gi No. 2654179
- % Identity 93
- Alignment Length 86
- Location of Alignment in SEQ ID NO 2611: from 38 to 123

- Alignment No. 15582
- gi No. 266018
- % Identity 91.2
- Alignment Length 34
- Location of Alignment in SEQ ID NO 2611: from 96 to 129

- Alignment No. 15583
- gi No. 2677834
- % Identity 93.6
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2611: from 20 to 129

- Alignment No. 15584
- gi No. 2809481

- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15585
- gi No. 2832598
- % Identity 91.8
- Alignment Length 134
- Location of Alignment in SEQ ID NO 2611: from 8 to 141
- Alignment No. 15586
- gi No. 289525
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15587
- gi No. 2959326
- % Identity 71.7
- Alignment Length 130
- Location of Alignment in SEQ ID NO 2611: from 8 to 129
- Alignment No. 15588
- gi No. 3021331
- % Identity 83.8
- Alignment Length 68
- Location of Alignment in SEQ ID NO 2611: from 74 to 141
- Alignment No. 15589
- gi No. 310563
- % Identity 78.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15590
- gi No. 3121848
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15591
- gi No. 3121849
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15592
- gi No. 3136336
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15593
- gi No. 3243222
- % Identity 88.6
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2611: from 77 to 111
- Alignment No. 15594
- gi No. 3336912
- % Identity 93.8

- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15595
- gi No. 3378652
- % Identity 100
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2611: from 28 to 145

- Alignment No. 15596
- gi No. 3415119
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15597
- gi No. 348265
- % Identity 100
- Alignment Length 29
- Location of Alignment in SEQ ID NO 2611: from 32 to 60

- Alignment No. 15598
- gi No. 348267
- % Identity 94.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2611: from 108 to 126

- Alignment No. 15599
- gi No. 348268
- % Identity 78.9
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2611: from 128 to 145

- Alignment No. 15600
- gi No. 3561059
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15601
- gi No. 3561061
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15602
- gi No. 3786339
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15603
- gi No. 3800845
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15604
- gi No. 3800847
- % Identity 74.7
- Alignment Length 146

- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15605
- gi No. 3800849
- % Identity 87.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15606
- gi No. 3800851
- % Identity 72.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15607
- gi No. 3913191
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15608
- gi No. 4028590
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15609
- gi No. 4033343
- % Identity 82.1
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
- Alignment No. 15610
- gi No. 4033509
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15611
- gi No. 4098293
- % Identity 95.3
- Alignment Length 107
- Location of Alignment in SEQ ID NO 2611: from 20 to 126
- Alignment No. 15612
- gi No. 4098295
- % Identity 86
- Alignment Length 107
- Location of Alignment in SEQ ID NO 2611: from 20 to 126
- Alignment No. 15613
- gi No. 4103778
- % Identity 94.1
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2611: from 130 to 145
- Alignment No. 15614
- gi No. 4103959
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15615
- gi No. 4103963
- % Identity 100
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2611: from 82 to 145

- Alignment No. 15616
- gi No. 4103965
- % Identity 100
- Alignment Length 64
- Location of Alignment in SEQ ID NO 2611: from 83 to 145

- Alignment No. 15617
- gi No. 4150908
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15618
- gi No. 4200039
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15619
- gi No. 4335787
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15620
- gi No. 4336136
- % Identity 87.2
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2611: from 21 to 67

- Alignment No. 15621
- gi No. 4379369
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15622
- gi No. 443167
- % Identity 87.6
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145

- Alignment No. 15623
- gi No. 4468115
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15624
- gi No. 4502549
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15625
- gi No. 4581211
- % Identity 87
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2611: from 70 to 145
- Alignment No. 15626
- gi No. 4581213
- % Identity 78.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15627
- gi No. 4585219
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15628
- gi No. 461684
- % Identity 85.1
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15629
- gi No. 476851
- % Identity 85.7
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2611: from 70 to 145
- Alignment No. 15630
- gi No. 484660
- % Identity 82.4
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2611: from 3 to 144
- Alignment No. 15631
- gi No. 4885109
- % Identity 89.3
- Alignment Length 149
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15632
- gi No. 4885111
- % Identity 82.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15633
- gi No. 4930156
- % Identity 95.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
- Alignment No. 15634
- gi No. 4959142
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15635

- gi No. 4959143
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15636
- gi No. 4959144
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15637
- gi No. 4959145
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15638
- gi No. 4959146
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15639
- gi No. 4959147
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15640
- gi No. 4959148
- % Identity 94
- Alignment Length 149
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15641
- gi No. 4959149
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15642
- gi No. 4959150
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15643
- gi No. 4959151
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15644
- gi No. 4959152
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15645
- gi No. 4959153

- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15646
- gi No. 4959154
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15647
- gi No. 4959155
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15648
- gi No. 4959156
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15649
- gi No. 4959157
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15650
- gi No. 4959159
- % Identity 89
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15651
- gi No. 4959160
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15652
- gi No. 4959161
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15653
- gi No. 4959162
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15654
- gi No. 4959163
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15655
- gi No. 4959164
- % Identity 95.9

- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15656
- gi No. 4959165
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15657
- gi No. 4959166
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15658
- gi No. 4959167
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15659
- gi No. 4959168
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15660
- gi No. 4959169
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15661
- gi No. 4959170
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15662
- gi No. 4959171
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15663
- gi No. 4959172
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15664
- gi No. 4959588
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15665
- gi No. 4959590
- % Identity 95.9
- Alignment Length 146

- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15666
- gi No. 4959593
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15667
- gi No. 4959594
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15668
- gi No. 4959598
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15669
- gi No. 4959599
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15670
- gi No. 4959600
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15671
- gi No. 4959602
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15672
- gi No. 4959604
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15673
- gi No. 4959612
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15674
- gi No. 4959613
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15675
- gi No. 4959614
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15676
- gi No. 4959615
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15677
- gi No. 4959616
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15678
- gi No. 4959617
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15679
- gi No. 4959618
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15680
- gi No. 4959621
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15681
- gi No. 4959622
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15682
- gi No. 4959625
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15683
- gi No. 4959626
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15684
- gi No. 4959629
- % Identity 94.6
- Alignment Length 149
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15685
- gi No. 4959630
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15686
- gi No. 4959635
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15687
- gi No. 4959636
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15688
- gi No. 4959637
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15689
- gi No. 4959638
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15690
- gi No. 4959640
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15691
- gi No. 4959645
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15692
- gi No. 4959646
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15693
- gi No. 4959647
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15694
- gi No. 4959648
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15695
- gi No. 4995673
- % Identity 100
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2611: from 49 to 70

- Alignment No. 15696

- gi No. 4995696
- % Identity 95.5
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2611: from 49 to 70

- Alignment No. 15697
- gi No. 4995737
- % Identity 82.6
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2611: from 49 to 71

- Alignment No. 15698
- gi No. 4995739
- % Identity 91.3
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2611: from 49 to 71

- Alignment No. 15699
- gi No. 508526
- % Identity 90.8
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2611: from 1 to 131

- Alignment No. 15700
- gi No. 535428
- % Identity 76
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15701
- gi No. 552252
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2611: from 75 to 100

- Alignment No. 15702
- gi No. 5640002
- % Identity 91.3
- Alignment Length 80
- Location of Alignment in SEQ ID NO 2611: from 61 to 140

- Alignment No. 15703
- gi No. 565166
- % Identity 86.2
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145

- Alignment No. 15704
- gi No. 576081
- % Identity 89.4
- Alignment Length 141
- Location of Alignment in SEQ ID NO 2611: from 6 to 145

- Alignment No. 15705
- gi No. 587454
- % Identity 90.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 2611: from 10 to 145

- Alignment No. 15706
- gi No. 625985

- % Identity 95.7
- Alignment Length 46
- Location of Alignment in SEQ ID NO 2611: from 1 to 46

- Alignment No. 15707
- gi No. 640285
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145

- Alignment No. 15708
- gi No. 640294
- % Identity 90.8
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2611: from 5 to 145

- Alignment No. 15709
- gi No. 71660
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145

- Alignment No. 15710
- gi No. 71662
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145

- Alignment No. 15711
- gi No. 71667
- % Identity 91.7
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145

- Alignment No. 15712
- gi No. 71673
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145

- Alignment No. 15713
- gi No. 71676
- % Identity 84.8
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145

- Alignment No. 15714
- gi No. 729010
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15715
- gi No. 729011
- % Identity 82.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15716
- gi No. 729012
- % Identity 87.3

- Alignment Length 142
- Location of Alignment in SEQ ID NO 2611: from 5 to 145
- Alignment No. 15717
- gi No. 809298
- % Identity 86.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
- Alignment No. 15718
- gi No. 85332
- % Identity 92.2
- Alignment Length 141
- Location of Alignment in SEQ ID NO 2611: from 2 to 142
- Alignment No. 15719
- gi No. 9874
- % Identity 85.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15720
- gi No. 99673
- % Identity 81.9
- Alignment Length 72
- Location of Alignment in SEQ ID NO 2611: from 3 to 74

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2612
- Ceres seq_id 1503991
- Location of start within SEQ ID NO 2610: at 175 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15721
- EF hand
- Location within SEQ ID NO 2612: from 12 to 40 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15722
- gi No. 100665
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15723
- gi No. 1076792
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15724
- gi No. 1076793
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15725
- gi No. 1084453
- % Identity 98.6
- Alignment Length 146

- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15726
- gi No. 1085679
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15727
- gi No. 115480
- % Identity 97.7
- Alignment Length 133
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15728
- gi No. 115484
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15729
- gi No. 115486
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15730
- gi No. 115489
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15731
- gi No. 115492
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15732
- gi No. 115500
- % Identity 91.9
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15733
- gi No. 115503
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15734
- gi No. 115504
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15735
- gi No. 115506
- % Identity 87.5
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15736
- gi No. 115508
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15737
- gi No. 115509
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15738
- gi No. 115510
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15739
- gi No. 115511
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15740
- gi No. 115513
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15741
- gi No. 115514
- % Identity 80
- Alignment Length 30
- Location of Alignment in SEQ ID NO 2612: from 39 to 68
- Alignment No. 15742
- gi No. 115515
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15743
- gi No. 115516
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15744
- gi No. 115518
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15745
- gi No. 115519
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15746
 - gi No. 115520
 - % Identity 87
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15747
 - gi No. 115521
 - % Identity 89.7
 - Alignment Length 145
 - Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15748
 - gi No. 115522
 - % Identity 91
 - Alignment Length 145
 - Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15749
 - gi No. 115523
 - % Identity 75.4
 - Alignment Length 142
 - Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15750
 - gi No. 115524
 - % Identity 92.5
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15751
 - gi No. 115525
 - % Identity 97.9
 - Alignment Length 145
 - Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15752
 - gi No. 115526
 - % Identity 91
 - Alignment Length 145
 - Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15753
 - gi No. 115527
 - % Identity 87
 - Alignment Length 77
 - Location of Alignment in SEQ ID NO 2612: from 34 to 109
- Alignment No. 15754
 - gi No. 115528
 - % Identity 90.4
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15755
 - gi No. 115530
 - % Identity 90.4
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15756

- gi No. 115531
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15757
- gi No. 115532
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15758
- gi No. 115534
- % Identity 93.1
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2612: from 1 to 106
- Alignment No. 15759
- gi No. 115541
- % Identity 83.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15760
- gi No. 1168748
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15761
- gi No. 1168749
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15762
- gi No. 1235664
- % Identity 85.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15763
- gi No. 1292710
- % Identity 97.3
- Alignment Length 147
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15764
- gi No. 1292853
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15765
- gi No. 1311052
- % Identity 88.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 2612: from 41 to 109
- Alignment No. 15766
- gi No. 1345451

- % Identity 94.8
- Alignment Length 58
- Location of Alignment in SEQ ID NO 2612: from 1 to 23

- Alignment No. 15767
- gi No. 1345660
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15768
- gi No. 1345661
- % Identity 87.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15769
- gi No. 1362058
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15770
- gi No. 1402947
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15771
- gi No. 1421816
- % Identity 85.5
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15772
- gi No. 1565285
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15773
- gi No. 162030
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15774
- gi No. 16225
- % Identity 99.3
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15775
- gi No. 166655
- % Identity 98.6
- Alignment Length 140
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15776
- gi No. 167676
- % Identity 87.4

- Alignment Length 135
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15777
- gi No. 168777
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15778
- gi No. 169406
- % Identity 88
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2612: from 5 to 79
- Alignment No. 15779
- gi No. 170076
- % Identity 79.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15780
- gi No. 1705567
- % Identity 85.4
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15781
- gi No. 1754997
- % Identity 98.3
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15782
- gi No. 1754999
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15783
- gi No. 1785953
- % Identity 84.1
- Alignment Length 63
- Location of Alignment in SEQ ID NO 2612: from 21 to 83
- Alignment No. 15784
- gi No. 1785955
- % Identity 72.5
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15785
- gi No. 1785958
- % Identity 87.3
- Alignment Length 63
- Location of Alignment in SEQ ID NO 2612: from 21 to 83
- Alignment No. 15786
- gi No. 20186
- % Identity 99.3
- Alignment Length 146

- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15787
- gi No. 208092
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15788
- gi No. 2119350
- % Identity 92.2
- Alignment Length 51
- Location of Alignment in SEQ ID NO 2612: from 41 to 91
- Alignment No. 15789
- gi No. 2119353
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15790
- gi No. 2119360
- % Identity 99.2
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15791
- gi No. 2119361
- % Identity 94.2
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15792
- gi No. 2119362
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15793
- gi No. 2119364
- % Identity 90
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2612: from 58 to 77
- Alignment No. 15794
- gi No. 2129978
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15795
- gi No. 2147165
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15796
- gi No. 2181205
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15797
- gi No. 222925
- % Identity 92.6
- Alignment Length 136
- Location of Alignment in SEQ ID NO 2612: from 1 to 107

- Alignment No. 15798
- gi No. 223036
- % Identity 88.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15799
- gi No. 223218
- % Identity 89
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15800
- gi No. 223872
- % Identity 86.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15801
- gi No. 2244820
- % Identity 75.4
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15802
- gi No. 225024
- % Identity 87.5
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15803
- gi No. 2267084
- % Identity 94.1
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15804
- gi No. 228408
- % Identity 97.7
- Alignment Length 133
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15805
- gi No. 2291247
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15806
- gi No. 230381
- % Identity 88.2
- Alignment Length 68
- Location of Alignment in SEQ ID NO 2612: from 43 to 109

- Alignment No. 15807
- gi No. 230382
- % Identity 86.4
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2612: from 45 to 109

- Alignment No. 15808
- gi No. 2388889
- % Identity 99.2
- Alignment Length 118
- Location of Alignment in SEQ ID NO 2612: from 1 to 90

- Alignment No. 15809
- gi No. 2388891
- % Identity 95.2
- Alignment Length 104
- Location of Alignment in SEQ ID NO 2612: from 1 to 68

- Alignment No. 15810
- gi No. 2392137
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15811
- gi No. 2464957
- % Identity 89.5
- Alignment Length 86
- Location of Alignment in SEQ ID NO 2612: from 25 to 109

- Alignment No. 15812
- gi No. 249170
- % Identity 92.3
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2612: from 1 to 34

- Alignment No. 15813
- gi No. 249171
- % Identity 75.4
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2612: from 41 to 97

- Alignment No. 15814
- gi No. 254773
- % Identity 100
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2612: from 72 to 91

- Alignment No. 15815
- gi No. 2554673
- % Identity 93.3
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2612: from 1 to 40

- Alignment No. 15816
- gi No. 2623680
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15817

- gi No. 2654179
- % Identity 93
- Alignment Length 86
- Location of Alignment in SEQ ID NO 2612: from 2 to 87

- Alignment No. 15818
- gi No. 266018
- % Identity 91.2
- Alignment Length 34
- Location of Alignment in SEQ ID NO 2612: from 60 to 93

- Alignment No. 15819
- gi No. 2677834
- % Identity 93.6
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2612: from 1 to 93

- Alignment No. 15820
- gi No. 2809481
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15821
- gi No. 2832598
- % Identity 91.8
- Alignment Length 134
- Location of Alignment in SEQ ID NO 2612: from 1 to 105

- Alignment No. 15822
- gi No. 289525
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15823
- gi No. 2959326
- % Identity 71.7
- Alignment Length 130
- Location of Alignment in SEQ ID NO 2612: from 1 to 93

- Alignment No. 15824
- gi No. 3021331
- % Identity 83.8
- Alignment Length 68
- Location of Alignment in SEQ ID NO 2612: from 38 to 105

- Alignment No. 15825
- gi No. 310563
- % Identity 78.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15826
- gi No. 3121848
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15827
- gi No. 3121849

- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15828
- gi No. 3136336
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15829
- gi No. 3243222
- % Identity 88.6
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2612: from 41 to 75

- Alignment No. 15830
- gi No. 3336912
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15831
- gi No. 3378652
- % Identity 100
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15832
- gi No. 3415119
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15833
- gi No. 348265
- % Identity 100
- Alignment Length 29
- Location of Alignment in SEQ ID NO 2612: from 1 to 24

- Alignment No. 15834
- gi No. 348267
- % Identity 94.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2612: from 72 to 90

- Alignment No. 15835
- gi No. 348268
- % Identity 78.9
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2612: from 92 to 109

- Alignment No. 15836
- gi No. 3561059
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15837
- gi No. 3561061
- % Identity 95.9

- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15838
- gi No. 3786339
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15839
- gi No. 3800845
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15840
- gi No. 3800847
- % Identity 74.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15841
- gi No. 3800849
- % Identity 87.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15842
- gi No. 3800851
- % Identity 72.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15843
- gi No. 3913191
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15844
- gi No. 4028590
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15845
- gi No. 4033343
- % Identity 82.1
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15846
- gi No. 4033509
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15847
- gi No. 4098293
- % Identity 95.3
- Alignment Length 107

- Location of Alignment in SEQ ID NO 2612: from 1 to 90
- Alignment No. 15848
- gi No. 4098295
- % Identity 86
- Alignment Length 107
- Location of Alignment in SEQ ID NO 2612: from 1 to 90
- Alignment No. 15849
- gi No. 4103778
- % Identity 94.1
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2612: from 94 to 109
- Alignment No. 15850
- gi No. 4103959
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15851
- gi No. 4103963
- % Identity 100
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2612: from 46 to 109
- Alignment No. 15852
- gi No. 4103965
- % Identity 100
- Alignment Length 64
- Location of Alignment in SEQ ID NO 2612: from 47 to 109
- Alignment No. 15853
- gi No. 4150908
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15854
- gi No. 4200039
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15855
- gi No. 4335787
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15856
- gi No. 4336136
- % Identity 87.2
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2612: from 1 to 31
- Alignment No. 15857
- gi No. 4379369
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15858
- gi No. 443167
- % Identity 87.6
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15859
- gi No. 4468115
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15860
- gi No. 4502549
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15861
- gi No. 4581211
- % Identity 87
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2612: from 34 to 109

- Alignment No. 15862
- gi No. 4581213
- % Identity 78.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15863
- gi No. 4585219
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15864
- gi No. 461684
- % Identity 85.1
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15865
- gi No. 476851
- % Identity 85.7
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2612: from 34 to 109

- Alignment No. 15866
- gi No. 484660
- % Identity 82.4
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2612: from 1 to 108

- Alignment No. 15867
- gi No. 4885109
- % Identity 89.3
- Alignment Length 149
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15868
- gi No. 4885111
- % Identity 82.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15869
- gi No. 4930156
- % Identity 95.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15870
- gi No. 4959142
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15871
- gi No. 4959143
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15872
- gi No. 4959144
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15873
- gi No. 4959145
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15874
- gi No. 4959146
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15875
- gi No. 4959147
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15876
- gi No. 4959148
- % Identity 94
- Alignment Length 149
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15877
- gi No. 4959149
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15878

- gi No. 4959150
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15879
- gi No. 4959151
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15880
- gi No. 4959152
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15881
- gi No. 4959153
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15882
- gi No. 4959154
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15883
- gi No. 4959155
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15884
- gi No. 4959156
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15885
- gi No. 4959157
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15886
- gi No. 4959159
- % Identity 89
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15887
- gi No. 4959160
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15888
- gi No. 4959161

- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15889
- gi No. 4959162
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15890
- gi No. 4959163
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15891
- gi No. 4959164
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15892
- gi No. 4959165
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15893
- gi No. 4959166
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15894
- gi No. 4959167
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15895
- gi No. 4959168
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15896
- gi No. 4959169
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15897
- gi No. 4959170
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15898
- gi No. 4959171
- % Identity 95.9

- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15899
- gi No. 4959172
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15900
- gi No. 4959588
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15901
- gi No. 4959590
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15902
- gi No. 4959593
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15903
- gi No. 4959594
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15904
- gi No. 4959598
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15905
- gi No. 4959599
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15906
- gi No. 4959600
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15907
- gi No. 4959602
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15908
- gi No. 4959604
- % Identity 95.9
- Alignment Length 146

- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15909
 - gi No. 4959612
 - % Identity 93.8
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15910
 - gi No. 4959613
 - % Identity 91.8
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15911
 - gi No. 4959614
 - % Identity 95.2
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15912
 - gi No. 4959615
 - % Identity 95.9
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15913
 - gi No. 4959616
 - % Identity 94.5
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15914
 - gi No. 4959617
 - % Identity 95.9
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15915
 - gi No. 4959618
 - % Identity 95.9
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15916
 - gi No. 4959621
 - % Identity 94.5
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15917
 - gi No. 4959622
 - % Identity 92.5
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15918
 - gi No. 4959625
 - % Identity 95.9
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15919
- gi No. 4959626
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15920
- gi No. 4959629
- % Identity 94.6
- Alignment Length 149
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15921
- gi No. 4959630
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15922
- gi No. 4959635
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15923
- gi No. 4959636
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15924
- gi No. 4959637
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15925
- gi No. 4959638
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15926
- gi No. 4959640
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15927
- gi No. 4959645
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15928
- gi No. 4959646
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15929
- gi No. 4959647
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15930
- gi No. 4959648
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15931
- gi No. 4995673
- % Identity 100
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2612: from 13 to 34
- Alignment No. 15932
- gi No. 4995696
- % Identity 95.5
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2612: from 13 to 34
- Alignment No. 15933
- gi No. 4995737
- % Identity 82.6
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2612: from 13 to 35
- Alignment No. 15934
- gi No. 4995739
- % Identity 91.3
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2612: from 13 to 35
- Alignment No. 15935
- gi No. 508526
- % Identity 90.8
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2612: from 1 to 95
- Alignment No. 15936
- gi No. 535428
- % Identity 76
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15937
- gi No. 552252
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2612: from 39 to 64
- Alignment No. 15938
- gi No. 5640002
- % Identity 91.3
- Alignment Length 80
- Location of Alignment in SEQ ID NO 2612: from 25 to 104
- Alignment No. 15939

- gi No. 565166
- % Identity 86.2
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15940
- gi No. 576081
- % Identity 89.4
- Alignment Length 141
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15941
- gi No. 587454
- % Identity 90.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15942
- gi No. 640285
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15943
- gi No. 640294
- % Identity 90.8
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15944
- gi No. 71660
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15945
- gi No. 71662
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15946
- gi No. 71667
- % Identity 91.7
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15947
- gi No. 71673
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15948
- gi No. 71676
- % Identity 84.8
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15949
- gi No. 729010

- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15950
- gi No. 729011
- % Identity 82.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15951
- gi No. 729012
- % Identity 87.3
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15952
- gi No. 809298
- % Identity 86.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15953
- gi No. 85332
- % Identity 92.2
- Alignment Length 141
- Location of Alignment in SEQ ID NO 2612: from 1 to 106

- Alignment No. 15954
- gi No. 9874
- % Identity 85.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15955
- gi No. 99673
- % Identity 81.9
- Alignment Length 72
- Location of Alignment in SEQ ID NO 2612: from 1 to 38

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2613
- Ceres seq_id 1503992
- Location of start within SEQ ID NO 2610: at 220 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15956
- EF hand
- Location within SEQ ID NO 2613: from 1 to 25 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15957
- gi No. 100665
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15958
- gi No. 1076792
- % Identity 97.9

- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15959
- gi No. 1076793
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15960
- gi No. 1084453
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15961
- gi No. 1085679
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15962
- gi No. 115480
- % Identity 97.7
- Alignment Length 133
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15963
- gi No. 115484
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15964
- gi No. 115486
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15965
- gi No. 115489
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15966
- gi No. 115492
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15967
- gi No. 115500
- % Identity 91.9
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15968
- gi No. 115503
- % Identity 89.7
- Alignment Length 146

- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15969
 - gi No. 115504
 - % Identity 82.2
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15970
 - gi No. 115506
 - % Identity 87.5
 - Alignment Length 144
 - Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15971
 - gi No. 115508
 - % Identity 91.8
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15972
 - gi No. 115509
 - % Identity 90.4
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15973
 - gi No. 115510
 - % Identity 90.3
 - Alignment Length 145
 - Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15974
 - gi No. 115511
 - % Identity 100
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15975
 - gi No. 115513
 - % Identity 93.2
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15976
 - gi No. 115514
 - % Identity 80
 - Alignment Length 30
 - Location of Alignment in SEQ ID NO 2613: from 24 to 53
- Alignment No. 15977
 - gi No. 115515
 - % Identity 98.6
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15978
 - gi No. 115516
 - % Identity 91
 - Alignment Length 145
 - Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15979
- gi No. 115518
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15980
- gi No. 115519
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15981
- gi No. 115520
- % Identity 87
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15982
- gi No. 115521
- % Identity 89.7
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15983
- gi No. 115522
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15984
- gi No. 115523
- % Identity 75.4
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15985
- gi No. 115524
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15986
- gi No. 115525
- % Identity 97.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15987
- gi No. 115526
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15988
- gi No. 115527
- % Identity 87
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2613: from 19 to 94

- Alignment No. 15989
- gi No. 115528
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15990
- gi No. 115530
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15991
- gi No. 115531
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15992
- gi No. 115532
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15993
- gi No. 115534
- % Identity 93.1
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2613: from 1 to 91

- Alignment No. 15994
- gi No. 115541
- % Identity 83.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15995
- gi No. 1168748
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15996
- gi No. 1168749
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15997
- gi No. 1235664
- % Identity 85.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15998
- gi No. 1292710
- % Identity 97.3
- Alignment Length 147
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15999

- gi No. 1292853
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16000
- gi No. 1311052
- % Identity 88.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 2613: from 26 to 94

- Alignment No. 16001
- gi No. 1345660
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16002
- gi No. 1345661
- % Identity 87.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16003
- gi No. 1362058
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16004
- gi No. 1402947
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16005
- gi No. 1421816
- % Identity 85.5
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16006
- gi No. 1565285
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16007
- gi No. 162030
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16008
- gi No. 16225
- % Identity 99.3
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16009
- gi No. 166655

- % Identity 98.6
- Alignment Length 140
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16010
- gi No. 167676
- % Identity 87.4
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16011
- gi No. 168777
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16012
- gi No. 169406
- % Identity 88
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2613: from 1 to 64

- Alignment No. 16013
- gi No. 170076
- % Identity 79.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16014
- gi No. 170567
- % Identity 85.4
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16015
- gi No. 1754997
- % Identity 98.3
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16016
- gi No. 1754999
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16017
- gi No. 1785953
- % Identity 84.1
- Alignment Length 63
- Location of Alignment in SEQ ID NO 2613: from 6 to 68

- Alignment No. 16018
- gi No. 1785955
- % Identity 72.5
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16019
- gi No. 1785958
- % Identity 87.3

- Alignment Length 63
- Location of Alignment in SEQ ID NO 2613: from 6 to 68
- Alignment No. 16020
- gi No. 20186
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16021
- gi No. 208092
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16022
- gi No. 2119350
- % Identity 92.2
- Alignment Length 51
- Location of Alignment in SEQ ID NO 2613: from 26 to 76
- Alignment No. 16023
- gi No. 2119353
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16024
- gi No. 2119360
- % Identity 99.2
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16025
- gi No. 2119361
- % Identity 94.2
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16026
- gi No. 2119362
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16027
- gi No. 2119364
- % Identity 90
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2613: from 43 to 62
- Alignment No. 16028
- gi No. 2129978
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16029
- gi No. 2147165
- % Identity 98.6
- Alignment Length 146

- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16030
- gi No. 2181205
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16031
- gi No. 222925
- % Identity 92.6
- Alignment Length 136
- Location of Alignment in SEQ ID NO 2613: from 1 to 92
- Alignment No. 16032
- gi No. 223036
- % Identity 88.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16033
- gi No. 223218
- % Identity 89
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16034
- gi No. 223872
- % Identity 86.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16035
- gi No. 2244820
- % Identity 75.4
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16036
- gi No. 225024
- % Identity 87.5
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16037
- gi No. 2267084
- % Identity 94.1
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16038
- gi No. 228408
- % Identity 97.7
- Alignment Length 133
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16039
- gi No. 2291247
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16040
- gi No. 230381
- % Identity 88.2
- Alignment Length 68
- Location of Alignment in SEQ ID NO 2613: from 28 to 94

- Alignment No. 16041
- gi No. 230382
- % Identity 86.4
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2613: from 30 to 94

- Alignment No. 16042
- gi No. 2388889
- % Identity 99.2
- Alignment Length 118
- Location of Alignment in SEQ ID NO 2613: from 1 to 75

- Alignment No. 16043
- gi No. 2388891
- % Identity 95.2
- Alignment Length 104
- Location of Alignment in SEQ ID NO 2613: from 1 to 53

- Alignment No. 16044
- gi No. 2392137
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16045
- gi No. 2464957
- % Identity 89.5
- Alignment Length 86
- Location of Alignment in SEQ ID NO 2613: from 10 to 94

- Alignment No. 16046
- gi No. 249170
- % Identity 92.3
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2613: from 1 to 19

- Alignment No. 16047
- gi No. 249171
- % Identity 75.4
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2613: from 26 to 82

- Alignment No. 16048
- gi No. 254773
- % Identity 100
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2613: from 57 to 76

- Alignment No. 16049
- gi No. 2554673
- % Identity 93.3
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2613: from 1 to 25

- Alignment No. 16050
 - gi No. 2623680
 - % Identity 98.6
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16051
 - gi No. 2654179
 - % Identity 93
 - Alignment Length 86
 - Location of Alignment in SEQ ID NO 2613: from 1 to 72
- Alignment No. 16052
 - gi No. 266018
 - % Identity 91.2
 - Alignment Length 34
 - Location of Alignment in SEQ ID NO 2613: from 45 to 78
- Alignment No. 16053
 - gi No. 2677834
 - % Identity 93.6
 - Alignment Length 110
 - Location of Alignment in SEQ ID NO 2613: from 1 to 78
- Alignment No. 16054
 - gi No. 2809481
 - % Identity 98.6
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16055
 - gi No. 2832598
 - % Identity 91.8
 - Alignment Length 134
 - Location of Alignment in SEQ ID NO 2613: from 1 to 90
- Alignment No. 16056
 - gi No. 289525
 - % Identity 98.6
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16057
 - gi No. 2959326
 - % Identity 71.7
 - Alignment Length 130
 - Location of Alignment in SEQ ID NO 2613: from 1 to 78
- Alignment No. 16058
 - gi No. 3021331
 - % Identity 83.8
 - Alignment Length 68
 - Location of Alignment in SEQ ID NO 2613: from 23 to 90
- Alignment No. 16059
 - gi No. 310563
 - % Identity 78.8
 - Alignment Length 146
 - Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16060

- gi No. 3121848
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16061
- gi No. 3121849
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16062
- gi No. 3136336
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16063
- gi No. 3243222
- % Identity 88.6
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2613: from 26 to 60

- Alignment No. 16064
- gi No. 3336912
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16065
- gi No. 3378652
- % Identity 100
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16066
- gi No. 3415119
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16067
- gi No. 348267
- % Identity 94.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2613: from 57 to 75

- Alignment No. 16068
- gi No. 348268
- % Identity 78.9
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2613: from 77 to 94

- Alignment No. 16069
- gi No. 3561059
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16070
- gi No. 3561061

- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16071
- gi No. 3786339
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16072
- gi No. 3800845
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16073
- gi No. 3800847
- % Identity 74.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16074
- gi No. 3800849
- % Identity 87.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16075
- gi No. 3800851
- % Identity 72.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16076
- gi No. 3913191
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16077
- gi No. 4028590
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16078
- gi No. 4033343
- % Identity 82.1
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16079
- gi No. 4033509
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16080
- gi No. 4098293
- % Identity 95.3

- Alignment Length 107
- Location of Alignment in SEQ ID NO 2613: from 1 to 75

- Alignment No. 16081
- gi No. 4098295
- % Identity 86
- Alignment Length 107
- Location of Alignment in SEQ ID NO 2613: from 1 to 75

- Alignment No. 16082
- gi No. 4103778
- % Identity 94.1
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2613: from 79 to 94

- Alignment No. 16083
- gi No. 4103959
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16084
- gi No. 4103963
- % Identity 100
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2613: from 31 to 94

- Alignment No. 16085
- gi No. 4103965
- % Identity 100
- Alignment Length 64
- Location of Alignment in SEQ ID NO 2613: from 32 to 94

- Alignment No. 16086
- gi No. 4150908
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16087
- gi No. 4200039
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16088
- gi No. 4335787
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16089
- gi No. 4336136
- % Identity 87.2
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2613: from 1 to 16

- Alignment No. 16090
- gi No. 4379369
- % Identity 93.2
- Alignment Length 146

- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16091
- gi No. 443167
- % Identity 87.6
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16092
- gi No. 4468115
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16093
- gi No. 4502549
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16094
- gi No. 4581211
- % Identity 87
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2613: from 19 to 94
- Alignment No. 16095
- gi No. 4581213
- % Identity 78.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16096
- gi No. 4585219
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16097
- gi No. 461684
- % Identity 85.1
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16098
- gi No. 476851
- % Identity 85.7
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2613: from 19 to 94
- Alignment No. 16099
- gi No. 484660
- % Identity 82.4
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2613: from 1 to 93
- Alignment No. 16100
- gi No. 4885109
- % Identity 89.3
- Alignment Length 149
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16101
- gi No. 4885111
- % Identity 82.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16102
- gi No. 4930156
- % Identity 95.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16103
- gi No. 4959142
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16104
- gi No. 4959143
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16105
- gi No. 4959144
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16106
- gi No. 4959145
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16107
- gi No. 4959146
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16108
- gi No. 4959147
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16109
- gi No. 4959148
- % Identity 94
- Alignment Length 149
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16110
- gi No. 4959149
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16111
- gi No. 4959150
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16112
- gi No. 4959151
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16113
- gi No. 4959152
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16114
- gi No. 4959153
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16115
- gi No. 4959154
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16116
- gi No. 4959155
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16117
- gi No. 4959156
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16118
- gi No. 4959157
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16119
- gi No. 4959159
- % Identity 89
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16120
- gi No. 4959160
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16121

- gi No. 4959161
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16122
- gi No. 4959162
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16123
- gi No. 4959163
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16124
- gi No. 4959164
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16125
- gi No. 4959165
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16126
- gi No. 4959166
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16127
- gi No. 4959167
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16128
- gi No. 4959168
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16129
- gi No. 4959169
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16130
- gi No. 4959170
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16131
- gi No. 4959171

- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16132
- gi No. 4959172
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16133
- gi No. 4959588
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16134
- gi No. 4959590
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16135
- gi No. 4959593
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16136
- gi No. 4959594
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16137
- gi No. 4959598
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16138
- gi No. 4959599
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16139
- gi No. 4959600
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16140
- gi No. 4959602
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16141
- gi No. 4959604
- % Identity 95.9

- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16142
- gi No. 4959612
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16143
- gi No. 4959613
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16144
- gi No. 4959614
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16145
- gi No. 4959615
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16146
- gi No. 4959616
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16147
- gi No. 4959617
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16148
- gi No. 4959618
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16149
- gi No. 4959621
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16150
- gi No. 4959622
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16151
- gi No. 4959625
- % Identity 95.9
- Alignment Length 146

- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16152
- gi No. 4959626
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16153
- gi No. 4959629
- % Identity 94.6
- Alignment Length 149
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16154
- gi No. 4959630
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16155
- gi No. 4959635
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16156
- gi No. 4959636
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16157
- gi No. 4959637
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16158
- gi No. 4959638
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16159
- gi No. 4959640
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16160
- gi No. 4959645
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16161
- gi No. 4959646
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16162
- gi No. 4959647
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16163
- gi No. 4959648
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16164
- gi No. 4995673
- % Identity 100
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2613: from 1 to 19
- Alignment No. 16165
- gi No. 4995696
- % Identity 95.5
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2613: from 1 to 19
- Alignment No. 16166
- gi No. 4995737
- % Identity 82.6
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2613: from 1 to 20
- Alignment No. 16167
- gi No. 4995739
- % Identity 91.3
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2613: from 1 to 20
- Alignment No. 16168
- gi No. 508526
- % Identity 90.8
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2613: from 1 to 80
- Alignment No. 16169
- gi No. 535428
- % Identity 76
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16170
- gi No. 552252
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2613: from 24 to 49
- Alignment No. 16171
- gi No. 5640002
- % Identity 91.3
- Alignment Length 80
- Location of Alignment in SEQ ID NO 2613: from 10 to 89

- Alignment No. 16172
- gi No. 565166
- % Identity 86.2
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16173
- gi No. 576081
- % Identity 89.4
- Alignment Length 141
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16174
- gi No. 587454
- % Identity 90.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16175
- gi No. 640285
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16176
- gi No. 640294
- % Identity 90.8
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16177
- gi No. 71660
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16178
- gi No. 71662
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16179
- gi No. 71667
- % Identity 91.7
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16180
- gi No. 71673
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16181
- gi No. 71676
- % Identity 84.8
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16182

- gi No. 729010
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16183
- gi No. 729011
- % Identity 82.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16184
- gi No. 729012
- % Identity 87.3
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16185
- gi No. 809298
- % Identity 86.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16186
- gi No. 85332
- % Identity 92.2
- Alignment Length 141
- Location of Alignment in SEQ ID NO 2613: from 1 to 91
- Alignment No. 16187
- gi No. 9874
- % Identity 85.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16188
- gi No. 99673
- % Identity 81.9
- Alignment Length 72
- Location of Alignment in SEQ ID NO 2613: from 1 to 23

Maximum Length Sequence corresponding to clone ID 316301

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2614
- Ceres seq_id 1504001

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2615
- Ceres seq_id 1504002
- Location of start within SEQ ID NO 2614: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2616
- Ceres seq_id 1504003
- Location of start within SEQ ID NO 2614: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

- Alignment No. 16189
- Ribosomal protein L5
- Location within SEQ ID NO 2616: from 34 to 79 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16190
- gi No. 1125808
- % Identity 80.4
- Alignment Length 51
- Location of Alignment in SEQ ID NO 2616: from 29 to 79
- Alignment No. 16191
- gi No. 1172816
- % Identity 90.7
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2616: from 26 to 79
- Alignment No. 16192
- gi No. 1172817
- % Identity 90.6
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2616: from 27 to 79
- Alignment No. 16193
- gi No. 1172952
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 2616: from 35 to 79
- Alignment No. 16194
- gi No. 1172954
- % Identity 70.6
- Alignment Length 51
- Location of Alignment in SEQ ID NO 2616: from 26 to 76
- Alignment No. 16195
- gi No. 1172969
- % Identity 90.7
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2616: from 26 to 79
- Alignment No. 16196
- gi No. 1173055
- % Identity 94.4
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2616: from 26 to 79
- Alignment No. 16197
- gi No. 132649
- % Identity 70.9
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2616: from 26 to 79
- Alignment No. 16198
- gi No. 132951
- % Identity 79.6
- Alignment Length 49
- Location of Alignment in SEQ ID NO 2616: from 31 to 79
- Alignment No. 16199
- gi No. 132992

- % Identity 75
- Alignment Length 44
- Location of Alignment in SEQ ID NO 2616: from 36 to 79

- Alignment No. 16200
- gi No. 1350658
- % Identity 70.9
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2616: from 26 to 79

- Alignment No. 16201
- gi No. 1350659
- % Identity 70.6
- Alignment Length 51
- Location of Alignment in SEQ ID NO 2616: from 26 to 76

- Alignment No. 16202
- gi No. 1710494
- % Identity 78
- Alignment Length 50
- Location of Alignment in SEQ ID NO 2616: from 30 to 79

- Alignment No. 16203
- gi No. 2500240
- % Identity 80.4
- Alignment Length 51
- Location of Alignment in SEQ ID NO 2616: from 29 to 79

- Alignment No. 16204
- gi No. 2500241
- % Identity 78.4
- Alignment Length 51
- Location of Alignment in SEQ ID NO 2616: from 29 to 79

- Alignment No. 16205
- gi No. 2570507
- % Identity 85.2
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2616: from 26 to 79

- Alignment No. 16206
- gi No. 4322
- % Identity 77.6
- Alignment Length 49
- Location of Alignment in SEQ ID NO 2616: from 31 to 79

- Alignment No. 16207
- gi No. 4432750
- % Identity 86.1
- Alignment Length 36
- Location of Alignment in SEQ ID NO 2616: from 41 to 76

- Alignment No. 16208
- gi No. 4512679
- % Identity 74.1
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2616: from 36 to 79

- Alignment No. 16209
- gi No. 4586222
- % Identity 76.5

- Alignment Length 51
- Location of Alignment in SEQ ID NO 2616: from 29 to 79
- Alignment No. 16210
- gi No. 71107
- % Identity 79.6
- Alignment Length 49
- Location of Alignment in SEQ ID NO 2616: from 31 to 79

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2617
- Ceres seq_id 1504004
- Location of start within SEQ ID NO 2614: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 316327

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2618
- Ceres seq_id 1504016

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2619
- Ceres seq_id 1504017
- Location of start within SEQ ID NO 2618: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2620
- Ceres seq_id 1504018
- Location of start within SEQ ID NO 2618: at 310 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16211
- gi No. 2224915
- % Identity 81.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2620: from 1 to 55
- Alignment No. 16212
- gi No. 729944
- % Identity 75
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2620: from 1 to 55

Maximum Length Sequence corresponding to clone ID 316354

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2621
- Ceres seq_id 1504025

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2622
- Ceres seq_id 1504026
- Location of start within SEQ ID NO 2621: at 133 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16213
- Sugar (and other) transporter
- Location within SEQ ID NO 2622: from 1 to 98 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16214
- gi No. 2760325
- % Identity 73.1
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2622: from 1 to 98

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2623
- Ceres seq_id 1504027
- Location of start within SEQ ID NO 2621: at 166 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16215
- Sugar (and other) transporter
- Location within SEQ ID NO 2623: from 1 to 87 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16216
- gi No. 2760325
- % Identity 73.1
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2623: from 1 to 87

Maximum Length Sequence corresponding to clone ID 316377

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2624
- Ceres seq_id 1504036

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2625
- Ceres seq_id 1504037
- Location of start within SEQ ID NO 2624: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16217
- gi No. 2505870
- % Identity 78.3
- Alignment Length 152
- Location of Alignment in SEQ ID NO 2625: from 1 to 152

- Alignment No. 16218
- gi No. 3287679
- % Identity 80.4
- Alignment Length 138
- Location of Alignment in SEQ ID NO 2625: from 1 to 138

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2626
- Ceres seq_id 1504038
- Location of start within SEQ ID NO 2624: at 75 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16219
- gi No. 2505870
- % Identity 78.3
- Alignment Length 152
- Location of Alignment in SEQ ID NO 2626: from 1 to 128

- Alignment No. 16220
- gi No. 3287679
- % Identity 80.4
- Alignment Length 138
- Location of Alignment in SEQ ID NO 2626: from 1 to 114

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2627
- Ceres seq_id 1504039
- Location of start within SEQ ID NO 2624: at 81 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16221
- gi No. 2505870
- % Identity 78.3
- Alignment Length 152
- Location of Alignment in SEQ ID NO 2627: from 1 to 126

- Alignment No. 16222
- gi No. 3287679
- % Identity 80.4
- Alignment Length 138
- Location of Alignment in SEQ ID NO 2627: from 1 to 112

Maximum Length Sequence corresponding to clone ID 316388

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2628
- Ceres seq_id 1504044

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2629
- Ceres seq_id 1504045
- Location of start within SEQ ID NO 2628: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16223
- gi No. 3057044
- % Identity 70.7
- Alignment Length 82
- Location of Alignment in SEQ ID NO 2629: from 61 to 142

- Alignment No. 16224
- gi No. 3337356
- % Identity 93.9
- Alignment Length 82
- Location of Alignment in SEQ ID NO 2629: from 61 to 142

- Alignment No. 16225
- gi No. 3834321

- % Identity 92.7
- Alignment Length 82
- Location of Alignment in SEQ ID NO 2629: from 61 to 142

- Alignment No. 16226
- gi No. 3881191
- % Identity 70.5
- Alignment Length 78
- Location of Alignment in SEQ ID NO 2629: from 65 to 142

- Alignment No. 16227
- gi No. 4689112
- % Identity 70.7
- Alignment Length 82
- Location of Alignment in SEQ ID NO 2629: from 61 to 142

- Alignment No. 16228
- gi No. 585957
- % Identity 70.7
- Alignment Length 82
- Location of Alignment in SEQ ID NO 2629: from 61 to 142

- Alignment No. 16229
- gi No. 585959
- % Identity 70.7
- Alignment Length 82
- Location of Alignment in SEQ ID NO 2629: from 61 to 142

Maximum Length Sequence corresponding to clone ID 316451

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2630
- Ceres seq_id 1504050

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2631
- Ceres seq_id 1504051
- Location of start within SEQ ID NO 2630: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16230
- WD domain, G-beta repeat
- Location within SEQ ID NO 2631: from 85 to 124 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16231
- gi No. 3122386
- % Identity 83.2
- Alignment Length 167
- Location of Alignment in SEQ ID NO 2631: from 1 to 166

- Alignment No. 16232
- gi No. 3122387
- % Identity 86.8
- Alignment Length 167
- Location of Alignment in SEQ ID NO 2631: from 1 to 166

Maximum Length Sequence corresponding to clone ID 316638

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2632
- Ceres seq_id 1504098

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2633
- Ceres seq_id 1504099
- Location of start within SEQ ID NO 2632: at 125 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16233
- ADP-ribosylation factor family
- Location within SEQ ID NO 2633: from 2 to 75 aa.
- Alignment No. 16234
- Ras family
- Location within SEQ ID NO 2633: from 19 to 80 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16235
- gi No. 114122
- % Identity 70.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2633: from 1 to 75
- Alignment No. 16236
- gi No. 3252999
- % Identity 74.1
- Alignment Length 58
- Location of Alignment in SEQ ID NO 2633: from 18 to 75
- Alignment No. 16237
- gi No. 3746799
- % Identity 71.9
- Alignment Length 57
- Location of Alignment in SEQ ID NO 2633: from 19 to 75
- Alignment No. 16238
- gi No. 3746801
- % Identity 71.9
- Alignment Length 57
- Location of Alignment in SEQ ID NO 2633: from 19 to 75
- Alignment No. 16239
- gi No. 461532
- % Identity 70.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2633: from 1 to 75
- Alignment No. 16240
- gi No. 89370
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2633: from 22 to 42

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2634
- Ceres seq_id 1504100
- Location of start within SEQ ID NO 2632: at 176 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16241
- ADP-ribosylation factor family
- Location within SEQ ID NO 2634: from 1 to 58 aa.

- Alignment No. 16242
- Ras family
- Location within SEQ ID NO 2634: from 2 to 63 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16243
- gi No. 114122
- % Identity 70.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2634: from 1 to 58

- Alignment No. 16244
- gi No. 3252999
- % Identity 74.1
- Alignment Length 58
- Location of Alignment in SEQ ID NO 2634: from 1 to 58

- Alignment No. 16245
- gi No. 3746799
- % Identity 71.9
- Alignment Length 57
- Location of Alignment in SEQ ID NO 2634: from 2 to 58

- Alignment No. 16246
- gi No. 3746801
- % Identity 71.9
- Alignment Length 57
- Location of Alignment in SEQ ID NO 2634: from 2 to 58

- Alignment No. 16247
- gi No. 461532
- % Identity 70.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2634: from 1 to 58

- Alignment No. 16248
- gi No. 89370
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2634: from 5 to 25

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2635
- Ceres seq_id 1504101
- Location of start within SEQ ID NO 2632: at 188 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16249
- ADP-ribosylation factor family
- Location within SEQ ID NO 2635: from 1 to 54 aa.

- Alignment No. 16250
- Ras family
- Location within SEQ ID NO 2635: from 1 to 59 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16251
- gi No. 114122
- % Identity 70.7

- Alignment Length 75
- Location of Alignment in SEQ ID NO 2635: from 1 to 54
- Alignment No. 16252
- gi No. 3252999
- % Identity 74.1
- Alignment Length 58
- Location of Alignment in SEQ ID NO 2635: from 1 to 54
- Alignment No. 16253
- gi No. 3746799
- % Identity 71.9
- Alignment Length 57
- Location of Alignment in SEQ ID NO 2635: from 1 to 54
- Alignment No. 16254
- gi No. 3746801
- % Identity 71.9
- Alignment Length 57
- Location of Alignment in SEQ ID NO 2635: from 1 to 54
- Alignment No. 16255
- gi No. 461532
- % Identity 70.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2635: from 1 to 54
- Alignment No. 16256
- gi No. 89370
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2635: from 1 to 21

Maximum Length Sequence corresponding to clone ID 316643

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2636
- Ceres seq_id 1504102

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2637
- Ceres seq_id 1504103
- Location of start within SEQ ID NO 2636: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16257
- gi No. 462338
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2637: from 95 to 108

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2638
- Ceres seq_id 1504104
- Location of start within SEQ ID NO 2636: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2639
- Ceres seq_id 1504105
- Location of start within SEQ ID NO 2636: at 94 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16258
- Merozoite Surface Antigen 2 (MSA-2) family
- Location within SEQ ID NO 2639: from 20 to 98 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 316664

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2640
- Ceres seq_id 1504107

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2641
- Ceres seq_id 1504108
- Location of start within SEQ ID NO 2640: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16259
- Eukaryotic ribosomal protein L18
- Location within SEQ ID NO 2641: from 65 to 155 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16260
- gi No. 1172977
- % Identity 78.4
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2641: from 55 to 155

- Alignment No. 16261
- gi No. 2529670
- % Identity 74.3
- Alignment Length 101
- Location of Alignment in SEQ ID NO 2641: from 56 to 155

- Alignment No. 16262
- gi No. 3021348
- % Identity 75.8
- Alignment Length 99
- Location of Alignment in SEQ ID NO 2641: from 58 to 155

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2642
- Ceres seq_id 1504109
- Location of start within SEQ ID NO 2640: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2643
- Ceres seq_id 1504110
- Location of start within SEQ ID NO 2640: at 164 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16263
- Eukaryotic ribosomal protein L18
- Location within SEQ ID NO 2643: from 11 to 101 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16264
- gi No. 1172977
- % Identity 78.4
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2643: from 1 to 101
- Alignment No. 16265
- gi No. 2529670
- % Identity 74.3
- Alignment Length 101
- Location of Alignment in SEQ ID NO 2643: from 2 to 101
- Alignment No. 16266
- gi No. 3021348
- % Identity 75.8
- Alignment Length 99
- Location of Alignment in SEQ ID NO 2643: from 4 to 101

Maximum Length Sequence corresponding to clone ID 316675

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2644
- Ceres seq_id 1504111

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2645
- Ceres seq_id 1504112
- Location of start within SEQ ID NO 2644: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16267
- gi No. 121928
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2645: from 30 to 40
- Alignment No. 16268
- gi No. 121950
- % Identity 92.3
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2645: from 17 to 42

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2646
- Ceres seq_id 1504113
- Location of start within SEQ ID NO 2644: at 49 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16269
- gi No. 121928
- % Identity 75
- Alignment Length 12

- Location of Alignment in SEQ ID NO 2646: from 14 to 24
- Alignment No. 16270
- gi No. 121950
- % Identity 92.3
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2646: from 1 to 26

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2647
- Ceres seq_id 1504114
- Location of start within SEQ ID NO 2644: at 212 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16271
 - linker histone H1 and H5 family
 - Location within SEQ ID NO 2647: from 1 to 65 aa.
-
- (D) Related Amino Acid Sequences
- Alignment No. 16272
 - gi No. 121906
 - % Identity 81.8
 - Alignment Length 22
 - Location of Alignment in SEQ ID NO 2647: from 1 to 22
-
- Alignment No. 16273
- gi No. 121950
- % Identity 87.6
- Alignment Length 97
- Location of Alignment in SEQ ID NO 2647: from 1 to 73
-
- Alignment No. 16274
- gi No. 121958
- % Identity 70.5
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2647: from 1 to 69
-
- Alignment No. 16275
- gi No. 5230781
- % Identity 70.5
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2647: from 1 to 69
-
- Alignment No. 16276
- gi No. 5230783
- % Identity 70.5
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2647: from 1 to 69
-
- Alignment No. 16277
- gi No. 5230785
- % Identity 76.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 2647: from 1 to 69
-
- Alignment No. 16278
- gi No. 5230788
- % Identity 71.6
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2647: from 1 to 69

- Alignment No. 16279
- gi No. 5230790
- % Identity 70.5
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2647: from 1 to 69

Maximum Length Sequence corresponding to clone ID 316686

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 2648
 - Ceres seq_id 1504119

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 2649
 - Ceres seq_id 1504120
 - Location of start within SEQ ID NO 2648: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 16280
 - gi No. 1085819
 - % Identity 72.7
 - Alignment Length 11
 - Location of Alignment in SEQ ID NO 2649: from 74 to 84

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 2650
 - Ceres seq_id 1504121
 - Location of start within SEQ ID NO 2648: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 16281
 - gi No. 137715
 - % Identity 71.4
 - Alignment Length 15
 - Location of Alignment in SEQ ID NO 2650: from 24 to 37
-
- Alignment No. 16282
 - gi No. 1389772
 - % Identity 76.9
 - Alignment Length 13
 - Location of Alignment in SEQ ID NO 2650: from 57 to 69
-
- Alignment No. 16283
 - gi No. 1914851
 - % Identity 78.6
 - Alignment Length 14
 - Location of Alignment in SEQ ID NO 2650: from 57 to 70
-
- Alignment No. 16284
 - gi No. 2388805
 - % Identity 76.9
 - Alignment Length 13
 - Location of Alignment in SEQ ID NO 2650: from 57 to 69
-
- Alignment No. 16285
 - gi No. 3183204
 - % Identity 76.9
 - Alignment Length 13

- Location of Alignment in SEQ ID NO 2650: from 57 to 69
- Alignment No. 16286
- gi No. 322755
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2650: from 25 to 38
- Alignment No. 16287
- gi No. 333063
- % Identity 71.4
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2650: from 24 to 37
- Alignment No. 16288
- gi No. 465445
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2650: from 57 to 69
- Alignment No. 16289
- gi No. 539029
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2650: from 25 to 38
- Alignment No. 16290
- gi No. 553165
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2650: from 58 to 69
- Alignment No. 16291
- gi No. 553165
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2650: from 57 to 69
- Alignment No. 16292
- gi No. 624076
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2650: from 59 to 69
- Alignment No. 16293
- gi No. 729462
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2650: from 57 to 69
- Alignment No. 16294
- gi No. 93144
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2650: from 57 to 69

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2651
- Ceres seq_id 1504122
- Location of start within SEQ ID NO 2648: at 90 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16295
- gi No. 1389772
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2651: from 28 to 40

- Alignment No. 16296
- gi No. 1914851
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2651: from 28 to 41

- Alignment No. 16297
- gi No. 2388805
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2651: from 28 to 40

- Alignment No. 16298
- gi No. 3183204
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2651: from 28 to 40

- Alignment No. 16299
- gi No. 465445
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2651: from 28 to 40

- Alignment No. 16300
- gi No. 553165
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2651: from 29 to 40

- Alignment No. 16301
- gi No. 553165
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2651: from 28 to 40

- Alignment No. 16302
- gi No. 624076
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2651: from 30 to 40

- Alignment No. 16303
- gi No. 729462
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2651: from 28 to 40

- Alignment No. 16304
- gi No. 93144
- % Identity 76.9
- Alignment Length 13

- Location of Alignment in SEQ ID NO 2651: from 28 to 40

Maximum Length Sequence corresponding to clone ID 316862

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2652
- Ceres seq_id 1504161

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2653
- Ceres seq_id 1504162
- Location of start within SEQ ID NO 2652: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16305
- gi No. 1916974
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2653: from 7 to 21
- Alignment No. 16306
- gi No. 477833
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2653: from 7 to 21

Maximum Length Sequence corresponding to clone ID 316893

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2654
- Ceres seq_id 1504170

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2655
- Ceres seq_id 1504171
- Location of start within SEQ ID NO 2654: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16307
- gi No. 404077
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2655: from 30 to 46

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2656
- Ceres seq_id 1504172
- Location of start within SEQ ID NO 2654: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16308
- gi No. 4972116
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2656: from 26 to 36

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2657
- Ceres seq_id 1504173

- Location of start within SEQ ID NO 2654: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16309
- gi No. 4996642
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2657: from 17 to 27

Maximum Length Sequence corresponding to clone ID 316929

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2658
- Ceres seq_id 1504178

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2659
- Ceres seq_id 1504179
- Location of start within SEQ ID NO 2658: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16310
- GDP dissociation inhibitor
- Location within SEQ ID NO 2659: from 1 to 60 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16311
- gi No. 1550740
- % Identity 73.8
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2659: from 1 to 60

- Alignment No. 16312
- gi No. 1655424
- % Identity 73.8
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2659: from 1 to 60

- Alignment No. 16313
- gi No. 2384758
- % Identity 88.5
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2659: from 1 to 60

- Alignment No. 16314
- gi No. 2384760
- % Identity 85.2
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2659: from 1 to 60

- Alignment No. 16315
- gi No. 2446981
- % Identity 73.8
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2659: from 1 to 60

- Alignment No. 16316
- gi No. 2501850
- % Identity 90.2
- Alignment Length 61

- Location of Alignment in SEQ ID NO 2659: from 1 to 60
- Alignment No. 16317
- gi No. 3175990
- % Identity 88.5
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2659: from 1 to 60

Maximum Length Sequence corresponding to clone ID 316935

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2660
- Ceres seq_id 1504180

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2661
- Ceres seq_id 1504181
- Location of start within SEQ ID NO 2660: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2662
- Ceres seq_id 1504182
- Location of start within SEQ ID NO 2660: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16318
- Globin
- Location within SEQ ID NO 2662: from 44 to 168 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2663
- Ceres seq_id 1504183
- Location of start within SEQ ID NO 2660: at 101 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16319
- Globin
- Location within SEQ ID NO 2663: from 11 to 135 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 316946

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2664
- Ceres seq_id 1504184

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2665
- Ceres seq_id 1504185
- Location of start within SEQ ID NO 2664: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16320
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 2665: from 1 to 134 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16321
- gi No. 1169128
- % Identity 70.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 2665: from 3 to 139

- Alignment No. 16322
- gi No. 2253010
- % Identity 74
- Alignment Length 154
- Location of Alignment in SEQ ID NO 2665: from 1 to 154

- Alignment No. 16323
- gi No. 3063459
- % Identity 86.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2665: from 1 to 145

- Alignment No. 16324
- gi No. 3201541
- % Identity 87.6
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2665: from 1 to 145

- Alignment No. 16325
- gi No. 322577
- % Identity 70.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 2665: from 3 to 139

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2666
- Ceres seq_id 1504186
- Location of start within SEQ ID NO 2664: at 6 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16326
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 2666: from 1 to 133 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16327
- gi No. 1169128
- % Identity 70.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 2666: from 2 to 138

- Alignment No. 16328
- gi No. 2253010
- % Identity 74
- Alignment Length 154
- Location of Alignment in SEQ ID NO 2666: from 1 to 153

- Alignment No. 16329
- gi No. 3063459
- % Identity 86.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2666: from 1 to 144

- Alignment No. 16330
- gi No. 3201541
- % Identity 87.6
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2666: from 1 to 144
- Alignment No. 16331
- gi No. 322577
- % Identity 70.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 2666: from 2 to 138

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2667
- Ceres seq_id 1504187
- Location of start within SEQ ID NO 2664: at 153 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16332
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 2667: from 1 to 84 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16333
- gi No. 1169128
- % Identity 70.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 2667: from 1 to 89
- Alignment No. 16334
- gi No. 2253010
- % Identity 74
- Alignment Length 154
- Location of Alignment in SEQ ID NO 2667: from 1 to 104
- Alignment No. 16335
- gi No. 3063459
- % Identity 86.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2667: from 1 to 95
- Alignment No. 16336
- gi No. 3201541
- % Identity 87.6
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2667: from 1 to 95
- Alignment No. 16337
- gi No. 322577
- % Identity 70.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 2667: from 1 to 89

Maximum Length Sequence corresponding to clone ID 316976

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2668
- Ceres seq_id 1504192

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2669

- Ceres seq_id 1504193
- Location of start within SEQ ID NO 2668: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16338
- gi No. 5042432
- % Identity 70.6
- Alignment Length 68
- Location of Alignment in SEQ ID NO 2669: from 93 to 159

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2670
- Ceres seq_id 1504194
- Location of start within SEQ ID NO 2668: at 87 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16339
- gi No. 5042432
- % Identity 70.6
- Alignment Length 68
- Location of Alignment in SEQ ID NO 2670: from 65 to 131

Maximum Length Sequence corresponding to clone ID 317012

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2671
- Ceres seq_id 1504201

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2672
- Ceres seq_id 1504202
- Location of start within SEQ ID NO 2671: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2673
- Ceres seq_id 1504203
- Location of start within SEQ ID NO 2671: at 369 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16340
- gi No. 2642447
- % Identity 76
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2673: from 23 to 46

- Alignment No. 16341
- gi No. 4335730
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2673: from 22 to 46

- Alignment No. 16342
- gi No. 4544385

- % Identity 76
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2673: from 23 to 46

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2674
- Ceres seq_id 1504204
- Location of start within SEQ ID NO 2671: at 378 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16343
- gi No. 2642447
- % Identity 76
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2674: from 20 to 43

- Alignment No. 16344
- gi No. 4335730
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2674: from 19 to 43

- Alignment No. 16345
- gi No. 4544385
- % Identity 76
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2674: from 20 to 43

Maximum Length Sequence corresponding to clone ID 317151

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2675
- Ceres seq_id 1504231

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2676
- Ceres seq_id 1504232
- Location of start within SEQ ID NO 2675: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16346
- gi No. 1076389
- % Identity 93.8
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2676: from 1 to 144

- Alignment No. 16347
- gi No. 1076390
- % Identity 95.2
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2676: from 1 to 144

- Alignment No. 16348
- gi No. 1076396
- % Identity 92.4
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2676: from 1 to 144

- Alignment No. 16349

- gi No. 1262171
- % Identity 92.4
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2676: from 1 to 144

- Alignment No. 16350
- gi No. 1568511
- % Identity 94.5
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2676: from 1 to 144

- Alignment No. 16351
- gi No. 2129734
- % Identity 92.4
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2676: from 1 to 144

- Alignment No. 16352
- gi No. 2146743
- % Identity 92.4
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2676: from 1 to 144

- Alignment No. 16353
- gi No. 261767
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2676: from 125 to 144

- Alignment No. 16354
- gi No. 3928142
- % Identity 93.8
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2676: from 1 to 144

- Alignment No. 16355
- gi No. 476923
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2676: from 125 to 144

- Alignment No. 16356
- gi No. 543715
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2676: from 1 to 144

- Alignment No. 16357
- gi No. 5679684
- % Identity 93.8
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2676: from 1 to 144

- Alignment No. 16358
- gi No. 683506
- % Identity 91.7
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2676: from 1 to 144

(B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 2677

- Ceres seq_id 1504233
- Location of start within SEQ ID NO 2675: at 44 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16359
 - gi No. 1076389
 - % Identity 93.8
 - Alignment Length 145
 - Location of Alignment in SEQ ID NO 2677: from 1 to 130
- Alignment No. 16360
 - gi No. 1076390
 - % Identity 95.2
 - Alignment Length 145
 - Location of Alignment in SEQ ID NO 2677: from 1 to 130
- Alignment No. 16361
 - gi No. 1076396
 - % Identity 92.4
 - Alignment Length 145
 - Location of Alignment in SEQ ID NO 2677: from 1 to 130
- Alignment No. 16362
 - gi No. 1262171
 - % Identity 92.4
 - Alignment Length 145
 - Location of Alignment in SEQ ID NO 2677: from 1 to 130
- Alignment No. 16363
 - gi No. 1568511
 - % Identity 94.5
 - Alignment Length 145
 - Location of Alignment in SEQ ID NO 2677: from 1 to 130
- Alignment No. 16364
 - gi No. 2129734
 - % Identity 92.4
 - Alignment Length 145
 - Location of Alignment in SEQ ID NO 2677: from 1 to 130
- Alignment No. 16365
 - gi No. 2146743
 - % Identity 92.4
 - Alignment Length 145
 - Location of Alignment in SEQ ID NO 2677: from 1 to 130
- Alignment No. 16366
 - gi No. 261767
 - % Identity 76.2
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2677: from 111 to 130
- Alignment No. 16367
 - gi No. 3928142
 - % Identity 93.8
 - Alignment Length 145
 - Location of Alignment in SEQ ID NO 2677: from 1 to 130
- Alignment No. 16368

- gi No. 476923
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2677: from 111 to 130
- Alignment No. 16369
- gi No. 543715
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2677: from 1 to 130
- Alignment No. 16370
- gi No. 5679684
- % Identity 93.8
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2677: from 1 to 130
- Alignment No. 16371
- gi No. 683506
- % Identity 91.7
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2677: from 1 to 130

Maximum Length Sequence corresponding to clone ID 317164

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2678
- Ceres seq_id 1504239

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2679
- Ceres seq_id 1504240
- Location of start within SEQ ID NO 2678: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16372
- PCI domain
- Location within SEQ ID NO 2679: from 7 to 86 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 317195

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2680
- Ceres seq_id 1504254

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2681
- Ceres seq_id 1504255
- Location of start within SEQ ID NO 2680: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16373
- gi No. 1076294
- % Identity 81.3
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2681: from 92 to 107
- Alignment No. 16374
- gi No. 1279640
- % Identity 71.1

- Alignment Length 45
- Location of Alignment in SEQ ID NO 2681: from 64 to 107
- Alignment No. 16375
- gi No. 1321924
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 2681: from 64 to 107
- Alignment No. 16376
- gi No. 1944132
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 2681: from 64 to 107
- Alignment No. 16377
- gi No. 4972066
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2681: from 89 to 107
- Alignment No. 16378
- gi No. 5679845
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2681: from 89 to 107

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2682
- Ceres seq_id 1504256
- Location of start within SEQ ID NO 2680: at 91 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16379
- gi No. 1279640
- % Identity 81.8
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2682: from 11 to 32
- Alignment No. 16380
- gi No. 1321924
- % Identity 81.8
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2682: from 11 to 32
- Alignment No. 16381
- gi No. 1944132
- % Identity 90.9
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2682: from 11 to 32
- Alignment No. 16382
- gi No. 2894607
- % Identity 81.8
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2682: from 11 to 32
- Alignment No. 16383
- gi No. 4585977

- % Identity 75
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2682: from 9 to 32

- Alignment No. 16384
- gi No. 5091624
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2682: from 13 to 32

- Alignment No. 16385
- gi No. 5091626
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2682: from 13 to 32

- Alignment No. 16386
- gi No. 5306267
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2682: from 13 to 32

- Alignment No. 16387
- gi No. 5679845
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2682: from 11 to 32

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2683
- Ceres seq_id 1504257
- Location of start within SEQ ID NO 2680: at 115 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16388
- gi No. 1279640
- % Identity 81.8
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2683: from 3 to 24

- Alignment No. 16389
- gi No. 1321924
- % Identity 81.8
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2683: from 3 to 24

- Alignment No. 16390
- gi No. 1944132
- % Identity 90.9
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2683: from 3 to 24

- Alignment No. 16391
- gi No. 2894607
- % Identity 81.8
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2683: from 3 to 24

- Alignment No. 16392

- gi No. 4585977
- % Identity 75
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2683: from 1 to 24

- Alignment No. 16393
- gi No. 5091624
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2683: from 5 to 24

- Alignment No. 16394
- gi No. 5091626
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2683: from 5 to 24

- Alignment No. 16395
- gi No. 5306267
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2683: from 5 to 24

- Alignment No. 16396
- gi No. 5679845
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2683: from 3 to 24

Maximum Length Sequence corresponding to clone ID 317200

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2684
- Ceres seq_id 1504258

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2685
- Ceres seq_id 1504259
- Location of start within SEQ ID NO 2684: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2686
- Ceres seq_id 1504260
- Location of start within SEQ ID NO 2684: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2687
- Ceres seq_id 1504261
- Location of start within SEQ ID NO 2684: at 195 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16397
- gi No. 2642154

- % Identity 74.3
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2687: from 1 to 35

Maximum Length Sequence corresponding to clone ID 317211

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2688
- Ceres seq_id 1504270

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2689
- Ceres seq_id 1504271
- Location of start within SEQ ID NO 2688: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2690
- Ceres seq_id 1504272
- Location of start within SEQ ID NO 2688: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16398
- gi No. 1546779
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2690: from 21 to 32

- Alignment No. 16399
- gi No. 2136108
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2690: from 21 to 32

- Alignment No. 16400
- gi No. 3858885
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2690: from 21 to 32

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2691
- Ceres seq_id 1504273
- Location of start within SEQ ID NO 2688: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 317217

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2692
- Ceres seq_id 1504274

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2693
- Ceres seq_id 1504275
- Location of start within SEQ ID NO 2692: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

- Alignment No. 16401
- Metallothionein
- Location within SEQ ID NO 2693: from 37 to 88 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16402
- gi No. 1944205
- % Identity 73
- Alignment Length 37
- Location of Alignment in SEQ ID NO 2693: from 37 to 73
- Alignment No. 16403
- gi No. 225131
- % Identity 70
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2693: from 40 to 59
- Alignment No. 16404
- gi No. 225144
- % Identity 71.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2693: from 39 to 59
- Alignment No. 16405
- gi No. 225146
- % Identity 70
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2693: from 40 to 59
- Alignment No. 16406
- gi No. 2407285
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 2693: from 37 to 73
- Alignment No. 16407
- gi No. 2497897
- % Identity 70.8
- Alignment Length 48
- Location of Alignment in SEQ ID NO 2693: from 37 to 84
- Alignment No. 16408
- gi No. 2497903
- % Identity 76.9
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2693: from 37 to 88
- Alignment No. 16409
- gi No. 2662415
- % Identity 72.5
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2693: from 38 to 88
- Alignment No. 16410
- gi No. 2815246
- % Identity 74.5
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2693: from 37 to 83

- Alignment No. 16411
- gi No. 541943
- % Identity 75
- Alignment Length 48
- Location of Alignment in SEQ ID NO 2693: from 37 to 84

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2694
- Ceres seq_id 1504276
- Location of start within SEQ ID NO 2692: at 110 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16412
- Metallothionein
- Location within SEQ ID NO 2694: from 1 to 52 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16413
- gi No. 1944205
- % Identity 73
- Alignment Length 37
- Location of Alignment in SEQ ID NO 2694: from 1 to 37
- Alignment No. 16414
- gi No. 225131
- % Identity 70
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2694: from 4 to 23
- Alignment No. 16415
- gi No. 225144
- % Identity 71.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2694: from 3 to 23
- Alignment No. 16416
- gi No. 225146
- % Identity 70
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2694: from 4 to 23
- Alignment No. 16417
- gi No. 2407285
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 2694: from 1 to 37
- Alignment No. 16418
- gi No. 2497897
- % Identity 70.8
- Alignment Length 48
- Location of Alignment in SEQ ID NO 2694: from 1 to 48
- Alignment No. 16419
- gi No. 2497903
- % Identity 76.9
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2694: from 1 to 52
- Alignment No. 16420

- gi No. 2662415
- % Identity 72.5
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2694: from 2 to 52
- Alignment No. 16421
- gi No. 2815246
- % Identity 74.5
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2694: from 1 to 47
- Alignment No. 16422
- gi No. 541943
- % Identity 75
- Alignment Length 48
- Location of Alignment in SEQ ID NO 2694: from 1 to 48

Maximum Length Sequence corresponding to clone ID 317283

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2695
- Ceres seq_id 1504277

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2696
- Ceres seq_id 1504278
- Location of start within SEQ ID NO 2695: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16423
- gi No. 2145062
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2696: from 70 to 80

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2697
- Ceres seq_id 1504279
- Location of start within SEQ ID NO 2695: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16424
- Collagen triple helix repeat (20 copies)
- Location within SEQ ID NO 2697: from 7 to 57 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16425
- gi No. 1042189
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2697: from 27 to 38
- Alignment No. 16426
- gi No. 1042189
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2697: from 27 to 38
- Alignment No. 16427
- gi No. 131036

- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2697: from 27 to 38

- Alignment No. 16428
- gi No. 131036
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2697: from 27 to 38

- Alignment No. 16429
- gi No. 1703594
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2697: from 3 to 13

- Alignment No. 16430
- gi No. 2134213
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2697: from 27 to 37

- Alignment No. 16431
- gi No. 2134213
- % Identity 91.7
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2697: from 27 to 38

- Alignment No. 16432
- gi No. 2134213
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2697: from 25 to 38

- Alignment No. 16433
- gi No. 2498095
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2697: from 27 to 38

- Alignment No. 16434
- gi No. 462338
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2697: from 27 to 38

- Alignment No. 16435
- gi No. 462338
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2697: from 27 to 38

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2698
- Ceres seq_id 1504280
- Location of start within SEQ ID NO 2695: at 119 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 16436

- gi No. 2145062
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2698: from 31 to 41

Maximum Length Sequence corresponding to clone ID 317408

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2699
- Ceres seq_id 1504299

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2700
- Ceres seq_id 1504300
- Location of start within SEQ ID NO 2699: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16437
- Chitin recognition protein
- Location within SEQ ID NO 2700: from 42 to 76 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16438
- gi No. 116329
- % Identity 71.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2700: from 26 to 76

- Alignment No. 16439
- gi No. 283037
- % Identity 71.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2700: from 26 to 76

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2701
- Ceres seq_id 1504301
- Location of start within SEQ ID NO 2699: at 34 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16440
- Chitin recognition protein
- Location within SEQ ID NO 2701: from 31 to 65 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16441
- gi No. 116329
- % Identity 71.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2701: from 15 to 65

- Alignment No. 16442
- gi No. 283037
- % Identity 71.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2701: from 15 to 65

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2702
- Ceres seq_id 1504302
- Location of start within SEQ ID NO 2699: at 40 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16443
- Chitin recognition protein
- Location within SEQ ID NO 2702: from 29 to 63 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16444
 - gi No. 116329
 - % Identity 71.2
 - Alignment Length 53
 - Location of Alignment in SEQ ID NO 2702: from 13 to 63
-
- Alignment No. 16445
 - gi No. 283037
 - % Identity 71.2
 - Alignment Length 53
 - Location of Alignment in SEQ ID NO 2702: from 13 to 63

Maximum Length Sequence corresponding to clone ID 317416

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2703
- Ceres seq_id 1504303

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2704
- Ceres seq_id 1504304
- Location of start within SEQ ID NO 2703: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16446
- PCI domain
- Location within SEQ ID NO 2704: from 99 to 149 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2705
- Ceres seq_id 1504305
- Location of start within SEQ ID NO 2703: at 106 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16447
- PCI domain
- Location within SEQ ID NO 2705: from 64 to 114 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2706
- Ceres seq_id 1504306
- Location of start within SEQ ID NO 2703: at 196 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16448
- PCI domain
- Location within SEQ ID NO 2706: from 34 to 84 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 317417

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2707
- Ceres seq_id 1504307

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2708
- Ceres seq_id 1504308
- Location of start within SEQ ID NO 2707: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2709
- Ceres seq_id 1504309
- Location of start within SEQ ID NO 2707: at 83 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16449
- gi No. 133902
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2709: from 8 to 54
- Alignment No. 16450
- gi No. 1350971
- % Identity 88.9
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2709: from 1 to 54
- Alignment No. 16451
- gi No. 1350972
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2709: from 8 to 54
- Alignment No. 16452
- gi No. 2078466
- % Identity 74.5
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2709: from 8 to 54
- Alignment No. 16453
- gi No. 2500501
- % Identity 96.3
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2709: from 1 to 54
- Alignment No. 16454
- gi No. 2979561
- % Identity 92.6
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2709: from 1 to 54
- Alignment No. 16455
- gi No. 3098456

- % Identity 72.7
- Alignment Length 44
- Location of Alignment in SEQ ID NO 2709: from 11 to 54

- Alignment No. 16456
- gi No. 4038471
- % Identity 98.1
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2709: from 1 to 54

- Alignment No. 16457
- gi No. 4193382
- % Identity 92.6
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2709: from 1 to 54

- Alignment No. 16458
- gi No. 4321094
- % Identity 70.8
- Alignment Length 48
- Location of Alignment in SEQ ID NO 2709: from 7 to 54

- Alignment No. 16459
- gi No. 4432748
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2709: from 8 to 54

- Alignment No. 16460
- gi No. 4506711
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2709: from 8 to 54

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2710
- Ceres seq_id 1504310
- Location of start within SEQ ID NO 2707: at 185 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16461
- gi No. 133902
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2710: from 1 to 20

- Alignment No. 16462
- gi No. 1350971
- % Identity 88.9
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2710: from 1 to 20

- Alignment No. 16463
- gi No. 1350972
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2710: from 1 to 20

- Alignment No. 16464

- gi No. 2078466
- % Identity 74.5
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2710: from 1 to 20

- Alignment No. 16465
- gi No. 2500501
- % Identity 96.3
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2710: from 1 to 20

- Alignment No. 16466
- gi No. 2979561
- % Identity 92.6
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2710: from 1 to 20

- Alignment No. 16467
- gi No. 3098456
- % Identity 72.7
- Alignment Length 44
- Location of Alignment in SEQ ID NO 2710: from 1 to 20

- Alignment No. 16468
- gi No. 4038471
- % Identity 98.1
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2710: from 1 to 20

- Alignment No. 16469
- gi No. 4193382
- % Identity 92.6
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2710: from 1 to 20

- Alignment No. 16470
- gi No. 4321094
- % Identity 70.8
- Alignment Length 48
- Location of Alignment in SEQ ID NO 2710: from 1 to 20

- Alignment No. 16471
- gi No. 4432748
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2710: from 1 to 20

- Alignment No. 16472
- gi No. 4506711
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2710: from 1 to 20

Maximum Length Sequence corresponding to clone ID 317418

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2711
- Ceres seq_id 1504311

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2712
- Ceres seq_id 1504312
- Location of start within SEQ ID NO 2711: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2713
- Ceres seq_id 1504313
- Location of start within SEQ ID NO 2711: at 118 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16473
- gi No. 100789
- % Identity 70.5
- Alignment Length 45
- Location of Alignment in SEQ ID NO 2713: from 1 to 43
- Alignment No. 16474
- gi No. 100883
- % Identity 93.2
- Alignment Length 44
- Location of Alignment in SEQ ID NO 2713: from 1 to 43
- Alignment No. 16475
- gi No. 1122313
- % Identity 79.5
- Alignment Length 44
- Location of Alignment in SEQ ID NO 2713: from 1 to 43
- Alignment No. 16476
- gi No. 1122315
- % Identity 75
- Alignment Length 44
- Location of Alignment in SEQ ID NO 2713: from 1 to 43
- Alignment No. 16477
- gi No. 123541
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2713: from 5 to 22
- Alignment No. 16478
- gi No. 123545
- % Identity 70.5
- Alignment Length 45
- Location of Alignment in SEQ ID NO 2713: from 1 to 43
- Alignment No. 16479
- gi No. 123546
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2713: from 5 to 22
- Alignment No. 16480
- gi No. 1536911
- % Identity 75
- Alignment Length 45
- Location of Alignment in SEQ ID NO 2713: from 1 to 43

- Alignment No. 16481
- gi No. 232272
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2713: from 5 to 21

- Alignment No. 16482
- gi No. 445136
- % Identity 70.5
- Alignment Length 45
- Location of Alignment in SEQ ID NO 2713: from 1 to 43

- Alignment No. 16483
- gi No. 507209
- % Identity 76.5
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2713: from 5 to 21

- Alignment No. 16484
- gi No. 81638
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2713: from 5 to 22

Maximum Length Sequence corresponding to clone ID 317460

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2714
- Ceres seq_id 1504333

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2715
- Ceres seq_id 1504334
- Location of start within SEQ ID NO 2714: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16485
- gi No. 4469020
- % Identity 88.9
- Alignment Length 99
- Location of Alignment in SEQ ID NO 2715: from 1 to 99

- Alignment No. 16486
- gi No. 4680205
- % Identity 98.8
- Alignment Length 83
- Location of Alignment in SEQ ID NO 2715: from 1 to 83

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2716
- Ceres seq_id 1504335
- Location of start within SEQ ID NO 2714: at 20 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16487
- gi No. 4469020
- % Identity 88.9
- Alignment Length 99
- Location of Alignment in SEQ ID NO 2716: from 1 to 93

- Alignment No. 16488
- gi No. 4680205
- % Identity 98.8
- Alignment Length 83
- Location of Alignment in SEQ ID NO 2716: from 1 to 77

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2717
- Ceres seq_id 1504336
- Location of start within SEQ ID NO 2714: at 107 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16489
- gi No. 4469020
- % Identity 88.9
- Alignment Length 99
- Location of Alignment in SEQ ID NO 2717: from 1 to 64
- Alignment No. 16490
- gi No. 4680205
- % Identity 98.8
- Alignment Length 83
- Location of Alignment in SEQ ID NO 2717: from 1 to 48

Maximum Length Sequence corresponding to clone ID 317528

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2718
- Ceres seq_id 1504370

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2719
- Ceres seq_id 1504371
- Location of start within SEQ ID NO 2718: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2720
- Ceres seq_id 1504372
- Location of start within SEQ ID NO 2718: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16491
- gi No. 2997589
- % Identity 87.1
- Alignment Length 116
- Location of Alignment in SEQ ID NO 2720: from 1 to 116
- Alignment No. 16492
- gi No. 2997591
- % Identity 84.6
- Alignment Length 117
- Location of Alignment in SEQ ID NO 2720: from 1 to 117
- Alignment No. 16493

- gi No. 2997593
- % Identity 86.3
- Alignment Length 117
- Location of Alignment in SEQ ID NO 2720: from 1 to 117
- Alignment No. 16494
- gi No. 3319374
- % Identity 79.2
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2720: from 93 to 116
- Alignment No. 16495
- gi No. 3367515
- % Identity 82.9
- Alignment Length 117
- Location of Alignment in SEQ ID NO 2720: from 1 to 117

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2721
- Ceres seq_id 1504373
- Location of start within SEQ ID NO 2718: at 23 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16496
- gi No. 2997589
- % Identity 87.1
- Alignment Length 116
- Location of Alignment in SEQ ID NO 2721: from 1 to 109
- Alignment No. 16497
- gi No. 2997591
- % Identity 84.6
- Alignment Length 117
- Location of Alignment in SEQ ID NO 2721: from 1 to 110
- Alignment No. 16498
- gi No. 2997593
- % Identity 86.3
- Alignment Length 117
- Location of Alignment in SEQ ID NO 2721: from 1 to 110
- Alignment No. 16499
- gi No. 3319374
- % Identity 79.2
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2721: from 86 to 109
- Alignment No. 16500
- gi No. 3367515
- % Identity 82.9
- Alignment Length 117
- Location of Alignment in SEQ ID NO 2721: from 1 to 110

Maximum Length Sequence corresponding to clone ID 317547

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2722
- Ceres seq_id 1504374

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2723

- Ceres seq_id 1504375
- Location of start within SEQ ID NO 2722: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16501
- E1-E2 ATPases
- Location within SEQ ID NO 2723: from 2 to 149 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16502
- gi No. 2668492
- % Identity 77.7
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2723: from 2 to 149

- Alignment No. 16503
- gi No. 3549654
- % Identity 77.7
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2723: from 2 to 149

- Alignment No. 16504
- gi No. 4490319
- % Identity 77.7
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2723: from 2 to 149

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2724
- Ceres seq_id 1504376
- Location of start within SEQ ID NO 2722: at 12 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16505
- E1-E2 ATPases
- Location within SEQ ID NO 2724: from 1 to 146 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16506
- gi No. 2668492
- % Identity 77.7
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2724: from 1 to 146

- Alignment No. 16507
- gi No. 3549654
- % Identity 77.7
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2724: from 1 to 146

- Alignment No. 16508
- gi No. 4490319
- % Identity 77.7
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2724: from 1 to 146

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2725
- Ceres seq_id 1504377

- Location of start within SEQ ID NO 2722: at 42 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16509
- E1-E2 ATPases
- Location within SEQ ID NO 2725: from 1 to 136 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16510
- gi No. 2666492
- % Identity 77.7
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2725: from 1 to 136
- Alignment No. 16511
- gi No. 3549654
- % Identity 77.7
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2725: from 1 to 136
- Alignment No. 16512
- gi No. 4490319
- % Identity 77.7
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2725: from 1 to 136

Maximum Length Sequence corresponding to clone ID 317650

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2726
- Ceres seq_id 1504382

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2727
- Ceres seq_id 1504383
- Location of start within SEQ ID NO 2726: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16513
- gi No. 100490
- % Identity 91.7
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2727: from 36 to 47
- Alignment No. 16514
- gi No. 100490
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16515
- gi No. 100490
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16516
- gi No. 100490
- % Identity 85.7
- Alignment Length 21

- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16517
- gi No. 100524
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16518
- gi No. 100524
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16519
- gi No. 100524
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16520
- gi No. 100524
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16521
- gi No. 100524
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16522
- gi No. 100524
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16523
- gi No. 100525
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16524
- gi No. 100525
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16525
- gi No. 100525
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16526
- gi No. 100525
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16527
- gi No. 100525
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16528
- gi No. 100598
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16529
- gi No. 100599
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16530
- gi No. 100812
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16531
- gi No. 100934
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16532
- gi No. 100934
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16533
- gi No. 100934
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16534
- gi No. 100934
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16535
- gi No. 100934
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16536
- gi No. 100934
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16537
- gi No. 100934
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16538
- gi No. 102062
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16539
- gi No. 102278
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16540
- gi No. 102278
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16541
- gi No. 102278
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16542
- gi No. 102278
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16543
- gi No. 102278
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16544
- gi No. 102278
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16545
- gi No. 102278
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16546
- gi No. 102279
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16547

- gi No. 102279
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16548
- gi No. 102279
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16549
- gi No. 102280
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16550
- gi No. 102280
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16551
- gi No. 102280
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16552
- gi No. 102280
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16553
- gi No. 102280
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16554
- gi No. 102281
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16555
- gi No. 102281
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16556
- gi No. 102281
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16557
- gi No. 102281

- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16558
- gi No. 102281
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16559
- gi No. 102389
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16560
- gi No. 103436
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16561
- gi No. 1044940
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16562
- gi No. 104829
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16563
- gi No. 104829
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16564
- gi No. 104829
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16565
- gi No. 1050930
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16566
- gi No. 1050930
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16567
- gi No. 10673
- % Identity 81

- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16568
- gi No. 1070590
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16569
- gi No. 1070590
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16570
- gi No. 1070590
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16571
- gi No. 1070591
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16572
- gi No. 1070591
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16573
- gi No. 1070591
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16574
- gi No. 1070591
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16575
- gi No. 1070591
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16576
- gi No. 1070591
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16577
- gi No. 1070591
- % Identity 85.7
- Alignment Length 21

- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16578
- gi No. 1070591
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16579
- gi No. 1070591
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16580
- gi No. 1076678
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16581
- gi No. 1076708
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16582
- gi No. 1076708
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16583
- gi No. 1076708
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16584
- gi No. 1076708
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16585
- gi No. 1078777
- % Identity 70.4
- Alignment Length 27
- Location of Alignment in SEQ ID NO 2727: from 27 to 51
- Alignment No. 16586
- gi No. 1078813
- % Identity 71.4
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2727: from 27 to 52
- Alignment No. 16587
- gi No. 1078813
- % Identity 71.4
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2727: from 27 to 52

- Alignment No. 16588
- gi No. 1078813
- % Identity 71.4
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2727: from 27 to 52

- Alignment No. 16589
- gi No. 1083758
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16590
- gi No. 1083758
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16591
- gi No. 1083758
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16592
- gi No. 1083758
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16593
- gi No. 1083758
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16594
- gi No. 1083758
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16595
- gi No. 1083758
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16596
- gi No. 1083758
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16597
- gi No. 1083758
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16598
- gi No. 1083758
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16599
- gi No. 1101011
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16600
- gi No. 1101011
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16601
- gi No. 1101011
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16602
- gi No. 1101011
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16603
- gi No. 1101011
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16604
- gi No. 1101011
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16605
- gi No. 1101011
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16606
- gi No. 1101011
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16607
- gi No. 1101011
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16608

- gi No. 1101011
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16609
- gi No. 1101013
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2727: from 33 to 47

- Alignment No. 16610
- gi No. 1101015
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2727: from 33 to 47

- Alignment No. 16611
- gi No. 1101021
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2727: from 33 to 47

- Alignment No. 16612
- gi No. 1101021
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16613
- gi No. 1107481
- % Identity 85
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2727: from 27 to 46

- Alignment No. 16614
- gi No. 1107481
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16615
- gi No. 1107481
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16616
- gi No. 1143188
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16617
- gi No. 1143188
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16618
- gi No. 1143188

- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16619
- gi No. 1167510
- % Identity 80
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2727: from 27 to 46

- Alignment No. 16620
- gi No. 1167510
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16621
- gi No. 1174859
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16622
- gi No. 1174860
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16623
- gi No. 1174861
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16624
- gi No. 1184755
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16625
- gi No. 1197093
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16626
- gi No. 1197093
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16627
- gi No. 1197093
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16628
- gi No. 1197093
- % Identity 85.7

- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16629
- gi No. 1304128
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16630
- gi No. 1304128
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16631
- gi No. 1304128
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16632
- gi No. 1304128
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16633
- gi No. 1304128
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16634
- gi No. 1304128
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16635
- gi No. 1304128
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16636
- gi No. 1304128
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16637
- gi No. 1304357
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16638
- gi No. 1321735
- % Identity 85.7
- Alignment Length 21

- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16639
- gi No. 1321735
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16640
- gi No. 1326022
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16641
- gi No. 1326022
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16642
- gi No. 1332579
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16643
- gi No. 1332579
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16644
- gi No. 1332579
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16645
- gi No. 1332579
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16646
- gi No. 1332579
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16647
- gi No. 1332579
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16648
- gi No. 1332579
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16649
- gi No. 1332579
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16650
- gi No. 1332579
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16651
- gi No. 1332579
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16652
- gi No. 1351348
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16653
- gi No. 1351349
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16654
- gi No. 1353755
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16655
- gi No. 1353757
- % Identity 80
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2727: from 28 to 47

- Alignment No. 16656
- gi No. 1353757
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16657
- gi No. 1362008
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16658
- gi No. 1362008
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16659
- gi No. 1362008
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16660
- gi No. 1362008
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16661
- gi No. 1362009
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16662
- gi No. 1362010
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16663
- gi No. 1362010
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16664
- gi No. 1362010
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16665
- gi No. 1362012
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16666
- gi No. 1362012
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16667
- gi No. 136665
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16668
- gi No. 136666
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16669

- gi No. 136667
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16670
- gi No. 136668
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16671
- gi No. 136669
- % Identity 71.4
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2727: from 27 to 52

- Alignment No. 16672
- gi No. 136670
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16673
- gi No. 136671
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16674
- gi No. 136672
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16675
- gi No. 136673
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16676
- gi No. 136674
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16677
- gi No. 136675
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16678
- gi No. 136676
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16679
- gi No. 136677

- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16680
- gi No. 136678
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16681
- gi No. 1421797
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16682
- gi No. 156480
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16683
- gi No. 158759
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16684
- gi No. 158763
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16685
- gi No. 158765
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16686
- gi No. 158767
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16687
- gi No. 158769
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16688
- gi No. 158771
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16689
- gi No. 161281
- % Identity 85.7

- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16690
- gi No. 163575
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16691
- gi No. 163575
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16692
- gi No. 166336
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16693
- gi No. 166336
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16694
- gi No. 166336
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16695
- gi No. 166336
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16696
- gi No. 166336
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16697
- gi No. 166336
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16698
- gi No. 1666175
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16699
- gi No. 1675359
- % Identity 81
- Alignment Length 21

- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16700
- gi No. 167935
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16701
- gi No. 167935
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16702
- gi No. 167935
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16703
- gi No. 167935
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16704
- gi No. 167935
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16705
- gi No. 167941
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 28 to 48
- Alignment No. 16706
- gi No. 167945
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16707
- gi No. 167945
- % Identity 81.8
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16708
- gi No. 167945
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16709
- gi No. 167947
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16710
- gi No. 167947
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16711
- gi No. 167947
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16712
- gi No. 167947
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16713
- gi No. 167947
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16714
- gi No. 167947
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16715
- gi No. 167947
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16716
- gi No. 167949
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16717
- gi No. 167949
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16718
- gi No. 167949
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16719
- gi No. 167949
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16720
- gi No. 167949
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 16721
- gi No. 1684855
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16722
- gi No. 1684855
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16723
- gi No. 1684855
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16724
- gi No. 1684855
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16725
- gi No. 1684857
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16726
- gi No. 1684857
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16727
- gi No. 170352
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16728
- gi No. 170352
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16729
- gi No. 170352
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16730

- gi No. 170352
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16731
- gi No. 170352
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16732
- gi No. 170352
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16733
- gi No. 170354
- % Identity 88.2
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2727: from 31 to 47

- Alignment No. 16734
- gi No. 170354
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16735
- gi No. 170354
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16736
- gi No. 170354
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16737
- gi No. 170354
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16738
- gi No. 1762374
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16739
- gi No. 1762935
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16740
- gi No. 1763015

- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16741
- gi No. 1771780
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16742
- gi No. 1778712
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16743
- gi No. 1778712
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16744
- gi No. 1778712
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16745
- gi No. 1778712
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16746
- gi No. 1778712
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16747
- gi No. 1800281
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16748
- gi No. 1800281
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16749
- gi No. 1800281
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16750
- gi No. 1800281
- % Identity 85.7

- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16751
- gi No. 1800281
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16752
- gi No. 1805696
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2727: from 34 to 47

- Alignment No. 16753
- gi No. 1805696
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16754
- gi No. 1839584
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16755
- gi No. 1841849
- % Identity 87.5
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2727: from 27 to 42

- Alignment No. 16756
- gi No. 208558
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16757
- gi No. 208560
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16758
- gi No. 208562
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16759
- gi No. 208564
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16760
- gi No. 208566
- % Identity 81
- Alignment Length 21

- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16761
 - gi No. 208568
 - % Identity 85.7
 - Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16762
 - gi No. 208891
 - % Identity 80
 - Alignment Length 20
- Location of Alignment in SEQ ID NO 2727: from 27 to 46
- Alignment No. 16763
 - gi No. 208891
 - % Identity 85.7
 - Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16764
 - gi No. 209603
 - % Identity 85.7
 - Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16765
 - gi No. 2118958
 - % Identity 85.7
 - Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16766
 - gi No. 2118958
 - % Identity 85.7
 - Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16767
 - gi No. 2118958
 - % Identity 85.7
 - Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16768
 - gi No. 2118958
 - % Identity 85.7
 - Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16769
 - gi No. 2118958
 - % Identity 85.7
 - Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16770
 - gi No. 2118959
 - % Identity 81.8
 - Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16771
- gi No. 2118959
- % Identity 77.3
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16772
- gi No. 2118959
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16773
- gi No. 2118960
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16774
- gi No. 2118960
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16775
- gi No. 2118961
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16776
- gi No. 2118961
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16777
- gi No. 2118962
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16778
- gi No. 2118962
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16779
- gi No. 2118964
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16780
- gi No. 2118964
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16781
- gi No. 2118964
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16782
- gi No. 2118965
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16783
- gi No. 2118965
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16784
- gi No. 2118965
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16785
- gi No. 2129452
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16786
- gi No. 2129452
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16787
- gi No. 2129452
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16788
- gi No. 2129452
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16789
- gi No. 2129452
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16790
- gi No. 2129452
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16791

- gi No. 2133278
- % Identity 75
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2727: from 27 to 52

- Alignment No. 16792
- gi No. 2133549
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16793
- gi No. 2144011
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16794
- gi No. 2144275
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16795
- gi No. 2144734
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16796
- gi No. 2144734
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16797
- gi No. 2144734
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16798
- gi No. 2144734
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16799
- gi No. 2149467
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16800
- gi No. 2209091
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16801
- gi No. 2209091

- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16802
- gi No. 223061
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16803
- gi No. 224321
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16804
- gi No. 224321
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16805
- gi No. 225317
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16806
- gi No. 225319
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16807
- gi No. 225320
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16808
- gi No. 2281952
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2727: from 34 to 47

- Alignment No. 16809
- gi No. 2281954
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2727: from 34 to 47

- Alignment No. 16810
- gi No. 2281955
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2727: from 34 to 47

- Alignment No. 16811
- gi No. 2281959
- % Identity 73.3

- Alignment Length 15
- Location of Alignment in SEQ ID NO 2727: from 33 to 47

- Alignment No. 16812
- gi No. 2330875
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16813
- gi No. 2408009
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16814
- gi No. 2437825
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16815
- gi No. 2437825
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16816
- gi No. 2437825
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16817
- gi No. 2437825
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16818
- gi No. 247308
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16819
- gi No. 248865
- % Identity 80
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2727: from 27 to 46

- Alignment No. 16820
- gi No. 2558539
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16821
- gi No. 2627129
- % Identity 85.7
- Alignment Length 21

- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16822
- gi No. 2627129
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16823
- gi No. 2627129
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16824
- gi No. 2627129
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16825
- gi No. 2627129
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16826
- gi No. 2627129
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16827
- gi No. 2627129
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16828
- gi No. 2627129
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16829
- gi No. 2627131
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16830
- gi No. 2627131
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16831
- gi No. 2627131
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16832
- gi No. 2627131
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16833
- gi No. 2627131
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16834
- gi No. 2627131
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16835
- gi No. 2627131
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16836
- gi No. 2627131
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16837
- gi No. 2627131
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16838
- gi No. 2627131
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16839
- gi No. 2627131
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16840
- gi No. 2627133
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16841
- gi No. 2627133
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16842
- gi No. 2627133
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16843
- gi No. 2627133
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16844
- gi No. 2627133
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16845
- gi No. 2627133
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16846
- gi No. 2627133
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16847
- gi No. 2627133
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16848
- gi No. 2627133
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16849
- gi No. 2627133
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16850
- gi No. 2627133
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16851
- gi No. 2627133
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16852

- gi No. 2627133
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16853
- gi No. 2641213
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16854
- gi No. 2641213
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16855
- gi No. 2654141
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16856
- gi No. 2654141
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16857
- gi No. 2654141
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16858
- gi No. 2654141
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16859
- gi No. 2654141
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16860
- gi No. 2707837
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16861
- gi No. 2707837
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16862
- gi No. 2707837

- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16863
- gi No. 2707837
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16864
- gi No. 2739333
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16865
- gi No. 2739333
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16866
- gi No. 2739333
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16867
- gi No. 2739333
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16868
- gi No. 2760345
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16869
- gi No. 2760345
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16870
- gi No. 2760345
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16871
- gi No. 2760345
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16872
- gi No. 2760347
- % Identity 85.7

- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16873
- gi No. 2760347
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16874
- gi No. 2760347
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16875
- gi No. 2760347
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16876
- gi No. 2760347
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16877
- gi No. 2760347
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16878
- gi No. 2760349
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16879
- gi No. 2760349
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16880
- gi No. 2760349
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16881
- gi No. 2760349
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16882
- gi No. 2760349
- % Identity 85.7
- Alignment Length 21

- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16883
- gi No. 279635
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16884
- gi No. 279636
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16885
- gi No. 280386
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16886
- gi No. 281276
- % Identity 80
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2727: from 27 to 46
- Alignment No. 16887
- gi No. 283496
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16888
- gi No. 283496
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16889
- gi No. 283496
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16890
- gi No. 283496
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16891
- gi No. 283496
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16892
- gi No. 2894304
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16893
- gi No. 2894304
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16894
- gi No. 2894304
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16895
- gi No. 2894304
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16896
- gi No. 2894306
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16897
- gi No. 2894308
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16898
- gi No. 2894308
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16899
- gi No. 2894308
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16900
- gi No. 2894308
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16901
- gi No. 2894308
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16902
- gi No. 2995949
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16903
- gi No. 3047314
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16904
- gi No. 3047316
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16905
- gi No. 3047318
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16906
- gi No. 3047318
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16907
- gi No. 3047318
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16908
- gi No. 3047318
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16909
- gi No. 3047318
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16910
- gi No. 3091264
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16911
- gi No. 3091264
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16912
- gi No. 3091264
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16913

- gi No. 3091264
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16914
- gi No. 3126967
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16915
- gi No. 3126967
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16916
- gi No. 3126967
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16917
- gi No. 3126967
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16918
- gi No. 3126967
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16919
- gi No. 3126967
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16920
- gi No. 3152950
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16921
- gi No. 3158372
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16922
- gi No. 3158372
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16923
- gi No. 320608

- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16924
- gi No. 320608
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16925
- gi No. 320608
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16926
- gi No. 320608
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16927
- gi No. 322750
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16928
- gi No. 323071
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16929
- gi No. 323157
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16930
- gi No. 323157
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16931
- gi No. 323157
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16932
- gi No. 323157
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16933
- gi No. 323157
- % Identity 85.7

- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16934
- gi No. 323157
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16935
- gi No. 323208
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16936
- gi No. 323230
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16937
- gi No. 3265058
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16938
- gi No. 3319208
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16939
- gi No. 3335355
- % Identity 85
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2727: from 27 to 46

- Alignment No. 16940
- gi No. 3335355
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16941
- gi No. 3335355
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16942
- gi No. 3335355
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16943
- gi No. 340062
- % Identity 88.2
- Alignment Length 17

- Location of Alignment in SEQ ID NO 2727: from 31 to 47
- Alignment No. 16944
 - gi No. 3452083
 - % Identity 85.7
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16945
 - gi No. 348148
 - % Identity 85.7
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16946
 - gi No. 3603456
 - % Identity 85.7
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16947
 - gi No. 3603456
 - % Identity 85.7
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16948
 - gi No. 3603456
 - % Identity 75
 - Alignment Length 28
 - Location of Alignment in SEQ ID NO 2727: from 27 to 52
- Alignment No. 16949
 - gi No. 3687425
 - % Identity 85.7
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16950
 - gi No. 3687425
 - % Identity 85.7
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16951
 - gi No. 3687425
 - % Identity 85.7
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16952
 - gi No. 3738185
 - % Identity 85.7
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16953
 - gi No. 3738185
 - % Identity 85.7
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16954
- gi No. 3738185
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16955
- gi No. 3738185
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16956
- gi No. 3738185
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16957
- gi No. 3776536
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16958
- gi No. 3776536
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16959
- gi No. 3776536
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16960
- gi No. 3776536
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16961
- gi No. 3776536
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16962
- gi No. 3776536
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16963
- gi No. 3776536
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16964
- gi No. 3776536
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16965
- gi No. 3789940
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16966
- gi No. 3789940
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16967
- gi No. 3789940
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16968
- gi No. 3789940
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16969
- gi No. 3789942
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16970
- gi No. 3789942
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16971
- gi No. 3789942
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16972
- gi No. 3789942
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16973
- gi No. 3789942
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16974

- gi No. 385076
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16975
- gi No. 3882081
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16976
- gi No. 3882081
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16977
- gi No. 3882081
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16978
- gi No. 3885463
- % Identity 83.3
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2727: from 30 to 47

- Alignment No. 16979
- gi No. 3892189
- % Identity 70.4
- Alignment Length 27
- Location of Alignment in SEQ ID NO 2727: from 27 to 51

- Alignment No. 16980
- gi No. 402242
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16981
- gi No. 4105408
- % Identity 91.7
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2727: from 36 to 47

- Alignment No. 16982
- gi No. 4105408
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16983
- gi No. 4105408
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16984
- gi No. 4105408

- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16985
- gi No. 4115337
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16986
- gi No. 4115337
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16987
- gi No. 4115337
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16988
- gi No. 4115337
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16989
- gi No. 4115337
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16990
- gi No. 4115337
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16991
- gi No. 4150898
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16992
- gi No. 4150898
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16993
- gi No. 4150898
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16994
- gi No. 4150898
- % Identity 85.7

- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16995
- gi No. 4150912
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16996
- gi No. 4150912
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16997
- gi No. 4150912
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16998
- gi No. 4150912
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16999
- gi No. 4150912
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17000
- gi No. 4150914
- % Identity 86.7
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2727: from 33 to 47
- Alignment No. 17001
- gi No. 4150914
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17002
- gi No. 4151082
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17003
- gi No. 418854
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17004
- gi No. 418854
- % Identity 85.7
- Alignment Length 21

- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17005
- gi No. 418854
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17006
- gi No. 418854
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17007
- gi No. 418854
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17008
- gi No. 418854
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17009
- gi No. 421735
- % Identity 88.9
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2727: from 27 to 44
- Alignment No. 17010
- gi No. 421867
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17011
- gi No. 421929
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17012
- gi No. 421929
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17013
- gi No. 421929
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17014
- gi No. 421929
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17015
- gi No. 421929
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17016
- gi No. 421929
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17017
- gi No. 421929
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17018
- gi No. 422248
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17019
- gi No. 422248
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17020
- gi No. 422248
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17021
- gi No. 422248
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17022
- gi No. 422248
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17023
- gi No. 422269
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17024
- gi No. 422270
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17025
- gi No. 422271
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17026
- gi No. 433970
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17027
- gi No. 433970
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17028
- gi No. 433970
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17029
- gi No. 433970
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17030
- gi No. 433970
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17031
- gi No. 444791
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17032
- gi No. 444791
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17033
- gi No. 444791
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17034
- gi No. 444791
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17035

- gi No. 4506713
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17036
- gi No. 4507761
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17037
- gi No. 456779
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17038
- gi No. 4586594
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17039
- gi No. 4586594
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17040
- gi No. 4587232
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17041
- gi No. 4587234
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17042
- gi No. 4587236
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17043
- gi No. 4587236
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17044
- gi No. 4587236
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17045
- gi No. 4587236

- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17046
- gi No. 4587236
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17047
- gi No. 4587236
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17048
- gi No. 4587236
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17049
- gi No. 4587236
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17050
- gi No. 4587236
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17051
- gi No. 4587236
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17052
- gi No. 4587236
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17053
- gi No. 4587236
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17054
- gi No. 4589760
- % Identity 75
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2727: from 27 to 52

- Alignment No. 17055
- gi No. 4589760
- % Identity 75

- Alignment Length 28
- Location of Alignment in SEQ ID NO 2727: from 27 to 52

- Alignment No. 17056
- gi No. 463363
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2727: from 27 to 46

- Alignment No. 17057
- gi No. 463369
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17058
- gi No. 463373
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17059
- gi No. 463375
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17060
- gi No. 464989
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17061
- gi No. 464990
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17062
- gi No. 468272
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17063
- gi No. 4737
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17064
- gi No. 477630
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17065
- gi No. 477815
- % Identity 81
- Alignment Length 21

- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17066
 - gi No. 478811
 - % Identity 85.7
 - Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17067
 - gi No. 478811
 - % Identity 85.7
 - Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17068
 - gi No. 478811
 - % Identity 85.7
 - Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17069
 - gi No. 478811
 - % Identity 85.7
 - Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17070
 - gi No. 4809266
 - % Identity 85.7
 - Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17071
 - gi No. 4809266
 - % Identity 85.7
 - Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17072
 - gi No. 4809266
 - % Identity 85.7
 - Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17073
 - gi No. 4809266
 - % Identity 85.7
 - Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17074
 - gi No. 4809266
 - % Identity 85.7
 - Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17075
 - gi No. 481477
 - % Identity 85.7
 - Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17076
- gi No. 481477
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17077
- gi No. 481477
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17078
- gi No. 481477
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17079
- gi No. 481477
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17080
- gi No. 481477
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17081
- gi No. 485427
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17082
- gi No. 485518
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17083
- gi No. 49586
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17084
- gi No. 49586
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17085
- gi No. 49586
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17086
- gi No. 510473
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17087
- gi No. 510473
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17088
- gi No. 510473
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17089
- gi No. 510473
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17090
- gi No. 510473
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17091
- gi No. 510473
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17092
- gi No. 510473
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17093
- gi No. 510473
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17094
- gi No. 510473
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17095
- gi No. 510476
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17096

- gi No. 5107695
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17097
- gi No. 539404
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17098
- gi No. 539935
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17099
- gi No. 539935
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17100
- gi No. 539935
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17101
- gi No. 539935
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17102
- gi No. 541546
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17103
- gi No. 541546
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17104
- gi No. 541546
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17105
- gi No. 541546
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17106
- gi No. 541546

- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17107
- gi No. 541953
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17108
- gi No. 541954
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17109
- gi No. 5441519
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17110
- gi No. 552237
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17111
- gi No. 5523967
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17112
- gi No. 5523969
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17113
- gi No. 5523969
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17114
- gi No. 5523971
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17115
- gi No. 5523973
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17116
- gi No. 5523975
- % Identity 85.7

- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17117
- gi No. 5523977
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17118
- gi No. 5523979
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17119
- gi No. 5523979
- % Identity 72.4
- Alignment Length 29
- Location of Alignment in SEQ ID NO 2727: from 19 to 47

- Alignment No. 17120
- gi No. 5523981
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17121
- gi No. 5523985
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17122
- gi No. 5523987
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17123
- gi No. 5531273
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17124
- gi No. 5531273
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17125
- gi No. 5531273
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17126
- gi No. 5531273
- % Identity 85.7
- Alignment Length 21

- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17127
- gi No. 5531273
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17128
- gi No. 5531278
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17129
- gi No. 5531281
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17130
- gi No. 554564
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17131
- gi No. 567767
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17132
- gi No. 567767
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17133
- gi No. 571519
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17134
- gi No. 571519
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17135
- gi No. 571519
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17136
- gi No. 571519
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17137
- gi No. 571519
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17138
- gi No. 571519
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17139
- gi No. 576773
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17140
- gi No. 576773
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17141
- gi No. 576773
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17142
- gi No. 576773
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17143
- gi No. 576773
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17144
- gi No. 576775
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17145
- gi No. 578545
- % Identity 77.3
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 17146
- gi No. 578545
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 17147
- gi No. 578546
- % Identity 81.8
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 17148
- gi No. 578546
- % Identity 77.3
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 17149
- gi No. 578546
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 17150
- gi No. 578549
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 17151
- gi No. 578549
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 17152
- gi No. 578551
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2727: from 29 to 47
- Alignment No. 17153
- gi No. 578551
- % Identity 77.3
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 17154
- gi No. 600539
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17155
- gi No. 602076
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17156
- gi No. 602076
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17157

- gi No. 602076
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17158
- gi No. 602076
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17159
- gi No. 602076
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17160
- gi No. 625174
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17161
- gi No. 625174
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17162
- gi No. 625509
- % Identity 85
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2727: from 27 to 46

- Alignment No. 17163
- gi No. 625509
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17164
- gi No. 625509
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17165
- gi No. 625509
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17166
- gi No. 630455
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17167
- gi No. 630479

- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17168
- gi No. 630479
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17169
- gi No. 630479
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17170
- gi No. 630479
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17171
- gi No. 630479
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17172
- gi No. 630479
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17173
- gi No. 70636
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17174
- gi No. 70636
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17175
- gi No. 70636
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17176
- gi No. 70637
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17177
- gi No. 70639
- % Identity 85.7

- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17178
- gi No. 70639
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17179
- gi No. 70639
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17180
- gi No. 70639
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17181
- gi No. 70640
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17182
- gi No. 70642
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17183
- gi No. 70642
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17184
- gi No. 70642
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17185
- gi No. 70642
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17186
- gi No. 70642
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17187
- gi No. 70643
- % Identity 85.7
- Alignment Length 21

- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17188
 - gi No. 70644
 - % Identity 85.7
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17189
 - gi No. 70644
 - % Identity 85.7
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17190
 - gi No. 70644
 - % Identity 85.7
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17191
 - gi No. 70644
 - % Identity 85.7
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17192
 - gi No. 70644
 - % Identity 85.7
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17193
 - gi No. 70645
 - % Identity 85.7
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17194
 - gi No. 70645
 - % Identity 85.7
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17195
 - gi No. 70645
 - % Identity 85.7
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17196
 - gi No. 70645
 - % Identity 85.7
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17197
 - gi No. 70645
 - % Identity 85.7
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17198
- gi No. 70646
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17199
- gi No. 70647
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17200
- gi No. 70647
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17201
- gi No. 70647
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17202
- gi No. 70648
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17203
- gi No. 70650
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2727: from 27 to 44
- Alignment No. 17204
- gi No. 70653
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 17205
- gi No. 70654
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17206
- gi No. 70657
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17207
- gi No. 70658
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17208
- gi No. 70659
- % Identity 87.5
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2727: from 32 to 47
- Alignment No. 17209
- gi No. 70660
- % Identity 81.8
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 17210
- gi No. 726391
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17211
- gi No. 726391
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17212
- gi No. 726391
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17213
- gi No. 726391
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17214
- gi No. 726391
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17215
- gi No. 726391
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17216
- gi No. 726391
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17217
- gi No. 726391
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17218

- gi No. 726391
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17219
- gi No. 726391
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17220
- gi No. 726391
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17221
- gi No. 82040
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17222
- gi No. 82040
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17223
- gi No. 82040
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17224
- gi No. 82040
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17225
- gi No. 82284
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17226
- gi No. 82287
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17227
- gi No. 82426
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17228
- gi No. 82426

- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17229
- gi No. 82512
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17230
- gi No. 82512
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17231
- gi No. 82733
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17232
- gi No. 82734
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17233
- gi No. 82734
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17234
- gi No. 82734
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17235
- gi No. 83594
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17236
- gi No. 83596
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17237
- gi No. 83596
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17238
- gi No. 83596
- % Identity 85.7

- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17239
- gi No. 83596
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17240
- gi No. 83596
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17241
- gi No. 84151
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 17242
- gi No. 84151
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 17243
- gi No. 84151
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 17244
- gi No. 84152
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 17245
- gi No. 84152
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 17246
- gi No. 84152
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 17247
- gi No. 84152
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 17248
- gi No. 84152
- % Identity 86.4
- Alignment Length 22

- Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 17249
 - gi No. 84337
 - % Identity 83.3
 - Alignment Length 18
 - Location of Alignment in SEQ ID NO 2727: from 27 to 44
- Alignment No. 17250
 - gi No. 84337
 - % Identity 81
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17251
 - gi No. 84478
 - % Identity 85.7
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17252
 - gi No. 84478
 - % Identity 85.7
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17253
 - gi No. 84478
 - % Identity 85.7
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17254
 - gi No. 84478
 - % Identity 85.7
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17255
 - gi No. 84478
 - % Identity 85.7
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17256
 - gi No. 84478
 - % Identity 85.7
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17257
 - gi No. 84478
 - % Identity 85.7
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17258
 - gi No. 84478
 - % Identity 85.7
 - Alignment Length 21
 - Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17259
- gi No. 84478
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17260
- gi No. 84478
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17261
- gi No. 84478
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17262
- gi No. 84834
- % Identity 87.5
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2727: from 27 to 42

- Alignment No. 17263
- gi No. 84834
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17264
- gi No. 84834
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17265
- gi No. 85106
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17266
- gi No. 85106
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17267
- gi No. 85106
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17268
- gi No. 870794
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17269
- gi No. 870794
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17270
- gi No. 89311
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17271
- gi No. 89311
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17272
- gi No. 89311
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17273
- gi No. 899115
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17274
- gi No. 899115
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17275
- gi No. 899608
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17276
- gi No. 899608
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17277
- gi No. 899608
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17278
- gi No. 899608
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17279

- gi No. 899608
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17280
- gi No. 902525
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17281
- gi No. 902584
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17282
- gi No. 902584
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17283
- gi No. 902584
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17284
- gi No. 902584
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17285
- gi No. 902584
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17286
- gi No. 902584
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17287
- gi No. 902584
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17288
- gi No. 902586
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17289
- gi No. 902586

- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17290
- gi No. 902586
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17291
- gi No. 902586
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17292
- gi No. 902586
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17293
- gi No. 91870
- % Identity 80
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2727: from 27 to 46

- Alignment No. 17294
- gi No. 91870
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17295
- gi No. 91871
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17296
- gi No. 940395
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17297
- gi No. 940395
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17298
- gi No. 940395
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17299
- gi No. 940395
- % Identity 85.7

- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17300
- gi No. 940395
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17301
- gi No. 940395
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17302
- gi No. 940395
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17303
- gi No. 940395
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17304
- gi No. 967985
- % Identity 88.9
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2727: from 27 to 44

- Alignment No. 17305
- gi No. 99771
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17306
- gi No. 99772
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17307
- gi No. 99975
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2728
- Ceres seq_id 1504384
- Location of start within SEQ ID NO 2726: at 166 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 17308
- Ubiquitin family
- Location within SEQ ID NO 2728: from 1 to 49 aa.

(D) Related Amino Acid Sequences

- Alignment No. 17309
 - gi No. 100490
 - % Identity 81.1
 - Alignment Length 53
 - Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17310
 - gi No. 100490
 - % Identity 81.1
 - Alignment Length 53
 - Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17311
 - gi No. 100490
 - % Identity 81.1
 - Alignment Length 53
 - Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17312
 - gi No. 100490
 - % Identity 81.1
 - Alignment Length 53
 - Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17313
 - gi No. 100524
 - % Identity 81.1
 - Alignment Length 53
 - Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17314
 - gi No. 100524
 - % Identity 81.1
 - Alignment Length 53
 - Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17315
 - gi No. 100524
 - % Identity 81.1
 - Alignment Length 53
 - Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17316
 - gi No. 100524
 - % Identity 81.1
 - Alignment Length 53
 - Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17317
 - gi No. 100524
 - % Identity 81.1
 - Alignment Length 53
 - Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17318
 - gi No. 100524
 - % Identity 79.6
 - Alignment Length 54
 - Location of Alignment in SEQ ID NO 2728: from 1 to 50

- Alignment No. 17319
- gi No. 100525
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17320
- gi No. 100525
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17321
- gi No. 100525
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17322
- gi No. 100525
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17323
- gi No. 100598
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
- Alignment No. 17324
- gi No. 100599
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
- Alignment No. 17325
- gi No. 100812
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17326
- gi No. 100934
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17327
- gi No. 100934
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17328
- gi No. 100934
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17329
- gi No. 100934
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17330
- gi No. 100934
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17331
- gi No. 100934
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17332
- gi No. 100934
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17333
- gi No. 100981
- % Identity 76.7
- Alignment Length 43
- Location of Alignment in SEQ ID NO 2728: from 9 to 51

- Alignment No. 17334
- gi No. 102062
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17335
- gi No. 102278
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17336
- gi No. 102278
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17337
- gi No. 102278
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17338
- gi No. 102278
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17339

- gi No. 102278
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17340
- gi No. 102278
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17341
- gi No. 102278
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17342
- gi No. 102279
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17343
- gi No. 102279
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17344
- gi No. 102279
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17345
- gi No. 102280
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17346
- gi No. 102280
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17347
- gi No. 102280
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17348
- gi No. 102280
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17349
- gi No. 102280

- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17350
- gi No. 102281
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17351
- gi No. 102281
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17352
- gi No. 102281
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17353
- gi No. 102281
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17354
- gi No. 102281
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17355
- gi No. 102389
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17356
- gi No. 103436
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17357
- gi No. 1044940
- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
- Alignment No. 17358
- gi No. 104829
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17359
- gi No. 104829
- % Identity 79.2

- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17360
- gi No. 104829
- % Identity 77.8
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50

- Alignment No. 17361
- gi No. 1050930
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17362
- gi No. 10673
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17363
- gi No. 1070590
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17364
- gi No. 1070590
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17365
- gi No. 1070590
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17366
- gi No. 1070591
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17367
- gi No. 1070591
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17368
- gi No. 1070591
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17369
- gi No. 1070591
- % Identity 79.2
- Alignment Length 53

- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17370
- gi No. 1070591
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17371
- gi No. 1070591
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17372
- gi No. 1070591
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17373
- gi No. 1070591
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17374
- gi No. 1070591
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17375
- gi No. 1076678
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
- Alignment No. 17376
- gi No. 1076708
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17377
- gi No. 1076708
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17378
- gi No. 1076708
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17379
- gi No. 1076708
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17380
- gi No. 1078777
- % Identity 73.1
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17381
- gi No. 1078813
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17382
- gi No. 1078813
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17383
- gi No. 1078813
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17384
- gi No. 1083758
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17385
- gi No. 1083758
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17386
- gi No. 1083758
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17387
- gi No. 1083758
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17388
- gi No. 1083758
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17389
- gi No. 1083758
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17390
- gi No. 1083758
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17391
- gi No. 1083758
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17392
- gi No. 1083758
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17393
- gi No. 1083758
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17394
- gi No. 1101011
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17395
- gi No. 1101011
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17396
- gi No. 1101011
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17397
- gi No. 1101011
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17398
- gi No. 1101011
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17399
- gi No. 1101011
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17400

- gi No. 1101011
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17401
- gi No. 1101011
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17402
- gi No. 1101011
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17403
- gi No. 1101013
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2728: from 1 to 18

- Alignment No. 17404
- gi No. 1101021
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17405
- gi No. 1101023
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2728: from 10 to 49

- Alignment No. 17406
- gi No. 1107481
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17407
- gi No. 1107481
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17408
- gi No. 1143188
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17409
- gi No. 1143188
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17410
- gi No. 1143188

- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17411
- gi No. 1167510
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17412
- gi No. 1174859
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17413
- gi No. 1174860
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17414
- gi No. 1174861
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17415
- gi No. 1184755
- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 17416
- gi No. 1197093
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17417
- gi No. 1197093
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17418
- gi No. 1197093
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17419
- gi No. 1197093
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17420
- gi No. 1304128
- % Identity 79.2

- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17421
- gi No. 1304128
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17422
- gi No. 1304128
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17423
- gi No. 1304128
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17424
- gi No. 1304128
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17425
- gi No. 1304128
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17426
- gi No. 1304128
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17427
- gi No. 1304128
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17428
- gi No. 1321735
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2728: from 1 to 36

- Alignment No. 17429
- gi No. 1321735
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17430
- gi No. 1326021
- % Identity 79.4
- Alignment Length 34

- Location of Alignment in SEQ ID NO 2728: from 16 to 49
- Alignment No. 17431
- gi No. 1326022
- % Identity 76.9
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2728: from 11 to 49
- Alignment No. 17432
- gi No. 1326022
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17433
- gi No. 1326022
- % Identity 74.1
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50
- Alignment No. 17434
- gi No. 1332579
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17435
- gi No. 1332579
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17436
- gi No. 1332579
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17437
- gi No. 1332579
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17438
- gi No. 1332579
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17439
- gi No. 1332579
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17440
- gi No. 1332579
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17441
- gi No. 1332579
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17442
- gi No. 1332579
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17443
- gi No. 1332579
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17444
- gi No. 1351348
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17445
- gi No. 1351349
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17446
- gi No. 1353755
- % Identity 80.6
- Alignment Length 36
- Location of Alignment in SEQ ID NO 2728: from 14 to 49
- Alignment No. 17447
- gi No. 1353755
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17448
- gi No. 1353757
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2728: from 1 to 18
- Alignment No. 17449
- gi No. 1353757
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17450
- gi No. 1362008
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17451
- gi No. 1362008
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17452
- gi No. 1362008
- % Identity 73.6
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17453
- gi No. 1362008
- % Identity 77.8
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50

- Alignment No. 17454
- gi No. 1362009
- % Identity 79.6
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50

- Alignment No. 17455
- gi No. 1362010
- % Identity 83
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17456
- gi No. 1362010
- % Identity 71.7
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17457
- gi No. 1362010
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17458
- gi No. 1362012
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17459
- gi No. 1362012
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17460
- gi No. 136665
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17461

- gi No. 136666
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17462
- gi No. 136667
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17463
- gi No. 136668
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17464
- gi No. 136669
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17465
- gi No. 136670
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17466
- gi No. 136671
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17467
- gi No. 136672
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17468
- gi No. 136673
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17469
- gi No. 136674
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17470
- gi No. 136675
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17471
- gi No. 136676

- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17472
- gi No. 136677
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17473
- gi No. 136678
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17474
- gi No. 1421797
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17475
- gi No. 1480012
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17476
- gi No. 158759
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17477
- gi No. 158763
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17478
- gi No. 158765
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17479
- gi No. 158767
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17480
- gi No. 158769
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17481
- gi No. 158771
- % Identity 77.4

- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17482
- gi No. 161281
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17483
- gi No. 163575
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17484
- gi No. 163575
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17485
- gi No. 166336
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17486
- gi No. 166336
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17487
- gi No. 166336
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17488
- gi No. 166336
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17489
- gi No. 166336
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17490
- gi No. 166336
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17491
- gi No. 1666175
- % Identity 81.1
- Alignment Length 53

- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17492
- gi No. 1675359
- % Identity 76.5
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2728: from 1 to 13

- Alignment No. 17493
- gi No. 167935
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17494
- gi No. 167935
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17495
- gi No. 167935
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17496
- gi No. 167935
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17497
- gi No. 167935
- % Identity 75.9
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50

- Alignment No. 17498
- gi No. 167941
- % Identity 77.2
- Alignment Length 57
- Location of Alignment in SEQ ID NO 2728: from 1 to 53

- Alignment No. 17499
- gi No. 167945
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17500
- gi No. 167945
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17501
- gi No. 167945
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17502
- gi No. 167947
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17503
- gi No. 167947
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17504
- gi No. 167947
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17505
- gi No. 167947
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17506
- gi No. 167947
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17507
- gi No. 167947
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17508
- gi No. 167947
- % Identity 77.8
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50

- Alignment No. 17509
- gi No. 167949
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17510
- gi No. 167949
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17511
- gi No. 167949
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17512
- gi No. 167949
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17513
- gi No. 167949
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17514
- gi No. 1684855
- % Identity 81.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 2728: from 17 to 49
- Alignment No. 17515
- gi No. 1684855
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17516
- gi No. 1684855
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17517
- gi No. 1684855
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17518
- gi No. 1684855
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17519
- gi No. 1684857
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17520
- gi No. 1684857
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17521
- gi No. 1684857
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17522

- gi No. 170352
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17523
- gi No. 170352
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17524
- gi No. 170352
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17525
- gi No. 170352
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17526
- gi No. 170352
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17527
- gi No. 170352
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17528
- gi No. 170354
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17529
- gi No. 170354
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17530
- gi No. 170354
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17531
- gi No. 170354
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17532
- gi No. 170354

- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17533
- gi No. 1762374
- % Identity 77.1
- Alignment Length 48
- Location of Alignment in SEQ ID NO 2728: from 1 to 44

- Alignment No. 17534
- gi No. 1762935
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17535
- gi No. 1763015
- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 17536
- gi No. 1771780
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 17537
- gi No. 1778712
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17538
- gi No. 1778712
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17539
- gi No. 1778712
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17540
- gi No. 1778712
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17541
- gi No. 1778712
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17542
- gi No. 1800281
- % Identity 81.1

- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17543
- gi No. 1800281
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17544
- gi No. 1800281
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17545
- gi No. 1800281
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17546
- gi No. 1800281
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17547
- gi No. 1805696
- % Identity 76.2
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2728: from 1 to 38

- Alignment No. 17548
- gi No. 1805696
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17549
- gi No. 1841849
- % Identity 81
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2728: from 8 to 49

- Alignment No. 17550
- gi No. 208558
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17551
- gi No. 208560
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17552
- gi No. 208562
- % Identity 79.2
- Alignment Length 53

- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17553
- gi No. 208564
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17554
- gi No. 208566
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17555
- gi No. 208568
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17556
- gi No. 208891
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17557
- gi No. 209603
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17558
- gi No. 2118958
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17559
- gi No. 2118958
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17560
- gi No. 2118958
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17561
- gi No. 2118958
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17562
- gi No. 2118958
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17563
 - gi No. 2118959
 - % Identity 73.6
 - Alignment Length 53
 - Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17564
 - gi No. 2118960
 - % Identity 79.2
 - Alignment Length 53
 - Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17565
 - gi No. 2118960
 - % Identity 79.2
 - Alignment Length 53
 - Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17566
 - gi No. 2118961
 - % Identity 79.2
 - Alignment Length 53
 - Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17567
 - gi No. 2118961
 - % Identity 77.4
 - Alignment Length 53
 - Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17568
 - gi No. 2118962
 - % Identity 79.2
 - Alignment Length 53
 - Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17569
 - gi No. 2118962
 - % Identity 79.2
 - Alignment Length 53
 - Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17570
 - gi No. 2118963
 - % Identity 76.2
 - Alignment Length 42
 - Location of Alignment in SEQ ID NO 2728: from 8 to 49
- Alignment No. 17571
 - gi No. 2118963
 - % Identity 75
 - Alignment Length 52
 - Location of Alignment in SEQ ID NO 2728: from 1 to 48
- Alignment No. 17572
 - gi No. 2118964
 - % Identity 78
 - Alignment Length 41
 - Location of Alignment in SEQ ID NO 2728: from 9 to 49

- Alignment No. 17573
- gi No. 2118964
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17574
- gi No. 2118964
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17575
- gi No. 2118964
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17576
- gi No. 2118965
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17577
- gi No. 2118965
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17578
- gi No. 2118965
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17579
- gi No. 2129452
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17580
- gi No. 2129452
- % Identity 73.6
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17581
- gi No. 2129452
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17582
- gi No. 2129452
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17583

- gi No. 2129452
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17584
- gi No. 2129452
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17585
- gi No. 2133278
- % Identity 70.9
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 17586
- gi No. 2133549
- % Identity 79.2
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2728: from 1 to 20

- Alignment No. 17587
- gi No. 2133549
- % Identity 79.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 2728: from 16 to 49

- Alignment No. 17588
- gi No. 2133549
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17589
- gi No. 2144011
- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 17590
- gi No. 2144275
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17591
- gi No. 2144734
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17592
- gi No. 2144734
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17593
- gi No. 2144734

- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17594
- gi No. 2144734
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17595
- gi No. 2149467
- % Identity 75
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17596
- gi No. 2209091
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17597
- gi No. 2209091
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17598
- gi No. 223061
- % Identity 76.9
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2728: from 1 to 48
- Alignment No. 17599
- gi No. 224321
- % Identity 76.9
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2728: from 11 to 49
- Alignment No. 17600
- gi No. 224321
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17601
- gi No. 224321
- % Identity 75.9
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50
- Alignment No. 17602
- gi No. 225317
- % Identity 78.3
- Alignment Length 46
- Location of Alignment in SEQ ID NO 2728: from 1 to 42
- Alignment No. 17603
- gi No. 225319
- % Identity 78.3

- Alignment Length 46
- Location of Alignment in SEQ ID NO 2728: from 1 to 42

- Alignment No. 17604
- gi No. 225320
- % Identity 76.1
- Alignment Length 46
- Location of Alignment in SEQ ID NO 2728: from 1 to 42

- Alignment No. 17605
- gi No. 2281952
- % Identity 78.3
- Alignment Length 46
- Location of Alignment in SEQ ID NO 2728: from 1 to 42

- Alignment No. 17606
- gi No. 2281954
- % Identity 78.3
- Alignment Length 46
- Location of Alignment in SEQ ID NO 2728: from 1 to 42

- Alignment No. 17607
- gi No. 2281955
- % Identity 75
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2728: from 1 to 24

- Alignment No. 17608
- gi No. 2281959
- % Identity 72.9
- Alignment Length 48
- Location of Alignment in SEQ ID NO 2728: from 1 to 44

- Alignment No. 17609
- gi No. 2330875
- % Identity 74.5
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 17610
- gi No. 2408009
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17611
- gi No. 2437825
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17612
- gi No. 2437825
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17613
- gi No. 2437825
- % Identity 77.4
- Alignment Length 53

- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17614
- gi No. 2437825
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17615
- gi No. 2558539
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17616
- gi No. 2627129
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17617
- gi No. 2627129
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17618
- gi No. 2627129
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17619
- gi No. 2627129
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17620
- gi No. 2627129
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17621
- gi No. 2627129
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17622
- gi No. 2627129
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17623
- gi No. 2627129
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17624
- gi No. 2627131
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17625
- gi No. 2627131
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17626
- gi No. 2627131
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17627
- gi No. 2627131
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17628
- gi No. 2627131
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17629
- gi No. 2627131
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17630
- gi No. 2627131
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17631
- gi No. 2627131
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17632
- gi No. 2627131
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17633
- gi No. 2627131
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17634
- gi No. 2627131
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17635
- gi No. 2627133
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17636
- gi No. 2627133
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17637
- gi No. 2627133
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17638
- gi No. 2627133
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17639
- gi No. 2627133
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17640
- gi No. 2627133
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17641
- gi No. 2627133
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17642
- gi No. 2627133
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17643
- gi No. 2627133
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17644

- gi No. 2627133
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17645
- gi No. 2627133
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17646
- gi No. 2627133
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17647
- gi No. 2627133
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17648
- gi No. 2641213
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2728: from 1 to 36

- Alignment No. 17649
- gi No. 2641213
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17650
- gi No. 2654141
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17651
- gi No. 2654141
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17652
- gi No. 2654141
- % Identity 71.7
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17653
- gi No. 2654141
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17654
- gi No. 2654141

- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17655
- gi No. 2707837
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17656
- gi No. 2707837
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17657
- gi No. 2707837
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17658
- gi No. 2707837
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17659
- gi No. 2739333
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17660
- gi No. 2739333
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17661
- gi No. 2739333
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17662
- gi No. 2739333
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17663
- gi No. 2760345
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17664
- gi No. 2760345
- % Identity 81.1

- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17665
- gi No. 2760345
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17666
- gi No. 2760345
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17667
- gi No. 2760347
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17668
- gi No. 2760347
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17669
- gi No. 2760347
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17670
- gi No. 2760347
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17671
- gi No. 2760347
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17672
- gi No. 2760347
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17673
- gi No. 2760349
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17674
- gi No. 2760349
- % Identity 81.1
- Alignment Length 53

- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17675
- gi No. 2760349
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17676
- gi No. 2760349
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17677
- gi No. 2760349
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17678
- gi No. 279635
- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
- Alignment No. 17679
- gi No. 279636
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
- Alignment No. 17680
- gi No. 280386
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17681
- gi No. 283496
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17682
- gi No. 283496
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17683
- gi No. 283496
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17684
- gi No. 283496
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17685
- gi No. 283496
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17686
- gi No. 2894304
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17687
- gi No. 2894304
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17688
- gi No. 2894304
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17689
- gi No. 2894304
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17690
- gi No. 2894306
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 17691
- gi No. 2894308
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17692
- gi No. 2894308
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17693
- gi No. 2894308
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17694
- gi No. 2894308
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17695
- gi No. 2894308
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17696
- gi No. 2995277
- % Identity 83.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 2728: from 20 to 49

- Alignment No. 17697
- gi No. 2995949
- % Identity 82.9
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2728: from 15 to 49

- Alignment No. 17698
- gi No. 2995949
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17699
- gi No. 3047314
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17700
- gi No. 3047316
- % Identity 74.5
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 17701
- gi No. 3047318
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17702
- gi No. 3047318
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17703
- gi No. 3047318
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17704
- gi No. 3047318
- % Identity 73.6
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17705

- gi No. 3047318
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17706
- gi No. 3091264
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17707
- gi No. 3091264
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17708
- gi No. 3091264
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17709
- gi No. 3091264
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17710
- gi No. 3126967
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17711
- gi No. 3126967
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17712
- gi No. 3126967
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17713
- gi No. 3126967
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17714
- gi No. 3126967
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17715
- gi No. 3126967

- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17716
- gi No. 3152950
- % Identity 74.5
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
- Alignment No. 17717
- gi No. 3158372
- % Identity 84.6
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2728: from 24 to 49
- Alignment No. 17718
- gi No. 3158372
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17719
- gi No. 320608
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17720
- gi No. 320608
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17721
- gi No. 320608
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17722
- gi No. 320608
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17723
- gi No. 322750
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17724
- gi No. 323157
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17725
- gi No. 323157
- % Identity 79.2

- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17726
- gi No. 323157
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17727
- gi No. 323157
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17728
- gi No. 323157
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17729
- gi No. 323157
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17730
- gi No. 323208
- % Identity 78.7
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2728: from 3 to 49

- Alignment No. 17731
- gi No. 323208
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17732
- gi No. 323230
- % Identity 76.9
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2728: from 1 to 48

- Alignment No. 17733
- gi No. 3265058
- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 17734
- gi No. 3319208
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 17735
- gi No. 3335355
- % Identity 86.4
- Alignment Length 22

- Location of Alignment in SEQ ID NO 2728: from 29 to 50
- Alignment No. 17736
- gi No. 3335355
- % Identity 77.8
- Alignment Length 27
- Location of Alignment in SEQ ID NO 2728: from 1 to 23
- Alignment No. 17737
- gi No. 3335355
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17738
- gi No. 3335355
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17739
- gi No. 3335355
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17740
- gi No. 340062
- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
- Alignment No. 17741
- gi No. 3452083
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17742
- gi No. 348148
- % Identity 79.2
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2728: from 1 to 20
- Alignment No. 17743
- gi No. 348148
- % Identity 79.4
- Alignment Length 34
- Location of Alignment in SEQ ID NO 2728: from 16 to 49
- Alignment No. 17744
- gi No. 348149
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17745
- gi No. 3603456
- % Identity 83.8
- Alignment Length 37
- Location of Alignment in SEQ ID NO 2728: from 13 to 49

- Alignment No. 17746
- gi No. 3603456
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17747
- gi No. 3603456
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17748
- gi No. 3603456
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17749
- gi No. 3687425
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17750
- gi No. 3687425
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17751
- gi No. 3687425
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17752
- gi No. 3738185
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17753
- gi No. 3738185
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17754
- gi No. 3738185
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17755
- gi No. 3738185
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17756
- gi No. 3738185
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17757
- gi No. 3776536
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17758
- gi No. 3776536
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17759
- gi No. 3776536
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17760
- gi No. 3776536
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17761
- gi No. 3776536
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17762
- gi No. 3776536
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17763
- gi No. 3776536
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17764
- gi No. 3776536
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17765
- gi No. 3789940
- % Identity 75
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17766

- gi No. 3789940
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17767
- gi No. 3789940
- % Identity 73.6
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17768
- gi No. 3789940
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17769
- gi No. 3789942
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17770
- gi No. 3789942
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17771
- gi No. 3789942
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17772
- gi No. 3789942
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17773
- gi No. 3789942
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17774
- gi No. 385076
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17775
- gi No. 3882081
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17776
- gi No. 3882081

- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17777
- gi No. 3882081
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17778
- gi No. 3885463
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17779
- gi No. 3892189
- % Identity 78.8
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17780
- gi No. 402242
- % Identity 74.5
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
- Alignment No. 17781
- gi No. 4049712
- % Identity 73.6
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17782
- gi No. 4102845
- % Identity 73.1
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17783
- gi No. 4105408
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17784
- gi No. 4105408
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17785
- gi No. 4105408
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17786
- gi No. 4105408
- % Identity 79.2

- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17787
- gi No. 4115337
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17788
- gi No. 4115337
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17789
- gi No. 4115337
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17790
- gi No. 4115337
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17791
- gi No. 4115337
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17792
- gi No. 4115337
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17793
- gi No. 4150898
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17794
- gi No. 4150898
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17795
- gi No. 4150898
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17796
- gi No. 4150898
- % Identity 79.2
- Alignment Length 53

- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17797
- gi No. 4150912
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17798
- gi No. 4150912
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17799
- gi No. 4150912
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17800
- gi No. 4150912
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17801
- gi No. 4150912
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17802
- gi No. 4150914
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17803
- gi No. 4150914
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17804
- gi No. 4151082
- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
- Alignment No. 17805
- gi No. 418854
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17806
- gi No. 418854
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17807
- gi No. 418854
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17808
- gi No. 418854
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17809
- gi No. 418854
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17810
- gi No. 418854
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17811
- gi No. 421867
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17812
- gi No. 421929
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17813
- gi No. 421929
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17814
- gi No. 421929
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17815
- gi No. 421929
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17816
- gi No. 421929
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17817
- gi No. 421929
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17818
- gi No. 421929
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17819
- gi No. 422248
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17820
- gi No. 422248
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17821
- gi No. 422248
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17822
- gi No. 422248
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17823
- gi No. 422248
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17824
- gi No. 422269
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17825
- gi No. 422270
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17826
- gi No. 422271
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17827

- gi No. 433970
- % Identity 81
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2728: from 8 to 49

- Alignment No. 17828
- gi No. 433970
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17829
- gi No. 433970
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17830
- gi No. 433970
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17831
- gi No. 433970
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17832
- gi No. 433970
- % Identity 75.9
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50

- Alignment No. 17833
- gi No. 444791
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17834
- gi No. 444791
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17835
- gi No. 444791
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17836
- gi No. 444791
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17837
- gi No. 4506713

- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 17838
- gi No. 4507761
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17839
- gi No. 4510359
- % Identity 81
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2728: from 8 to 49

- Alignment No. 17840
- gi No. 4586594
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17841
- gi No. 4587232
- % Identity 77.8
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50

- Alignment No. 17842
- gi No. 4587234
- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 17843
- gi No. 4587236
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17844
- gi No. 4587236
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17845
- gi No. 4587236
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17846
- gi No. 4587236
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17847
- gi No. 4587236
- % Identity 79.2

- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17848
- gi No. 4587236
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17849
- gi No. 4587236
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17850
- gi No. 4587236
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17851
- gi No. 4587236
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17852
- gi No. 4587236
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17853
- gi No. 4587236
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17854
- gi No. 4587236
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17855
- gi No. 4589760
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17856
- gi No. 4589760
- % Identity 75.9
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50
- Alignment No. 17857
- gi No. 463363
- % Identity 73.6
- Alignment Length 53

- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17858
- gi No. 463365
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17859
- gi No. 463367
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17860
- gi No. 463369
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17861
- gi No. 463371
- % Identity 83
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17862
- gi No. 463373
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17863
- gi No. 463375
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17864
- gi No. 464990
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17865
- gi No. 468272
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17866
- gi No. 4737
- % Identity 73.9
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2728: from 1 to 19
- Alignment No. 17867
- gi No. 477630
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17868
- gi No. 477630
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17869
- gi No. 477815
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17870
- gi No. 478811
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17871
- gi No. 478811
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17872
- gi No. 478811
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17873
- gi No. 478811
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17874
- gi No. 4809266
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17875
- gi No. 4809266
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17876
- gi No. 4809266
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17877
- gi No. 4809266
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17878
- gi No. 4809266
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17879
- gi No. 481477
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17880
- gi No. 481477
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17881
- gi No. 481477
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17882
- gi No. 481477
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17883
- gi No. 481477
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17884
- gi No. 481477
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17885
- gi No. 485427
- % Identity 76.1
- Alignment Length 46
- Location of Alignment in SEQ ID NO 2728: from 1 to 42

- Alignment No. 17886
- gi No. 485518
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17887
- gi No. 49586
- % Identity 77.1
- Alignment Length 48
- Location of Alignment in SEQ ID NO 2728: from 1 to 44

- Alignment No. 17888

- gi No. 49586
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17889
- gi No. 49586
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17890
- gi No. 510473
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17891
- gi No. 510473
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17892
- gi No. 510473
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17893
- gi No. 510473
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17894
- gi No. 510473
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17895
- gi No. 510473
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17896
- gi No. 510473
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17897
- gi No. 510473
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17898
- gi No. 510473

- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 17899
- gi No. 510476
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17900
- gi No. 5107695
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17901
- gi No. 539404
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17902
- gi No. 539935
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17903
- gi No. 539935
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17904
- gi No. 539935
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17905
- gi No. 539935
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17906
- gi No. 541546
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17907
- gi No. 541546
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17908
- gi No. 541546
- % Identity 81.1

- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17909
- gi No. 541546
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17910
- gi No. 541546
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17911
- gi No. 541953
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 17912
- gi No. 541954
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 17913
- gi No. 542395
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17914
- gi No. 5441519
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17915
- gi No. 552237
- % Identity 78.6
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2728: from 8 to 49

- Alignment No. 17916
- gi No. 5523967
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17917
- gi No. 5523969
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17918
- gi No. 5523969
- % Identity 77.4
- Alignment Length 53

- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17919
- gi No. 5523971
- % Identity 78.9
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2728: from 31 to 49
- Alignment No. 17920
- gi No. 5523971
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17921
- gi No. 5523973
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17922
- gi No. 5523975
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17923
- gi No. 5523977
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17924
- gi No. 5523979
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17925
- gi No. 5523979
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17926
- gi No. 5523981
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17927
- gi No. 5523983
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17928
- gi No. 5523985
- % Identity 77.1
- Alignment Length 48
- Location of Alignment in SEQ ID NO 2728: from 2 to 49

- Alignment No. 17929
- gi No. 5523985
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17930
- gi No. 5523987
- % Identity 79.2
- Alignment Length 48
- Location of Alignment in SEQ ID NO 2728: from 2 to 49

- Alignment No. 17931
- gi No. 5523987
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17932
- gi No. 5531273
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17933
- gi No. 5531273
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17934
- gi No. 5531273
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17935
- gi No. 5531273
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17936
- gi No. 5531273
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17937
- gi No. 5531278
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17938
- gi No. 5531281
- % Identity 74.5
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 17939
- gi No. 554564
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17940
- gi No. 567767
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17941
- gi No. 567767
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17942
- gi No. 571519
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17943
- gi No. 571519
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17944
- gi No. 571519
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17945
- gi No. 571519
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17946
- gi No. 571519
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17947
- gi No. 571519
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17948
- gi No. 576773
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17949

- gi No. 576773
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17950
- gi No. 576773
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17951
- gi No. 576773
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17952
- gi No. 576773
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17953
- gi No. 576775
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17954
- gi No. 578545
- % Identity 75
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2728: from 1 to 48

- Alignment No. 17955
- gi No. 578545
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17956
- gi No. 578545
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17957
- gi No. 578545
- % Identity 73.6
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17958
- gi No. 578545
- % Identity 71.7
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17959
- gi No. 578546

- % Identity 73.1
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2728: from 1 to 48
- Alignment No. 17960
- gi No. 578546
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17961
- gi No. 578546
- % Identity 73.6
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17962
- gi No. 578549
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17963
- gi No. 578549
- % Identity 71.7
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17964
- gi No. 578551
- % Identity 75
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17965
- gi No. 578551
- % Identity 75
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2728: from 1 to 48
- Alignment No. 17966
- gi No. 578551
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17967
- gi No. 578551
- % Identity 73.6
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17968
- gi No. 578551
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17969
- gi No. 600539
- % Identity 76.4

- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 17970
- gi No. 602076
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17971
- gi No. 602076
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17972
- gi No. 602076
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17973
- gi No. 602076
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17974
- gi No. 625174
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17975
- gi No. 625174
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17976
- gi No. 625174
- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 17977
- gi No. 625509
- % Identity 85
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2728: from 30 to 49

- Alignment No. 17978
- gi No. 625509
- % Identity 77.8
- Alignment Length 27
- Location of Alignment in SEQ ID NO 2728: from 1 to 23

- Alignment No. 17979
- gi No. 625509
- % Identity 81.1
- Alignment Length 53

- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17980
- gi No. 625509
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17981
- gi No. 625509
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17982
- gi No. 630455
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17983
- gi No. 630479
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17984
- gi No. 630479
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17985
- gi No. 630479
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17986
- gi No. 630479
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17987
- gi No. 630479
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17988
- gi No. 630479
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17989
- gi No. 70636
- % Identity 78.3
- Alignment Length 46
- Location of Alignment in SEQ ID NO 2728: from 1 to 42

- Alignment No. 17990
- gi No. 70636
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17991
- gi No. 70636
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17992
- gi No. 70637
- % Identity 78.4
- Alignment Length 51
- Location of Alignment in SEQ ID NO 2728: from 1 to 47

- Alignment No. 17993
- gi No. 70639
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17994
- gi No. 70639
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17995
- gi No. 70639
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17996
- gi No. 70639
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17997
- gi No. 70640
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17998
- gi No. 70642
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17999
- gi No. 70642
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18000
- gi No. 70642
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18001
- gi No. 70642
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18002
- gi No. 70642
- % Identity 81.5
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50
- Alignment No. 18003
- gi No. 70643
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18004
- gi No. 70644
- % Identity 83.3
- Alignment Length 30
- Location of Alignment in SEQ ID NO 2728: from 20 to 49
- Alignment No. 18005
- gi No. 70644
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18006
- gi No. 70644
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18007
- gi No. 70644
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18008
- gi No. 70644
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18009
- gi No. 70644
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18010

- gi No. 70645
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18011
- gi No. 70645
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18012
- gi No. 70645
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18013
- gi No. 70645
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18014
- gi No. 70645
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18015
- gi No. 70646
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18016
- gi No. 70647
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18017
- gi No. 70647
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18018
- gi No. 70647
- % Identity 75.9
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50

- Alignment No. 18019
- gi No. 70648
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18020
- gi No. 70653

- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18021
- gi No. 70654
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18022
- gi No. 70657
- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
- Alignment No. 18023
- gi No. 70658
- % Identity 74.5
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
- Alignment No. 18024
- gi No. 70659
- % Identity 74.5
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
- Alignment No. 18025
- gi No. 70660
- % Identity 77.2
- Alignment Length 57
- Location of Alignment in SEQ ID NO 2728: from 1 to 53
- Alignment No. 18026
- gi No. 726391
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18027
- gi No. 726391
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18028
- gi No. 726391
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18029
- gi No. 726391
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18030
- gi No. 726391
- % Identity 79.2

- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18031
- gi No. 726391
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18032
- gi No. 726391
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18033
- gi No. 726391
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18034
- gi No. 726391
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18035
- gi No. 726391
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18036
- gi No. 726391
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18037
- gi No. 82040
- % Identity 81
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2728: from 8 to 49

- Alignment No. 18038
- gi No. 82040
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18039
- gi No. 82040
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18040
- gi No. 82040
- % Identity 81.1
- Alignment Length 53

- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18041
- gi No. 82284
- % Identity 78.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 2728: from 1 to 29
- Alignment No. 18042
- gi No. 82286
- % Identity 85
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2728: from 30 to 49
- Alignment No. 18043
- gi No. 82287
- % Identity 79.2
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2728: from 1 to 20
- Alignment No. 18044
- gi No. 82288
- % Identity 80.5
- Alignment Length 41
- Location of Alignment in SEQ ID NO 2728: from 9 to 49
- Alignment No. 18045
- gi No. 82426
- % Identity 83.3
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2728: from 32 to 49
- Alignment No. 18046
- gi No. 82426
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18047
- gi No. 82426
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18048
- gi No. 82512
- % Identity 83.8
- Alignment Length 37
- Location of Alignment in SEQ ID NO 2728: from 13 to 49
- Alignment No. 18049
- gi No. 82512
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18050
- gi No. 82512
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18051
- gi No. 825728
- % Identity 78.9
- Alignment Length 38
- Location of Alignment in SEQ ID NO 2728: from 12 to 49

- Alignment No. 18052
- gi No. 82733
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 18053
- gi No. 82734
- % Identity 81.4
- Alignment Length 43
- Location of Alignment in SEQ ID NO 2728: from 7 to 49

- Alignment No. 18054
- gi No. 82734
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18055
- gi No. 82734
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18056
- gi No. 82734
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18057
- gi No. 829173
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18058
- gi No. 83594
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18059
- gi No. 83596
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18060
- gi No. 83596
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18061
- gi No. 83596
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18062
- gi No. 83596
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18063
- gi No. 83596
- % Identity 75.9
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50
- Alignment No. 18064
- gi No. 84151
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18065
- gi No. 84151
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18066
- gi No. 84151
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18067
- gi No. 84152
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18068
- gi No. 84152
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18069
- gi No. 84152
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18070
- gi No. 84152
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18071

- gi No. 84152
- % Identity 75.9
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50
- Alignment No. 18072
- gi No. 84336
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
- Alignment No. 18073
- gi No. 84337
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18074
- gi No. 84478
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18075
- gi No. 84478
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18076
- gi No. 84478
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18077
- gi No. 84478
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18078
- gi No. 84478
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18079
- gi No. 84478
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18080
- gi No. 84478
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18081
- gi No. 84478

- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18082
- gi No. 84478
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18083
- gi No. 84478
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18084
- gi No. 84478
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18085
- gi No. 84834
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18086
- gi No. 84834
- % Identity 77.8
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50

- Alignment No. 18087
- gi No. 85106
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18088
- gi No. 85106
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18089
- gi No. 85106
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18090
- gi No. 86473
- % Identity 76.5
- Alignment Length 34
- Location of Alignment in SEQ ID NO 2728: from 17 to 50

- Alignment No. 18091
- gi No. 86474
- % Identity 87.5

- Alignment Length 16
- Location of Alignment in SEQ ID NO 2728: from 34 to 49

- Alignment No. 18092
- gi No. 870794
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18093
- gi No. 870794
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18094
- gi No. 89311
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2728: from 24 to 49

- Alignment No. 18095
- gi No. 89311
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18096
- gi No. 89311
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18097
- gi No. 89311
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18098
- gi No. 899115
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18099
- gi No. 899608
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18100
- gi No. 899608
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18101
- gi No. 899608
- % Identity 81.1
- Alignment Length 53

- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18102
- gi No. 899608
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18103
- gi No. 899608
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18104
- gi No. 902525
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
- Alignment No. 18105
- gi No. 902584
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18106
- gi No. 902584
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18107
- gi No. 902584
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18108
- gi No. 902584
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18109
- gi No. 902584
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18110
- gi No. 902584
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 18111
- gi No. 902584
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18112
- gi No. 902586
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18113
- gi No. 902586
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18114
- gi No. 902586
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18115
- gi No. 902586
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18116
- gi No. 902586
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18117
- gi No. 91870
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18118
- gi No. 91871
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18119
- gi No. 9295
- % Identity 73.1
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18120
- gi No. 940395
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18121
- gi No. 940395
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18122
- gi No. 940395
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18123
- gi No. 940395
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18124
- gi No. 940395
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18125
- gi No. 940395
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18126
- gi No. 940395
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18127
- gi No. 940395
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 18128
- gi No. 967985
- % Identity 74.5
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 18129
- gi No. 99469
- % Identity 80
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2728: from 10 to 49

- Alignment No. 18130
- gi No. 99771
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 18131
- gi No. 99772
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51

- Alignment No. 18132

- gi No. 99975
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

Maximum Length Sequence corresponding to clone ID 317675

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2729
- Ceres seq_id 1504393

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2730
- Ceres seq_id 1504394
- Location of start within SEQ ID NO 2729: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2731
- Ceres seq_id 1504395
- Location of start within SEQ ID NO 2729: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 18133
- gi No. 132962
- % Identity 88
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2731: from 22 to 46

- Alignment No. 18134
- gi No. 132963
- % Identity 80
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2731: from 22 to 46

- Alignment No. 18135
- gi No. 2500379
- % Identity 80
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2731: from 22 to 46

- Alignment No. 18136
- gi No. 3142154
- % Identity 82.4
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2731: from 22 to 38

- Alignment No. 18137
- gi No. 3142154
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2731: from 22 to 40

- Alignment No. 18138
- gi No. 3492819
- % Identity 80
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2731: from 22 to 46

- Alignment No. 18139
- gi No. 3914754
- % Identity 85
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2731: from 27 to 46

- Alignment No. 18140
- gi No. 4581465
- % Identity 80
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2731: from 22 to 46

- Alignment No. 18141
- gi No. 464638
- % Identity 92
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2731: from 22 to 46

Maximum Length Sequence corresponding to clone ID 317687

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2732
- Ceres seq_id 1504400

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2733
- Ceres seq_id 1504401
- Location of start within SEQ ID NO 2732: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 18142
- Mitochondrial carrier proteins
- Location within SEQ ID NO 2733: from 1 to 64 aa.

(D) Related Amino Acid Sequences

- Alignment No. 18143
- gi No. 2398829
- % Identity 85.5
- Alignment Length 69
- Location of Alignment in SEQ ID NO 2733: from 1 to 69

- Alignment No. 18144
- gi No. 3115108
- % Identity 83.3
- Alignment Length 67
- Location of Alignment in SEQ ID NO 2733: from 1 to 66

- Alignment No. 18145
- gi No. 3451392
- % Identity 83.3
- Alignment Length 67
- Location of Alignment in SEQ ID NO 2733: from 1 to 66

- Alignment No. 18146
- gi No. 4063007
- % Identity 72.7
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2733: from 1 to 66

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2734

- Ceres seq_id 1504402
- Location of start within SEQ ID NO 2732: at 26 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 18147
- Mitochondrial carrier proteins
- Location within SEQ ID NO 2734: from 1 to 56 aa.

(D) Related Amino Acid Sequences

- Alignment No. 18148
- gi No. 2398829
- % Identity 85.5
- Alignment Length 69
- Location of Alignment in SEQ ID NO 2734: from 1 to 61

- Alignment No. 18149
- gi No. 3115108
- % Identity 83.3
- Alignment Length 67
- Location of Alignment in SEQ ID NO 2734: from 1 to 58

- Alignment No. 18150
- gi No. 3451392
- % Identity 83.3
- Alignment Length 67
- Location of Alignment in SEQ ID NO 2734: from 1 to 58

- Alignment No. 18151
- gi No. 4063007
- % Identity 72.7
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2734: from 1 to 58

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2735
- Ceres seq_id 1504403
- Location of start within SEQ ID NO 2732: at 29 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 18152
- Mitochondrial carrier proteins
- Location within SEQ ID NO 2735: from 1 to 55 aa.

(D) Related Amino Acid Sequences

- Alignment No. 18153
- gi No. 2398829
- % Identity 85.5
- Alignment Length 69
- Location of Alignment in SEQ ID NO 2735: from 1 to 60

- Alignment No. 18154
- gi No. 3115108
- % Identity 83.3
- Alignment Length 67
- Location of Alignment in SEQ ID NO 2735: from 1 to 57

- Alignment No. 18155
- gi No. 3451392
- % Identity 83.3

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..789
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497851

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

atcatcaaca	aaaacaattc	tcaatacaca	aaacacaaaa	cacaaagaag	ttaaattctc	60
tgaagaagaa	tgagttctac	aagcaaatgc	tggacagtgg	cagtgagcat	cgagccgcta	120
gaggcattaa	aaagccaact	aggctcttgt	cggtggaaact	acatactccg	gtcggttaat	180
caacatctcc	ggaacaacgt	tagatctggt	tctcaaggga	aaaggtttct	tcgtctttct	240
gtctccgcag	ccgttacctc	ctctggtgag	agcgagaaga	cgaagagaac	cttttccctt	300
gagaaacaat	tgatcagaga	tttaaagaaa	aagatggaat	tcaccgcaga	gcagctaagc	360
caatacaacg	gcaccgacga	atcaaaagcc	atctacgtcg	caatcaaaag	ccgtgtgttc	420
gaygtcacca	ccgaaaaatc	cttctacggc	tccggagcg	attactcgat	gttcgcggga	480
aaagacgcga	gcagagcttt	gggtaagatg	agtaagaacg	aagaagatgt	gtctctctct	540
cttgaaggct	ctactgagaa	agagatcaat	actcttaagt	attgggagac	caaatttgaa	600
gctaagtatc	ctgtcggttg	ccgtgttgct	tcttagtgtc	ctcttctgag	attgcactat	660
gttatgtaac	tattgtgtgt	gaggatcttt	gtgtgtgtgt	ttttctgatt	tcgtgttttg	720
atctgatcgt	tttgatacaa	ttaccataag	taccaaatta	tctatgaaat	aaatcgggga	780
tttcgtgtt						

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..188
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ser	Ser	Thr	Ser	Lys	Ala	Trp	Thr	Val	Ala	Val	Ser	Ile	Gly	Ala
1				5				10						15	
Val	Glu	Ala	Leu	Lys	Asp	Gln	Leu	Gly	Leu	Cys	Arg	Trp	Asn	Trp	Ile
				20				25						30	
Leu	Arg	Ser	Val	Asn	Gln	His	Leu	Arg	Asn	Asn	Val	Arg	Ser	Val	Ser
				35				40						45	
Gln	Gly	Lys	Arg	Phe	Ser	Ser	Ser	Val	Ser	Ala	Ala	Val	Thr	Ser	
				50				55						60	
Ser	Gly	Glu	Ser	Glu	Lys	Thr	Lys	Arg	Thr	Phe	Ser	Leu	Glu	Lys	Gln
				65				70						80	
Leu	Ile	Arg	Ala	Leu	Lys	Lys	Lys	Met	Glu	Phe	Thr	Ala	Glu	Gln	Leu
				85				90						95	
Ser	Gln	Tyr	Asn	Gly	Thr	Asp	Glu	Ser	Lys	Pro	Ile	Tyr	Val	Ala	Ile
				100				105						110	
Lys	Gly	Arg	Val	Phe	Xaa	Val	Thr	Thr	Gly	Lys	Ser	Phe	Tyr	Gly	Ser
				115				120						125	
Gly	Gly	Asp	Tyr	Ser	Met	Phe	Ala	Gly	Lys	Asp	Ala	Ser	Arg	Ala	Leu
				130				135						140	
Gly	Lys	Met	Ser	Lys	Asn	Glu	Glu	Asp	Val	Ser	Pro	Ser	Leu	Glu	Gly
				145				150						155	
Leu	Thr	Glu	Lys	Glu	Ile	Asn	Thr	Leu	Asn	Asp	Trp	Glu	Thr	Lys	Phe
				165				170						175	
Glu	Ala	Lys	Tyr	Pro	Val	Val	Gly	Arg	Val	Val	Ser				

180 185
(2) INFORMATION FOR SEQ ID NO:3:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 100 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..100
 (D) OTHER INFORMATION: / Ceres Seq. ID 1497853
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
Met Glu Phe Thr Ala Glu Gln Leu Ser Gln Tyr Asn Gly Thr Asp Glu
1 5 10 15
Ser Lys Pro Ile Tyr Val Ala Ile Lys Gly Arg Val Phe Xaa Val Thr
20 25 30
Thr Gly Lys Ser Phe Tyr Gly Ser Gly Gly Asp Tyr Ser Met Phe Ala
35 40 45
Gly Lys Asp Ala Ser Arg Ala Leu Gly Lys Met Ser Lys Asn Glu Glu
50 55 60
Asp Val Ser Pro Ser Leu Glu Gly Leu Thr Glu Lys Glu Ile Asn Thr
65 70 75 80
Leu Asn Asp Trp Glu Thr Lys Phe Glu Ala Lys Tyr Pro Val Val Gly
85 90 95
Arg Val Val Ser
100

(2) INFORMATION FOR SEQ ID NO:4:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1005 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..1005
 (D) OTHER INFORMATION: / Ceres Seq. ID 1497854
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
aaaaacaacac aaaaaaatca gtgttcggct ctaacacgct cgacgaccaa ggcgggtctcg 60
tttaatacaac cgctttcacca gcctttctctg agtcccagct gtgacatcaa gctttattct 120
gggttaaagc ctcaatctgc aagctttttg gcaagtgggt atcagaattt gaataaggag 180
ttctatggaa gagttcataa gagttctgcaa tctgggactg gcaaaagcgag caggtoacgg 240
gtaaagatga tgccaatagg aacaccgaga gtgccctaca gaaaccgtga agaaggcact 300
tggaakggg ttgatatatg gaatgccctt tctcgagagc gtgtaattct cattggacaa 360
aacattgatg aagagtttag caaccagata ttgacaacca tgttgtacct tgatactatt 420
gatgactcga ggaggattta tatgtaccta aatggtccgg gtggtgattc tactccaagt 480
ctagccattct atgatacaat gaagagcttg aaaaagtcgg ttgggacaca ttgcgttggg 540
cttgccttca accttgcagg tttttcttct gcggctggag aaaaagggta ccgatttgcg 600
atgccattgt caagaatcgc cctccaatca ccagctgggt cagcccgtgg ccaggctgat 660
gatattcaaa atgaagcaaa agagctttca aggataaagc actacctctt caatgaacta 720
gccaaagaata caggccagcc tcgcgaaagg gtcttcaaa acttgagccg ggtgaaaagg 780
ttcaatgcag aggaagcaat cgagtatgga ctatttgata agattgttag accaccgcgc 840
atcaaaagaag acgctcctcg ccaagacgaa agcgcagggc taggctagtc tttttgtttt 900
gtttgttatg tcaaaagttt taattcttat gtattgtga ttgtgattgt tacctaaaaa 960
aatcactgat tattgttttt tcattccacc gattttctga ttct

(2) INFORMATION FOR SEQ ID NO:5:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 295 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..295
 (D) OTHER INFORMATION: / Ceres Seq. ID 1497855
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
Lys Asn Lys Gln Lys Asn Gln Cys Ser Ala Leu Thr Arg Ser Thr Thr
1 5 10 15
Met Ala Val Ser Phe Asn Thr Thr Leu His Gln Pro Ser Leu Ser Pro
 20 25 30
Ser Cys Ser Ile Lys Leu Tyr Ser Gly Leu Lys Pro Gln Ser Ala Ser
 35 40 45
Phe Leu Ala Ser Gly Tyr Gln Asn Leu Asn Lys Glu Phe Tyr Gly Arg
50 55 60
Val His Lys Ser Leu Gln Ser Gly Thr Gly Lys Ala Ser Arg Ser Arg
65 70 75 80
Val Lys Met Met Pro Ile Gly Thr Pro Arg Val Pro Tyr Arg Asn Arg
 85 90 95
Glu Glu Gly Thr Trp Gln Xaa Val Asp Ile Trp Asn Ala Leu Tyr Arg
 100 105 110
Glu Arg Val Ile Phe Ile Gly Gln Asn Ile Asp Glu Glu Phe Ser Asn
 115 120 125
Gln Ile Leu Ala Thr Met Leu Tyr Leu Asp Thr Leu Asp Asp Ser Arg
130 135 140
Arg Ile Tyr Met Tyr Leu Asn Gly Pro Gly Gly Asp Leu Thr Pro Ser
145 150 155 160
Leu Ala Ile Tyr Asp Thr Met Lys Ser Leu Lys Ser Pro Val Gly Thr
 165 170 175
His Cys Val Gly Leu Ala Tyr Asn Leu Ala Gly Phe Leu Leu Ala Ala
 180 185 190
Gly Glu Lys Gly His Arg Phe Ala Met Pro Leu Ser Arg Ile Ala Leu
 195 200 205
Gln Ser Pro Ala Gly Ala Ala Arg Gly Gln Ala Asp Asp Ile Gln Asn
210 215 220
Glu Ala Lys Glu Leu Ser Arg Ile Arg Asp Tyr Leu Phe Asn Glu Leu
225 230 235 240
Ala Lys Asn Thr Gly Gln Pro Ala Glu Arg Val Phe Lys Asp Leu Ser
 245 250 255
Arg Val Lys Arg Phe Asn Ala Glu Glu Ala Ile Glu Tyr Gly Leu Ile
260 265 270
Asp Lys Ile Val Arg Pro Pro Arg Ile Lys Glu Asp Ala Pro Arg Gln
275 280 285
Asp Glu Ser Ala Gly Leu Gly
290 295
(2) INFORMATION FOR SEQ ID NO:6:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 279 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..279
 (D) OTHER INFORMATION: / Ceres Seq. ID 1497856
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
Met Ala Val Ser Phe Asn Thr Thr Leu His Gln Pro Ser Leu Ser Pro
1 5 10 15
Ser Cys Ser Ile Lys Leu Tyr Ser Gly Leu Lys Pro Gln Ser Ala Ser
 20 25 30

```

Phe Leu Ala Ser Gly Tyr Gln Asn Leu Asn Lys Glu Phe Tyr Gly Arg
    35                      40                      45
Val His Lys Ser Leu Gln Ser Gly Thr Gly Lys Ala Ser Arg Ser Arg
    50                      55                      60
Val Lys Met Met Pro Ile Gly Thr Pro Arg Val Pro Tyr Arg Asn Arg
    65                      70                      75                      80
Glu Glu Gly Thr Trp Gln Xaa Val Asp Ile Trp Asn Ala Leu Tyr Arg
    85                      90                      95
Glu Arg Val Ile Phe Ile Gly Gln Asn Ile Asp Glu Glu Phe Tyr Asn
    100                      105                      110
Gln Ile Leu Ala Thr Met Leu Tyr Leu Asp Thr Leu Asp Asp Ser Arg
    115                      120                      125
Arg Ile Tyr Met Tyr Leu Asn Gly Pro Gly Gly Asp Leu Thr Pro Ser
    130                      135                      140
Leu Ala Ile Tyr Asp Thr Met Lys Ser Leu Lys Ser Pro Val Gly Thr
    145                      150                      155                      160
His Cys Val Gly Leu Ala Tyr Asn Leu Ala Gly Phe Leu Leu Ala Ala
    165                      170                      175
Gly Glu Lys Gly His Arg Phe Ala Met Pro Leu Ser Arg Ile Ala Leu
    180                      185                      190
Gln Ser Pro Ala Gly Ala Ala Arg Gly Gln Ala Asp Asp Ile Gln Asn
    195                      200                      205
Glu Ala Lys Glu Leu Ser Arg Ile Arg Asp Tyr Leu Phe Asn Glu Leu
    210                      215                      220
Ala Lys Asn Thr Gly Gln Pro Ala Glu Arg Val Phe Lys Asp Leu Ser
    225                      230                      235                      240
Arg Val Lys Arg Phe Asn Ala Glu Glu Ala Ile Glu Tyr Gly Leu Ile
    245                      250                      255
Asp Lys Ile Val Arg Pro Pro Arg Ile Lys Glu Asp Ala Pro Arg Gln
    260                      265                      270
Asp Glu Ser Ala Gly Leu Gly
    275

```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..213
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497857

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```

Met Met Pro Ile Gly Thr Pro Arg Val Pro Tyr Arg Asn Arg Glu Glu
1          5          10          15
Gly Thr Trp Gln Xaa Val Asp Ile Trp Asn Ala Leu Tyr Arg Glu Arg
    20          25          30
Val Ile Phe Ile Gly Gln Asn Ile Asp Glu Glu Phe Ser Asn Gln Ile
    35          40          45
Leu Ala Thr Met Leu Tyr Leu Asp Thr Leu Asp Asp Ser Arg Arg Ile
    50          55          60
Tyr Met Tyr Leu Asn Gly Pro Gly Gly Asp Leu Thr Pro Ser Leu Ala
    65          70          75          80
Ile Tyr Asp Thr Met Lys Ser Leu Lys Ser Pro Val Gly Thr His Cys
    85          90          95
Val Gly Leu Ala Tyr Asn Leu Ala Gly Phe Leu Leu Ala Ala Gly Glu
    100          105          110
Lys Gly His Arg Phe Ala Met Pro Leu Ser Arg Ile Ala Leu Gln Ser
    115          120          125
Pro Ala Gly Ala Ala Arg Gly Gln Ala Asp Asp Ile Gln Asn Glu Ala

```

130 135 140
Lys Glu Leu Ser Arg Ile Arg Asp Tyr Leu Phe Asn Glu Leu Ala Lys
145 150 155
Asn Thr Gly Gln Pro Ala Glu Arg Val Phe Lys Asp Leu Ser Arg Val
165 170 175
Lys Arg Phe Asn Ala Glu Glu Ala Ile Glu Tyr Gly Leu Ile Asp Lys
180 185 190
Ile Val Arg Pro Pro Arg Ile Lys Glu Asp Ala Pro Arg Gln Asp Glu
195 200 205
Ser Ala Gly Leu Gly
210

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 678 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..678
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

aatcgcatc	tccgatgaa	tagccgacg	agaaatgacc	aagttcagga	agctcggccg	60
cccagcaggt	caccgtatgt	ccatgctcag	gactatgggt	tctcaattgg	tgcaacacaga	120
gcgaattgag	accactgtta	caaaggctat	agaagtctgt	cgtcttgctg	ataatatgat	180
tcaactcgga	aaagaggggt	caactagctgc	agcaagaaga	gctgctgggt	ttgttagagg	240
agatgatgta	cttcacaaga	tttttacaga	attggckcat	cgatacaaa	atagagctgg	300
tggataacca	agaatgcttc	gtactcgcat	tcgtgttggt	gatgctgccc	caatggccta	360
tatcgatctt	atcgatagag	agaacgagct	aggccaatca	aaaccagcta	ctcctcaacc	420
tcacacctga	gtgcacctgt	atccatgggc	tagatccctg	ctcaccaggg	agtatgctcc	480
accaaaggag	gcataaaact	tctgattctg	acctataaat	agaagaagat	ctctctcgct	540
ctctcacacc	agaagatcat	gttttttttc	cccttgccca	tgttggttct	ccttcaaccc	600
atagctttgt	atgtctggca	ccttatccat	cactgtcatt	cacaatgtgt	ttaaaaacgt	660
ttaaatgtag	tttctctg					

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..167
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497861

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ile	Ala	Phe	Ser	Asp	Arg	Ile	Ala	Asp	Gly	Glu	Met	Thr	Lys	Phe	Arg
1			5						10					15	
Lys	Leu	Gly	Arg	Pro	Ala	Gly	His	Arg	Met	Ser	Met	Leu	Arg	Thr	Met
			20					25					30		
Val	Ser	Gln	Leu	Val	Gln	His	Glu	Arg	Ile	Glu	Thr	Thr	Val	Thr	Lys
			35				40				45				
Ala	Ile	Glu	Val	Arg	Arg	Leu	Ala	Asp	Asn	Met	Ile	Gln	Leu	Gly	Lys
			50			55				60					
Glu	Gly	Ser	Leu	Ala	Ala	Ala	Arg	Arg	Ala	Ala	Gly	Phe	Val	Arg	Gly
			65			70			75					80	
Asp	Asp	Val	Leu	His	Lys	Ile	Phe	Thr	Glu	Leu	Xaa	His	Arg	Tyr	Lys
			85					90					95		
Asp	Arg	Ala	Gly	Gly	Tyr	Thr	Arg	Met	Leu	Arg	Thr	Arg	Ile	Arg	Val
			100				105						110		

Gly Asp Ala Ala Pro Met Ala Tyr Ile Glu Phe Ile Asp Arg Glu Asn
115 120 125
Glu Leu Arg Gln Ser Lys Pro Ala Thr Pro Gln Pro Pro Arg Val
130 135 140
Pro Leu Asp Pro Trp Ala Arg Ser Arg Leu Thr Arg Gln Tyr Ala Pro
145 150 155 160
Pro Lys Glu Ala Lys Asn Phe
165

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..156
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497862

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Thr Lys Phe Arg Lys Leu Gly Arg Pro Ala Gly His Arg Met Ser
1 5 10 15
Met Leu Arg Thr Met Val Ser Gln Leu Val Gln His Glu Arg Ile Glu
20 25 30
Thr Thr Val Thr Lys Ala Ile Glu Val Arg Arg Leu Ala Asp Asn Met
35 40 45
Ile Gln Leu Gly Lys Glu Gly Ser Leu Ala Ala Arg Arg Ala Ala
50 55 60
Gly Phe Val Arg Gly Asp Asp Val Leu His Lys Ile Phe Thr Glu Leu
65 70 75 80
Xaa His Arg Tyr Lys Asp Arg Ala Gly Gly Tyr Thr Arg Met Leu Arg
85 90 95
Thr Arg Ile Arg Val Gly Asp Ala Ala Pro Met Ala Tyr Ile Glu Phe
100 105 110
Ile Asp Arg Glu Asn Glu Leu Arg Gln Ser Lys Pro Ala Thr Pro Gln
115 120 125
Pro Pro Pro Arg Val Pro Leu Asp Pro Trp Ala Arg Ser Arg Leu Thr
130 135 140
Arg Gln Tyr Ala Pro Pro Lys Glu Ala Lys Asn Phe
145 150 155

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497863

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Ser Met Leu Arg Thr Met Val Ser Gln Leu Val Gln His Glu Arg
1 5 10 15
Ile Glu Thr Thr Val Thr Lys Ala Ile Glu Val Arg Arg Leu Ala Asp
20 25 30
Asn Met Ile Gln Leu Gly Lys Glu Gly Ser Leu Ala Ala Arg Arg
35 40 45
Ala Ala Gly Phe Val Arg Gly Asp Asp Val Leu His Lys Ile Phe Thr
50 55 60
Glu Leu Xaa His Arg Tyr Lys Asp Arg Ala Gly Gly Tyr Thr Arg Met

65 70 75 80
Leu Arg Thr Arg Ile Arg Val Gly Asp Ala Ala Pro Met Ala Tyr Ile
85 90 95
Glu Phe Ile Asp Arg Glu Asn Glu Leu Arg Gln Ser Lys Pro Ala Thr
100 105 110
Pro Gln Pro Pro Arg Val Pro Leu Asp Pro Trp Ala Arg Ser Arg
115 120 125
Leu Thr Arg Gln Tyr Ala Pro Pro Lys Glu Ala Lys Asn Phe
130 135 140

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..505
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

atcaatcgga ttatctgcac ttgtttcaat ggtgcatcta atatctctca agctggtgct 60
cttgcttgcc ttacaccgga aggacttgag gcaatgcata aggtgattgg attctataaa 120
gaaacacaaa acataatcat tgacacattc acatctctcg ggtatgatgt atatggagga 180
aatgcgcctt acgtatgggt tcacttcccg aaccaaagct catgggatgt gttgctgag 240
attctggaga agactcatgt ggttacaact ccaggaaagt ggtttggacc agggggtgaa 300
gggttcgttc gtgtcagtc ctttggtcac agagagaaca tcttagagcg atgtcgaaga 360
ttcaagcagc tttaacaaatg aagaaccttg tttgtaatcg tctctcatca tcatcacocc 420
ctttaatgac atgatttgag ttaaaaat gtcgtttcca ttgkktstg gaatttgtag 480
aagacacttt tgacaccagt gtttc

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..126
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497865

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ile Asn Arg Ile Ile Cys Thr Cys Phe Asn Gly Ala Ser Asn Ile Ser
1 5 10 15
Gln Ala Gly Ala Leu Ala Cys Leu Thr Pro Glu Gly Leu Glu Ala Met
20 25 30
His Lys Val Ile Gly Phe Tyr Lys Glu Asn Thr Asn Ile Ile Asp
35 40 45
Thr Phe Thr Ser Leu Gly Tyr Asp Val Tyr Gly Gly Asn Ala Pro Tyr
50 55 60
Val Trp Val His Phe Pro Asn Gln Ser Ser Trp Asp Val Phe Ala Glu
65 70 75 80
Ile Leu Glu Lys Thr His Val Val Thr Thr Pro Gly Ser Gly Phe Gly
85 90 95
Pro Gly Gly Glu Gly Phe Val Arg Val Ser Ala Phe Gly His Arg Glu
100 105 110
Asn Ile Leu Glu Ala Cys Arg Arg Phe Lys Gln Leu Tyr Lys
115 120 125

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..95
(D) OTHER INFORMATION: / Ceres Seq. ID 1497866
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
Met His Lys Val Ile Gly Phe Tyr Lys Glu Asn Thr Asn Ile Ile Ile
1 5 10 15
Asp Thr Phe Thr Ser Leu Gly Tyr Asp Val Tyr Gly Gly Asn Ala Pro
20 25 30
Tyr Val Trp Val His Phe Pro Asn Gln Ser Ser Trp Asp Val Phe Ala
35 40 45
Glu Ile Leu Glu Lys Thr His Val Val Thr Thr Pro Gly Ser Gly Phe
50 55 60
Gly Pro Gly Gly Glu Gly Phe Val Arg Val Ser Ala Phe Gly His Arg
65 70 75 80
Glu Asn Ile Leu Glu Ala Cys Arg Arg Phe Lys Gln Leu Tyr Lys
85 90 95

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 431 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..431
(D) OTHER INFORMATION: / Ceres Seq. ID 1497867
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
atttctaaaa agaacgaacg acgccaatata caccgagaag ctcaacgcttc gtcacacttc 60
ttctcgcttc tcggcgctctc catcgccgctc tctatctaatt ttctgctctgc gtcgacgttg 120
tgagctactt cagattccgg ccattcacgca gctccagttg tatgcttttg ggctaataca 180
aagatgacaa caatcaaaac cggtcagaaa actcaaaagt cttctctcttc cggttctgct 240
actaccgcta ctgtgtactct taagcagtc tcaagcatcgt ttaawaggtg gggaaggaga 300
caccggtttg taagatatgg acttcgatg atatctctca ctgtatttgg agccctcgga 360
ctcgcccaac tccttcaagg cagtaaggat attgcaaaagg taaaagatga ccaagaatgg 420
gagattatag a

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..61
(D) OTHER INFORMATION: / Ceres Seq. ID 1497868
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
Phe Pro Lys Arg Thr Asn Asp Ala Ile Tyr Thr Glu Lys Leu Asn Val
1 5 10 15
Arg His His Ser Ser Arg Phe Ser Ala Ser Pro Ser Pro Ser Leu Ser
20 25 30
Asn Phe Val Leu Arg Arg Pro Gly Glu Leu Leu Gln Ile Pro Ala Ile
35 40 45
Thr Gln Leu Gln Leu Tyr Ala Leu Trp Leu Ile Gln Arg
50 55 60

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..57
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497869

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Phe	Leu	Lys	Glu	Arg	Thr	Thr	Pro	Tyr	Thr	Pro	Arg	Ser	Ser	Thr	Phe
1			5					10					15		
Val	Ile	Thr	Leu	Leu	Ala	Ser	Arg	Arg	Leu	His	Arg	Arg	Leu	Tyr	Leu
			20				25						30		
Ile	Ser	Ser	Cys	Val	Asp	Leu	Val	Ser	Tyr	Phe	Arg	Phe	Arg	Pro	Ser
			35				40					45			
Arg	Ser	Ser	Ser	Cys	Met	Leu	Cys	Gly							
			50				55								

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..82
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met	Thr	Thr	Ile	Lys	Thr	Gly	Gln	Lys	Thr	Gln	Lys	Ser	Ser	Pro	Ser
1			5					10					15		
Gly	Ser	Ala	Thr	Thr	Ala	Thr	Gly	Thr	Leu	Lys	Gln	Ser	Ser	Ala	Ser
			20				25						30		
Phe	Xaa	Arg	Trp	Gly	Arg	Arg	His	Pro	Phe	Val	Arg	Tyr	Gly	Leu	Pro
			35				40					45			
Met	Ile	Ser	Leu	Thr	Val	Phe	Gly	Ala	Leu	Gly	Leu	Gly	Gln	Leu	Leu
			50				55				60				
Gln	Gly	Ser	Lys	Asp	Ile	Ala	Lys	Val	Lys	Asp	Gln	Glu	Trp	Glu	
65					70					75				80	
Ile	Ile														

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2584 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2584
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497875

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

aaacacacca	aaatcaaaag	ctgagagctc	tcttacattg	aagctacttt	cgaagatagc	60
attactgat	tggtaaagag	ttctagaagc	gacgagcatc	ttctttagtt	cccgagtttt	120
ctgcggttga	gaagctctgt	ctagaaaagta	atgggtgaca	gcgagggccat	ggtttccgag	180
ggttatactt	ctgctccata	tggagactat	aatgcttctg	ctgctactgt	ggaatcgacc	240
gggcaagaga	ctgcaccaat	tgttgatgca	tcaactcgg	tcaacaatga	ttcttttggtc	300

aatggtactg	cgccagttga	gaacggaagt	gcaacagata	atgtggctgt	gactgtctca	360
gcagcggagc	atggagacaa	tactggctct	acactctcaa	cggaagaggga	gcgcttgtgg	420
aatattgtaa	gggcaaatct	tttagagttt	aatgctttga	ctgccttgat	tgatgagacg	480
gagaggatag	cgccagacaa	tatagcaaaa	atccggaagg	tctatgatgc	ttctttagct	540
gaatttcctc	tggtttatgg	ctatttgaaa	aagtttgccg	atcatgaggc	tcgggtgggg	600
ccaattggaca	aagctgtgga	ggtttatgaa	agagcagtg	tgaggagtgc	atatcagtg	660
gatatctggg	tgcatattgt	cacttttgcc	atcaatacat	atggagatcc	agaaacgac	720
agaaggcttt	ttgaacgagc	tttggtttac	gttggaaact	attttcttct	ctctccgttg	780
tgggacaaa	acattgagta	tgagtacatg	cagcaggact	ggagccgagt	tgcccttgatt	840
tacaccagaa	tattggagaa	tccaattcaa	aatctggata	gatatttcag	cagttttaag	900
gagctagctg	aaacacggcc	ctctgctgaa	ctaaggagtg	ctgaggaaac	cgacgctgct	960
gctgttgctg	ttgcttggtg	tgcttctgaa	agtgccagcat	ctgagtcogg	tgaaaaggca	1020
gatgaaggac	gatctcaagt	tgatggttcc	accgaacaat	ccctcaaat	ggaaagctgt	1080
agttcaactg	aacctgagga	gttgaagaag	tatgtaggca	tcaggggaagc	catgtacata	1140
aaatcgaaag	agttttgaat	taaaatcatt	ggttatgaaa	tggtctataag	gaggccctat	1200
ttccatgtgc	gtccctcgaa	gtgcgcagaa	ctggagaatt	ggcacaacta	cttgatttcc	1260
attgagaggg	atggagactg	caataaagggt	gtcaagctgt	atgaaaagtg	tggtgttacc	1320
tgtgcaaat	acccagaata	ctggattcgt	tatgtgacaa	acatggaaagc	aagtgggaagt	1380
gcggaccttg	cagaaaaatgc	cttgctcgca	gcaactcaag	tctttgtcaa	gaaacaaaca	1440
gagattcacc	tatttgctgc	tcgattaaaa	gagcagaatg	gagatatagc	tggtgctaga	1500
gctgcatacc	aattagtgca	ctctgaaatt	tctctggac	tcttggaagc	agtaaatcaag	1560
catgcaaat	tggaataacc	actaggtaat	ctggatgatg	ctttctcttt	gtatgagcaa	1620
gtgattgctg	ttgaaaaggg	gaaagaacat	tccacaatac	tgccactgct	gtatgcgag	1680
tattcaaggt	tttcaactgt	ggctctcagg	gatgctgaga	aagctaggag	gattattgtc	1740
gaagcacttg	accatgtaca	accgtcaaaa	cctctcatgg	agcactgat	ctattttgag	1800
gcgattcagc	caccaccaag	agagattgat	taccttgagc	cacttgtaga	gaaagtata	1860
aagccagatg	cagatgcacca	aaacattgca	agttccactg	agaggggaag	gaactcttta	1920
atatatatag	agttcctggg	tatttttgga	gatgtgaagt	ccattaaaaa	agcggaagat	1980
caacatgtta	aactgtttta	tctctcatcg	agcacgtcgg	agctgaaaaa	gcgtagcgca	2040
gatgatgttt	tcgcatcaga	taggaagaaa	atggcaaaaa	cttcaaacgc	cactccacct	2100
gctcagccag	tatccaatgc	atatccaaat	gctcaggctc	aatggctctg	tggttatgct	2160
gcgcagcctc	agacttgccc	accagcacaa	gctgctcctg	ctcaaccaca	gcaatggaac	2220
cctgcctacg	gtcaaacaggc	tgcttatggt	gcataatggg	gatatacctg	tcgtctaac	2280
gctccacacg	cccaaacacc	tggtgccacg	gccgcagcct	atggagcgtg	tctgctcag	2340
acatacccaa	cgcagagtta	tgacacctca	gttgcaagcag	cagcaccagc	ggctgcaccg	2400
gtgcagcaac	cggtgctg	gtgtgctcct	caagcgtact	acaacacgta	ctacttgagc	2460
tattactgct	gctggtcggt	ttgttagtgt	aattgataac	catttgcttc	tatctactca	2520
aatttagtgt	ctggatgttt	acatgtctct	cttttctcga	tcagtgcaca	tagatattta	2580
cttt						

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 768 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..768
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met	Gly	Asp	Ser	Glu	Ala	Met	Val	Ser	Glu	Gly	Tyr	Thr	Ser	Ala	Pro
1				5					10					15	
Tyr	Gly	Asp	Tyr	Asn	Ala	Ser	Ala	Ala	Thr	Val	Glu	Ser	Thr	Gly	Gln
				20				25					30		
Glu	Thr	Ala	Pro	Ile	Val	Asp	Ala	Ser	His	Ser	Val	Asn	Asn	Asp	Ser
				35				40				45			
Leu	Val	Asn	Gly	Thr	Ala	Pro	Val	Glu	Asn	Gly	Ser	Ala	Thr	Asp	Asn
				50				55				60			
Val	Ala	Val	Thr	Ala	Pro	Ala	Ala	Glu	His	Gly	Asp	Asn	Thr	Gly	Ser
65				70				75				80			

Thr	Leu	Ser	Thr	Glu	Glu	Glu	Arg	Leu	Trp	Asn	Ile	Val	Arg	Ala	Asn	
				85					90					95		
Ser	Leu	Glu	Phe	Asn	Ala	Trp	Thr	Ala	Leu	Ile	Asp	Glu	Thr	Glu	Arg	
			100					105					110			
Ile	Ala	Gln	Asp	Asn	Ile	Ala	Lys	Ile	Arg	Lys	Val	Tyr	Asp	Ala	Phe	
		115					120					125				
Leu	Ala	Glu	Phe	Pro	Leu	Cys	Tyr	Gly	Trp	Lys	Lys	Phe	Ala	Asp		
	130					135					140					
His	Glu	Ala	Arg	Val	Gly	Ala	Met	Asp	Lys	Val	Val	Glu	Val	Tyr	Glu	
	145				150					155					160	
Arg	Ala	Val	Leu	Gly	Val	Thr	Tyr	Ser	Val	Asp	Ile	Trp	Leu	His	Tyr	
			165						170					175		
Cys	Thr	Phe	Ala	Ile	Asn	Thr	Tyr	Gly	Asp	Pro	Glu	Thr	Ile	Arg	Arg	
		180						185					190			
Leu	Phe	Glu	Arg	Ala	Leu	Val	Tyr	Val	Gly	Thr	Asp	Phe	Leu	Ser	Ser	
	195						200				205					
Pro	Leu	Trp	Asp	Lys	Tyr	Ile	Glu	Tyr	Glu	Tyr	Met	Gln	Gln	Asp	Trp	
	210				215						220					
Ser	Arg	Val	Ala	Leu	Ile	Tyr	Thr	Arg	Ile	Leu	Glu	Asn	Pro	Ile	Gln	
	225				230					235					240	
Asn	Leu	Asp	Arg	Tyr	Phe	Ser	Ser	Phe	Lys	Glu	Leu	Ala	Glu	Thr	Arg	
			245						250					255		
Pro	Leu	Ser	Glu	Leu	Arg	Ser	Ala	Glu	Glu	Ser	Ala	Ala	Ala	Ala	Val	
			260					265					270			
Ala	Val	Ala	Gly	Asp	Ala	Ser	Glu	Ser	Ala	Ala	Ser	Glu	Ser	Gly	Glu	
	275						280					285				
Lys	Ala	Asp	Glu	Gly	Arg	Ser	Gln	Val	Asp	Gly	Ser	Thr	Glu	Gln	Ser	
	290					295					300					
Pro	Lys	Leu	Glu	Ser	Ala	Ser	Ser	Thr	Glu	Pro	Glu	Glu	Leu	Lys	Lys	
	305				310					315				320		
Tyr	Val	Gly	Ile	Arg	Glu	Ala	Met	Tyr	Ile	Lys	Ser	Lys	Glu	Phe	Glu	
			325						330					335		
Ser	Lys	Ile	Ile	Gly	Tyr	Glu	Met	Ala	Ile	Arg	Arg	Pro	Tyr	Phe	His	
		340						345					350			
Val	Arg	Pro	Leu	Asn	Val	Ala	Glu	Leu	Glu	Asn	Trp	His	Asn	Tyr	Leu	
		355				360										
Asp	Phe	Ile	Glu	Arg	Asp	Gly	Asp	Phe	Asn	Lys	Val	Val	Lys	Leu	Tyr	
	370				375						380					
Glu	Arg	Cys	Val	Val	Thr	Cys	Ala	Asn	Tyr	Pro	Glu	Tyr	Trp	Ile	Arg	
	385				390					395				400		
Tyr	Val	Thr	Asn	Met	Glu	Ala	Ser	Gly	Ser	Ala	Asp	Leu	Ala	Glu	Asn	
			405						410					415		
Ala	Leu	Ala	Arg	Ala	Thr	Gln	Val	Phe	Val	Lys	Lys	Gln	Pro	Glu	Ile	
			420					425					430			
His	Leu	Phe	Ala	Ala	Arg	Leu	Lys	Glu	Gln	Asn	Gly	Asp	Ile	Ala	Gly	
	435					440					445					
Ala	Arg	Ala	Ala	Tyr	Gln	Leu	Val	His	Ser	Glu	Ile	Ser	Pro	Gly	Leu	
	450					455					460					
Leu	Glu	Ala	Val	Ile	Lys	His	Ala	Asn	Met	Glu	Tyr	Arg	Leu	Gly	Asn	
	465				470					475				480		
Leu	Asp	Asp	Ala	Phe	Ser	Leu	Tyr	Glu	Gln	Val	Ile	Ala	Val	Glu	Lys	
			485						490					495		
Gly	Lys	Glu	His	Ser	Thr	Ile	Leu	Pro	Leu	Leu	Tyr	Ala	Gln	Tyr	Ser	
		500						505					510			
Arg	Phe	Ser	Tyr	Leu	Val	Ser	Arg	Asp	Ala	Glu	Lys	Ala	Arg	Arg	Ile	
		515					520					525				
Ile	Val	Glu	Ala	Leu	Asp	His	Val	Gln	Pro	Ser	Lys	Pro	Leu	Met	Glu	
	530					535					540					
Ala	Leu	Ile	His	Phe	Glu	Ala	Ile	Gln	Pro	Pro	Pro	Arg	Glu	Ile	Asp	
	545				550					555					560	
Tyr	Leu	Glu	Pro	Leu	Val	Glu	Lys	Val	Ile	Lys	Pro	Asp	Ala	Asp	Ala	

	565		570		575
Gln Asn Ile Ala Ser Ser Thr Glu Arg Glu Glu Leu Ser Leu Ile Tyr					
	580		585		590
Ile Glu Phe Leu Gly Ile Phe Gly Asp Val Lys Ser Ile Lys Lys Ala					
	595		600		605
Glu Asp Gln His Val Lys Leu Phe Tyr Pro His Arg Ser Thr Ser Glu					
	610		615		620
Leu Lys Lys Arg Ser Ala Asp Asp Phe Leu Ala Ser Asp Arg Thr Lys					
	625		630		635
Met Ala Lys Thr Tyr Asn Gly Thr Pro Pro Ala Gln Pro Val Ser Asn					
	645		650		655
Ala Tyr Pro Asn Ala Gln Ala Gln Trp Ser Gly Gly Tyr Ala Ala Gln					
	660		665		670
Pro Gln Thr Trp Pro Pro Ala Gln Ala Ala Pro Ala Gln Pro Gln Gln					
	675		680		685
Trp Asn Pro Ala Tyr Gly Gln Gln Ala Ala Tyr Gly Ala Tyr Gly Gly					
	690		695		700
Tyr Pro Ala Gly Tyr Thr Ala Pro Gln Ala Pro Thr Pro Val Pro Gln					
	705		710		715
Ala Ala Ala Tyr Gly Ala Tyr Pro Ala Gln Thr Tyr Pro Thr Gln Ser					
	725		730		735
Tyr Ala Pro Pro Val Ala Ala Ala Ala Pro Ala Ala Ala Pro Val Gln					
	740		745		750
Gln Pro Ala Ala Ala Val Ala Pro Gln Ala Tyr Tyr Asn Thr Tyr Tyr					
	755		760		765

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 762 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..762

(D) OTHER INFORMATION: / Ceres Seq. ID 1497877

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Val Ser Glu Gly Tyr Thr Ser Ala Pro Tyr Gly Asp Tyr Asn Ala					
1	5		10		15
Ser Ala Ala Thr Val Glu Ser Thr Gly Gln Glu Thr Ala Pro Ile Val					
	20		25		30
Asp Ala Ser His Ser Val Asn Asn Asp Ser Leu Val Asn Gly Thr Ala					
	35		40		45
Pro Val Glu Asn Gly Ser Ala Thr Asp Asn Val Ala Val Thr Ala Pro					
	50		55		60
Ala Ala Glu His Gly Asp Asn Thr Gly Ser Thr Leu Ser Thr Glu Glu					
	65		70		75
Glu Arg Leu Trp Asn Ile Val Arg Ala Asn Ser Leu Glu Phe Asn Ala					
	85		90		95
Trp Thr Ala Leu Ile Asp Glu Thr Glu Arg Ile Ala Gln Asp Asn Ile					
	100		105		110
Ala Lys Ile Arg Lys Val Tyr Asp Ala Phe Leu Ala Glu Phe Pro Leu					
	115		120		125
Cys Tyr Gly Tyr Trp Lys Lys Phe Ala Asp His Glu Ala Arg Val Gly					
	130		135		140
Ala Met Asp Lys Val Val Glu Val Tyr Glu Arg Ala Val Leu Gly Val					
	145		150		155
Thr Tyr Ser Val Asp Ile Trp Leu His Tyr Cys Thr Phe Ala Ile Asn					
	165		170		175

Thr	Tyr	Gly	Asp	Pro	Glu	Thr	Ile	Arg	Arg	Leu	Phe	Glu	Arg	Ala	Leu	
			180					185					190			
Val	Tyr	Val	Gly	Thr	Asp	Phe	Leu	Ser	Ser	Pro	Leu	Trp	Asp	Lys	Tyr	
		195					200					205				
Ile	Glu	Tyr	Glu	Tyr	Met	Gln	Gln	Asp	Trp	Ser	Arg	Val	Ala	Leu	Ile	
	210					215					220					
Tyr	Thr	Arg	Ile	Leu	Glu	Asn	Pro	Ile	Gln	Asn	Leu	Asp	Arg	Tyr	Phe	
	225				230				235						240	
Ser	Ser	Phe	Lys	Glu	Leu	Ala	Glu	Thr	Arg	Pro	Leu	Ser	Glu	Leu	Arg	
			245						250					255		
Ser	Ala	Glu	Glu	Ser	Ala	Ala	Ala	Val	Ala	Val	Ala	Gly	Asp	Ala		
		260					265					270				
Ser	Glu	Ser	Ala	Ala	Ser	Glu	Ser	Gly	Glu	Lys	Ala	Asp	Glu	Gly	Arg	
		275					280					285				
Ser	Gln	Val	Asp	Gly	Ser	Thr	Glu	Gln	Ser	Pro	Lys	Leu	Glu	Ser	Ala	
	290					295					300					
Ser	Ser	Thr	Glu	Pro	Glu	Glu	Leu	Lys	Lys	Tyr	Val	Gly	Ile	Arg	Glu	
	305				310					315					320	
Ala	Met	Tyr	Ile	Lys	Ser	Lys	Glu	Phe	Glu	Ser	Lys	Ile	Ile	Gly	Tyr	
				325					330					335		
Glu	Met	Ala	Ile	Arg	Arg	Pro	Tyr	Phe	His	Val	Arg	Pro	Leu	Asn	Val	
		340						345					350			
Ala	Glu	Leu	Glu	Asn	Trp	His	Asn	Tyr	Leu	Asp	Phe	Ile	Glu	Arg	Asp	
		355					360					365				
Gly	Asp	Phe	Asn	Lys	Val	Val	Lys	Leu	Tyr	Glu	Arg	Cys	Val	Val	Thr	
	370					375					380					
Cys	Ala	Asn	Tyr	Pro	Glu	Tyr	Trp	Ile	Arg	Tyr	Val	Thr	Asn	Met	Glu	
	385				390					395					400	
Ala	Ser	Gly	Ser	Ala	Asp	Leu	Ala	Glu	Asn	Ala	Leu	Ala	Arg	Ala	Thr	
				405					410					415		
Gln	Val	Phe	Val	Lys	Lys	Gln	Pro	Glu	Ile	His	Leu	Phe	Ala	Ala	Arg	
		420					425						430			
Leu	Lys	Glu	Gln	Asn	Gly	Asp	Ile	Ala	Gly	Ala	Arg	Ala	Ala	Tyr	Gln	
		435				440						445				
Leu	Val	His	Ser	Glu	Ile	Ser	Pro	Gly	Leu	Leu	Glu	Ala	Val	Ile	Lys	
	450					455					460					
His	Ala	Asn	Met	Glu	Tyr	Arg	Leu	Gly	Asn	Leu	Asp	Asp	Ala	Phe	Ser	
	465				470					475					480	
Leu	Tyr	Glu	Gln	Val	Ile	Ala	Val	Glu	Lys	Gly	Lys	Glu	His	Ser	Thr	
			485						490					495		
Ile	Leu	Pro	Leu	Leu	Tyr	Ala	Gln	Tyr	Ser	Arg	Phe	Ser	Tyr	Leu	Val	
			500					505					510			
Ser	Arg	Asp	Ala	Glu	Lys	Ala	Arg	Arg	Ile	Ile	Val	Glu	Ala	Leu	Asp	
		515					520					525				
His	Val	Gln	Pro	Ser	Lys	Pro	Leu	Met	Glu	Ala	Leu	Ile	His	Phe	Glu	
		530				535					540					
Ala	Ile	Gln	Pro	Pro	Pro	Arg	Glu	Ile	Asp	Tyr	Leu	Glu	Pro	Leu	Val	
	545				550				555						560	
Glu	Lys	Val	Ile	Lys	Pro	Asp	Ala	Asp	Ala	Gln	Asn	Ile	Ala	Ser	Ser	
				565					570					575		
Thr	Glu	Arg	Glu	Glu	Leu	Ser	Leu	Ile	Tyr	Ile	Glu	Phe	Leu	Gly	Ile	
			580					585					590			
Phe	Gly	Asp	Val	Lys	Ser	Ile	Lys	Lys	Ala	Glu	Asp	Gln	His	Val	Lys	
		595					600					605				
Leu	Phe	Tyr	Pro	His	Arg	Ser	Thr	Ser	Glu	Leu	Lys	Lys	Arg	Ser	Ala	
	610					615					620					
Asp	Asp	Phe	Leu	Ala	Ser	Asp	Arg	Thr	Lys	Met	Ala	Lys	Thr	Tyr	Asn	
	625				630					635					640	
Gly	Thr	Pro	Pro	Ala	Gln	Pro	Val	Ser	Asn	Ala	Tyr	Pro	Asn	Ala	Gln	
				645					650					655		
Ala	Gln	Trp	Ser	Gly	Gly	Tyr	Ala	Ala	Gln	Pro	Gln	Thr	Trp	Pro	Pro	

660	665	670
Ala Gln Ala Ala Pro Ala Gln Pro Gln Gln Trp Asn Pro Ala Tyr Gly		
675	680	685
Gln Gln Ala Ala Tyr Gly Ala Tyr Gly Gly Tyr Pro Ala Gly Tyr Thr		
690	695	700
Ala Pro Gln Ala Pro Thr Pro Val Pro Gln Ala Ala Tyr Gly Ala		
705	710	715
Tyr Pro Ala Gln Thr Tyr Pro Thr Gln Ser Tyr Ala Pro Pro Val Ala		
725	730	735
Ala Ala Ala Pro Ala Ala Ala Pro Val Gln Gln Pro Ala Ala Ala Val		
740	745	750
Ala Pro Gln Ala Tyr Tyr Asn Thr Tyr Tyr		
755	760	

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 617 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..617

(D) OTHER INFORMATION: / Ceres Seq. ID 1497878

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met	Asp	Lys	Val	Val	Glu	Val	Tyr	Glu	Arg	Ala	Val	Leu	Gly	Val	Thr
1			5					10					15		
Tyr	Ser	Val	Asp	Ile	Trp	Leu	His	Tyr	Cys	Thr	Phe	Ala	Ile	Asn	Thr
		20					25						30		
Tyr	Gly	Asp	Pro	Glu	Thr	Ile	Arg	Arg	Leu	Phe	Glu	Arg	Ala	Leu	Val
		35				40					45				
Tyr	Val	Gly	Thr	Asp	Phe	Leu	Ser	Ser	Pro	Leu	Trp	Asp	Lys	Tyr	Ile
		50			55						60				
Glu	Tyr	Glu	Tyr	Met	Gln	Gln	Asp	Trp	Ser	Arg	Val	Ala	Leu	Ile	Tyr
65				70				75						80	
Thr	Arg	Ile	Leu	Glu	Asn	Pro	Ile	Gln	Asn	Leu	Asp	Arg	Tyr	Phe	Ser
		85						90					95		
Ser	Phe	Lys	Glu	Leu	Ala	Glu	Thr	Arg	Pro	Leu	Ser	Glu	Leu	Arg	Ser
		100					105						110		
Ala	Glu	Glu	Ser	Ala	Ala	Ala	Ala	Val	Ala	Val	Ala	Gly	Asp	Ala	Ser
		115					120					125			
Glu	Ser	Ala	Ala	Ser	Glu	Ser	Gly	Glu	Lys	Ala	Asp	Glu	Gly	Arg	Ser
		130				135					140				
Gln	Val	Asp	Gly	Ser	Thr	Glu	Gln	Ser	Pro	Lys	Leu	Glu	Ser	Ala	Ser
145				150						155				160	
Ser	Thr	Glu	Pro	Glu	Glu	Leu	Lys	Lys	Tyr	Val	Gly	Ile	Arg	Glu	Ala
		165							170					175	
Met	Tyr	Ile	Lys	Ser	Lys	Glu	Phe	Glu	Ser	Lys	Ile	Ile	Gly	Tyr	Glu
		180						185						190	
Met	Ala	Ile	Arg	Arg	Pro	Tyr	Phe	His	Val	Arg	Pro	Leu	Asn	Val	Ala
		195					200				205				
Glu	Leu	Glu	Asn	Trp	His	Asn	Tyr	Leu	Asp	Phe	Ile	Glu	Arg	Asp	Gly
		210			215						220				
Asp	Phe	Asn	Lys	Val	Val	Lys	Leu	Tyr	Glu	Arg	Cys	Val	Val	Thr	Cys
225				230						235				240	
Ala	Asn	Tyr	Pro	Glu	Tyr	Trp	Ile	Arg	Tyr	Val	Thr	Asn	Met	Glu	Ala
		245							250				255		
Ser	Gly	Ser	Ala	Asp	Leu	Ala	Glu	Asn	Ala	Leu	Ala	Arg	Ala	Thr	Gln
		260					265						270		
Val	Phe	Val	Lys	Lys	Gln	Pro	Glu	Ile	His	Leu	Phe	Ala	Ala	Arg	Leu
		275				280						285			

Lys Glu Gln Asn Gly Asp Ile Ala Gly Ala Arg Ala Ala Tyr Gln Leu
290 295 300
Val His Ser Glu Ile Ser Pro Gly Leu Leu Glu Ala Val Ile Lys His
305 310 315 320
Ala Asn Met Glu Tyr Arg Leu Gly Asn Leu Asp Asp Ala Phe Ser Leu
325 330 335
Tyr Glu Gln Val Ile Ala Val Glu Lys Gly Lys Glu His Ser Thr Ile
340 345 350
Leu Pro Leu Leu Tyr Ala Gln Tyr Ser Arg Phe Ser Tyr Leu Val Ser
355 360 365
Arg Asp Ala Glu Lys Ala Arg Arg Ile Ile Val Glu Ala Leu Asp His
370 375 380
Val Gln Pro Ser Lys Pro Leu Met Glu Ala Leu Ile His Phe Glu Ala
385 390 395 400
Ile Gln Pro Pro Pro Arg Glu Ile Asp Tyr Leu Glu Pro Leu Val Glu
405 410 415
Lys Val Ile Lys Pro Asp Ala Asp Ala Gln Asn Ile Ala Ser Ser Thr
420 425 430
Glu Arg Glu Glu Leu Ser Leu Ile Tyr Ile Glu Phe Leu Gly Ile Phe
435 440 445
Gly Asp Val Lys Ser Ile Lys Lys Ala Glu Asp Gln His Val Lys Leu
450 455 460
Phe Tyr Pro His Arg Ser Thr Ser Glu Leu Lys Lys Arg Ser Ala Asp
465 470 475 480
Asp Phe Leu Ala Ser Asp Arg Thr Lys Met Ala Lys Thr Tyr Asn Gly
485 490 495
Thr Pro Pro Ala Gln Pro Val Ser Asn Ala Tyr Pro Asn Ala Gln Ala
500 505 510
Gln Trp Ser Gly Gly Tyr Ala Ala Gln Pro Gln Thr Trp Pro Pro Ala
515 520 525
Gln Ala Ala Pro Ala Gln Pro Gln Gln Trp Asn Pro Ala Tyr Gly Gln
530 535 540
Gln Ala Ala Tyr Gly Ala Tyr Gly Gly Tyr Pro Ala Gly Tyr Thr Ala
545 550 555 560
Pro Gln Ala Pro Thr Pro Val Pro Gln Ala Ala Ala Tyr Gly Ala Tyr
565 570 575
Pro Ala Gln Thr Tyr Pro Thr Gln Ser Tyr Ala Pro Pro Val Ala Ala
580 585 590
Ala Ala Pro Ala Ala Ala Pro Val Gln Gln Pro Ala Ala Ala Val Ala
595 600 605
Pro Gln Ala Tyr Tyr Asn Thr Tyr Tyr
610 615

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..833
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

caaaccaagt	ttcttcttaa	gctgtatttg	aatgtgtata	tatttcacac	accaaacaga	60
tcagaagcta	aaaggttaata	atataatggc	ggatttgagg	gacgaaaaag	gtaacccaat	120
ccatctaacc	gacacacagg	gaaccccaat	tgctgacctg	actgatgagc	acggtaacc	180
catgtaccta	accggtgttg	ttagctccac	tcctcagcat	aaggagagta	ctaccagcga	240
catcgacagc	caccctacta	gcacogttgg	agaaacacat	ccggcagctg	ctccaactgg	300
tgctggtgct	gccaccgctg	ccaactgcgc	aggagtctct	gctgggtactg	gagcaaccac	360
cacagggcag	caacaccatg	ggtcgcttga	agagcatctt	cgctgggtctg	gaagttcatc	420

tagctctagc	tcgggagatg	acgggcaag	agggaggagg	aagaagagca	taaaggagaa	480
aattaaagag	aagttcagta	gcggcaaa	caaggacgaa	caaacaccaa	ccaccgccc	540
aacaacagga	cctgccacta	ccgaccaacc	tcacgagaag	aagggcattc	tcgagaagat	600
caaggacaag	cttcccggcc	accataacca	caaccaccca	tgaacaccaa	tcatatgacg	660
tcctttgttac	atgaataaat	cgtttgacag	aatttcatta	gggcttatga	agaatcaata	720
tatatgtcta	gtgaagttta	ctaaatttta	gttgtgtttg	cttcgagttt	gtgaatgtga	780
ccatcgtggt	atcatgttct	tgttttat	taaagaagga	actgtat	gct	

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..185
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met	Ala	Asp	Leu	Arg	Asp	Glu	Lys	Gly	Asn	Pro	Ile	His	Leu	Thr	Asp
1			5						10					15	
Thr	Gln	Gly	Asn	Pro	Ile	Val	Asp	Leu	Thr	Asp	Glu	His	Gly	Asn	Pro
			20				25						30		
Met	Tyr	Leu	Thr	Gly	Val	Val	Ser	Ser	Thr	Pro	Gln	His	Lys	Glu	Ser
			35				40				45				
Thr	Thr	Ser	Asp	Ile	Ala	Glu	His	Pro	Thr	Ser	Thr	Val	Gly	Glu	Thr
			50				55				60				
His	Pro	Ala	Ala	Ala	Pro	Thr	Gly	Ala	Gly	Ala	Ala	Thr	Ala	Ala	Thr
			65				70				75			80	
Ala	Thr	Gly	Val	Ser	Ala	Gly	Thr	Gly	Ala	Thr	Thr	Thr	Gly	Gln	Gln
			85						90				95		
His	His	Gly	Ser	Leu	Glu	Glu	His	Leu	Arg	Arg	Ser	Gly	Ser	Ser	Ser
			100					105					110		
Ser	Ser	Ser	Ser	Glu	Asp	Asp	Gly	Gln	Gly	Arg	Arg	Lys	Lys	Ser	Ser
			115				120					125			
Ile	Lys	Glu	Lys	Ile	Lys	Glu	Lys	Phe	Ser	Ser	Gly	Lys	His	Lys	Asp
			130				135				140				
Glu	Gln	Thr	Pro	Thr	Thr	Ala	Thr	Thr	Gly	Pro	Ala	Thr	Thr	Asp	
			145				150				155				
Gln	Pro	His	Glu	Lys	Lys	Gly	Ile	Leu	Glu	Lys	Ile	Lys	Asp	Lys	Leu
			165						170					175	
Pro	Gly	His	His	Asn	His	Asn	His	Pro							
			180				185								

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met	Tyr	Leu	Thr	Gly	Val	Val	Ser	Ser	Thr	Pro	Gln	His	Lys	Glu	Ser
1				5					10					15	
Thr	Thr	Ser	Asp	Ile	Ala	Glu	His	Pro	Thr	Ser	Thr	Val	Gly	Glu	Thr
			20				25					30			
His	Pro	Ala	Ala	Ala	Pro	Thr	Gly	Ala	Gly	Ala	Ala	Thr	Ala	Ala	Thr
			35				40					45			

Ala Thr Gly Val Ser Ala Gly Thr Gly Ala Thr Thr Thr Gly Gln Gln
50 55 60
His His Gly Ser Leu Glu Glu His Leu Arg Arg Ser Gly Ser Ser Ser
65 70 75 80
Ser Ser Ser Ser Glu Asp Asp Gly Gln Gly Gly Arg Arg Lys Lys Ser
85 90 95
Ile Lys Glu Lys Ile Lys Glu Lys Phe Ser Ser Gly Lys His Lys Asp
100 105 110
Glu Gln Thr Thr Thr Thr Ala Thr Thr Thr Gly Pro Ala Thr Thr Asp
115 120 125
Gln Pro His Glu Lys Lys Gly Ile Leu Glu Lys Ile Lys Asp Lys Leu
130 135 140
Pro Gly His His Asn His Asn His Pro
145 150

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1122 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1122

(D) OTHER INFORMATION: / Ceres Seq. ID 1497886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

agtctagtca	tttctcagac	tctgacctca	ctgatctcca	atggcgaaaa	ccctagctcg	60
ctccacagcg	tcacgcacat	ccaagcgctt	attctccacc	tcoggagcca	ccactccttc	120
ccctctcttat	attctctccc	gtcgatcaac	cccgggtgtc	tcocatgcgc	tcggattctat	180
ctcttcccttg	aatcggttca	caacgattcg	aactcgaatg	gataggctcg	gtggatcgta	240
ctctctctcta	aaatccgggt	cgaatttcag	cgaccgagca	cccactgaga	tggcgccggt	300
gtttctcggc	tgcgattatg	agcattgggt	gattgtaatg	gacaaacctg	gaggcgaaaa	360
cgctactaag	cagcaaatga	ttgattgta	tgttcaaac	ctagctaaaa	ttatcgcgag	420
tgaggagaaga	gctaagaaga	agatttataa	tgatcgtgt	gaaaggatt	ttggatttgg	480
ttgtgagatt	gatgaagaga	catcaaacaa	actgaaggga	cttccgtgtg	ttctcttcat	540
caatctcaca	accaaactcca	aaaaactttt	ctctccatc	aaaatcctcc	gacgatgaca	600
accatagctg	cagctggcct	caacgtgcgc	actccacgag	tggtcggtcg	acctgtggct	660
cgtgtattag	gtccgggtccg	gttgaattac	ccgtggaaat	tcggttcgat	gaagcggatg	720
gttgtggtta	aggctacatc	ggaaggagag	atatcgagga	aggtggagaa	gagtatacaa	780
gaagctaagg	agacatcgcc	tgatgatccg	gtgagcgggg	agtggtgtagc	ggcttgggac	840
gaggtggagg	agctgagtcg	ggcggcgag	catgctaggg	acaaagaaga	agcgtgtggc	900
tcgatctctt	tggaagagta	ttgcaatgat	aaycctgaga	ctgatgagtg	tcgtacttat	960
gataattaaa	aaatatgttt	ttgatgttgc	aattatgaaa	cttaggtgat	ggtacaaagt	1020
ttgtctctct	tgctccttgt	tgttatgttt	gtgtttttgg	tttggttgat	gattgtaagt	1080
tgataaatga	atatgaatag	tacaatacac	aacatatgtt	tc		

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..185

(D) OTHER INFORMATION: / Ceres Seq. ID 1497887

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met	Ala	Lys	Thr	Leu	Ala	Arg	Ser	Thr	Ala	Ser	Arg	Ile	Thr	Lys	Arg
1				5				10				15			
Leu	Phe	Ser	Thr	Ser	Gly	Ala	Thr	Thr	Pro	Ser	Pro	Ser	Thr	Ile	Leu
				20				25					30		

Ser Arg Arg Ser Thr Pro Val Phe Ser His Ala Val Gly Phe Ile Ser
35 40 45
Ser Leu Asn Arg Phe Thr Thr Ile Arg Thr Arg Met Asp Arg Ser Gly
50 55 60
Gly Ser Tyr Ser Pro Leu Lys Ser Gly Ser Asn Phe Ser Asp Arg Ala
65 70 75 80
Pro Thr Glu Met Ala Pro Leu Phe Pro Gly Cys Asp Tyr Glu His Trp
85 90 95
Leu Ile Val Met Asp Lys Pro Gly Gly Glu Asn Ala Thr Lys Gln Gln
100 105 110
Met Ile Asp Cys Tyr Val Gln Thr Leu Ala Lys Ile Ile Gly Ser Glu
115 120 125
Glu Glu Ala Lys Lys Lys Ile Tyr Asn Val Ser Cys Glu Arg Tyr Phe
130 135 140
Gly Phe Gly Cys Glu Ile Asp Glu Glu Thr Ser Asn Lys Leu Glu Gly
145 150 155 160
Leu Pro Gly Val Leu Phe Ile Asn Leu Thr Thr Lys Ser Lys Lys Leu
165 170 175
Phe Ser Ser Ile Lys Ile Leu Arg Arg
180 185

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..126
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497888

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Asp Arg Ser Gly Gly Ser Tyr Ser Pro Leu Lys Ser Gly Ser Asn
1 5 10 15
Phe Ser Asp Arg Ala Pro Thr Glu Met Ala Pro Leu Phe Pro Gly Cys
20 25 30
Asp Tyr Glu His Trp Leu Ile Val Met Asp Lys Pro Gly Gly Glu Asn
35 40 45
Ala Thr Lys Gln Gln Met Ile Asp Cys Tyr Val Gln Thr Leu Ala Lys
50 55 60
Ile Ile Gly Ser Glu Glu Glu Ala Lys Lys Lys Ile Tyr Asn Val Ser
65 70 75 80
Cys Glu Arg Tyr Phe Gly Phe Gly Cys Glu Ile Asp Glu Glu Thr Ser
85 90 95
Asn Lys Leu Glu Gly Leu Pro Gly Val Leu Phe Ile Asn Leu Thr Thr
100 105 110
Lys Ser Lys Lys Leu Phe Ser Ser Ile Lys Ile Leu Arg Arg
115 120 125

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..124
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497889

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Thr Thr Ile Ala Ala Gly Leu Asn Val Ala Thr Pro Arg Val

Met	Ala	Gly	Arg	Gly	Gly	Val	Val	Lys	Asp	His	His	His	Asn	Arg	Trp
1			5						10					15	
Val	Trp	Asp	Lys	Ile	Leu	Pro	Pro	Glu	Cys	Ala	Pro	Asn	Ser	Ser	Ile
			20					25					30		

Leu Arg Leu Ser Ala Asp Leu Arg Trp Glu Glu Ala His Glu Pro Leu
35 40 45
His Val Asp Ile Asp Thr Gly Lys Val Cys Gly Val Gly Pro Gly Met
50 55 60
Ala Phe Ala Asn Ala Val Lys Asn Arg Val Glu Thr Asp Ser Ala Val
65 70 75 80
Ile Gly Leu Val Pro Cys Ala Ser Gly Gly Thr Ala Ile Lys Glu Trp
85 90 95
Glu Arg Gly Ser His Leu Tyr Glu Arg Met Val Lys Arg Thr Glu Glu
100 105 110
Ser Arg Lys Cys Gly Gly Glu Ile Lys Ala Val Leu Trp Tyr Gln Gly
115 120 125
Glu Ser Asp Val Leu Asp Ile His Asp Ala Glu Ser Tyr Gly Asn Asn
130 135 140
Met Asp Arg Leu Ile Lys Asn Leu Arg His Asp Leu Asn Leu Pro Ser
145 150 155 160
Leu Pro Ile Ile Gln Val Ala Ile Ala Ser Gly Gly Gly Tyr Ile Asp
165 170 175
Lys Val Arg Glu Ala Gln Leu Gly Leu Lys Leu Ser Asn Val Val Cys
180 185 190
Val Asp Ala Lys Gly Leu Pro Leu Lys Ser Asp Asn Leu His Leu Thr
195 200 205
Thr Glu Ala Gln Val Gln Leu Gly Leu Ser Leu Ala Gln Ala Tyr Leu
210 215 220
Ser Asn Phe Cys
225

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..165
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497892

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Ala Phe Ala Asn Ala Val Lys Asn Arg Val Glu Thr Asp Ser Ala
1 5 10 15
Val Ile Gly Leu Val Pro Cys Ala Ser Gly Gly Thr Ala Ile Lys Glu
20 25 30
Trp Glu Arg Gly Ser His Leu Tyr Glu Arg Met Val Lys Arg Thr Glu
35 40 45
Glu Ser Arg Lys Cys Gly Gly Glu Ile Lys Ala Val Leu Trp Tyr Gln
50 55 60
Gly Glu Ser Asp Val Leu Asp Ile His Asp Ala Glu Ser Tyr Gly Asn
65 70 75 80
Asn Met Asp Arg Leu Ile Lys Asn Leu Arg His Asp Leu Asn Leu Pro
85 90 95
Ser Leu Pro Ile Ile Gln Val Ala Ile Ala Ser Gly Gly Gly Tyr Ile
100 105 110
Asp Lys Val Arg Glu Ala Gln Leu Gly Leu Lys Leu Ser Asn Val Val
115 120 125
Cys Val Asp Ala Lys Gly Leu Pro Leu Lys Ser Asp Asn Leu His Leu
130 135 140
Thr Thr Glu Ala Gln Val Gln Leu Gly Leu Ser Leu Ala Gln Ala Tyr
145 150 155 160
Leu Ser Asn Phe Cys
165

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 123 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..123
 (D) OTHER INFORMATION: / Ceres Seq. ID 1497893
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:
Met Val Lys Arg Thr Glu Glu Ser Arg Lys Cys Gly Gly Glu Ile Lys
1 5 10 15
Ala Val Leu Trp Tyr Gln Gly Glu Ser Asp Val Leu Asp Ile His Asp
 20 25 30
Ala Glu Ser Tyr Gly Asn Asn Met Asp Arg Leu Ile Lys Asn Leu Arg
 35 40 45
His Asp Leu Asn Leu Pro Ser Leu Pro Ile Ile Gln Val Ala Ile Ala
 50 55 60
Ser Gly Gly Gly Tyr Ile Asp Lys Val Arg Glu Ala Gln Leu Gly Leu
65 70 75 80
Lys Leu Ser Asn Val Val Cys Val Asp Ala Lys Gly Leu Pro Leu Lys
 85 90 95
Ser Asp Asn Leu His Leu Thr Thr Glu Ala Gln Val Gln Leu Gly Leu
 100 105 110
Ser Leu Ala Gln Ala Tyr Leu Ser Asn Phe Cys
 115 120

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1166 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1166
(D) OTHER INFORMATION: / Ceres Seq. ID 1497894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

```
atatatacaa cgaggaaaaa tagtactatt ttctacgaac ttcagaatct ttcgtctctc 60
ttaattattt ttctcaaat ttctgaaaca tctagttttc ttctcaacca gccaatcatg 120
ggtagtgatc atcatcatcg aaagctccac gttatgttct tccctttcat ggcttatggg 180
cacatgatac caactctaga catggctaag ctttctctta gcagaggagc caaatccaca 240
atcctcacca catctctcaa ctccaagatc ctccaaaaac ccactgcacac attcaagaat 300
ctgaatccgg gtctcgaaat cgacatccag atcttcgatt tccttgcggt ggagctgggg 360
ttaccagaag gatgtgaaaa cggttgatttc ttacattcaa acaaccaatga tgataaaaaa 420
gagatgatcg tgaattctta ttctcgaca aggtttttca aagaccagct tgagaaactc 480
ctcgggacaa cgagaccaga ctgtctttatc gccgacatgt tcttcccctg ggctactgta 540
gctgctggga agttcaatgt gccaaagactt gtgttccacg gcaactggcta cttctcttaa 600
tgcgctgggt attgcatcgg agtgcataaa ccacagaaga gagtgcttc aagctctgag 660
ccattttgta ttcccagact cctcggggaa atgtgtataa ctgaagaaca gatcatagat 720
ggcgatggag aatccgacat cggaaaagtt atgactgaag ttagggaatc ggaagtgaag 780
agctcaggag ttgttttgaa tagttttctac gagctagaac atgattacgc cgatttttac 840
aaaagtgtgt tacaaaagag agcgtggcat atcggttccg tatcggttta caacagggga 900
tttgaggaga aggcgtgagag aggaagaaaa gcgaacattg atgasgctga atgcctcaaa 960
tggcttgact ccaagaaacc aaattcagtc atttatgttt cctttgggag cgtggtcttc 1020
ttcaagaatg aacagttatt cgagatcgct gcaggggttag aagcttccgg tacaagtttc 1080
atttgggttg ttaggaaaaa caaaggtatt gaaattgacg tttagagcct atattatata 1140
actgtaattt gggtagcttt gatttt
```

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..374
(D) OTHER INFORMATION: / Ceres Seq. ID 1497895

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Ile	Tyr	Thr	Thr	Arg	Lys	Asn	Ser	Thr	Ile	Phe	Tyr	Glu	Leu	Gln	Asn
1				5				10						15	
Leu	Ser	Ser	Leu	Leu	Ile	Ile	Phe	Leu	Lys	Phe	Leu	Glu	Thr	Ser	Ser
				20			25					30			
Phe	Leu	Phe	Asn	Gln	Pro	Ile	Met	Gly	Ser	Asp	His	His	Arg	Lys	
		35					40				45				
Leu	His	Val	Met	Phe	Phe	Pro	Phe	Met	Ala	Tyr	Gly	His	Met	Ile	Pro
		50				55					60				
Thr	Leu	Asp	Met	Ala	Lys	Leu	Phe	Ser	Ser	Arg	Gly	Ala	Lys	Ser	Thr
		65				70				75				80	
Ile	Leu	Thr	Thr	Ser	Leu	Asn	Ser	Lys	Ile	Leu	Gln	Lys	Pro	Ile	Asp
				85					90					95	
Thr	Phe	Lys	Asn	Leu	Asn	Pro	Gly	Leu	Glu	Ile	Asp	Ile	Gln	Ile	Phe
			100				105						110		
Asp	Phe	Pro	Cys	Val	Glu	Leu	Gly	Leu	Pro	Glu	Gly	Cys	Glu	Asn	Val
		115					120					125			
Asp	Phe	Phe	Thr	Ser	Asn	Asn	Asp	Asp	Lys	Asn	Glu	Met	Ile	Val	
		130				135				140					
Lys	Phe	Phe	Phe	Ser	Thr	Arg	Phe	Phe	Lys	Asp	Gln	Leu	Glu	Lys	Leu
		145				150				155				160	
Leu	Gly	Thr	Thr	Arg	Pro	Asp	Cys	Leu	Ile	Ala	Asp	Met	Phe	Phe	Pro
				165				170						175	
Trp	Ala	Thr	Glu	Ala	Ala	Gly	Lys	Phe	Asn	Val	Pro	Arg	Leu	Val	Phe
		180					185						190		
His	Gly	Thr	Gly	Tyr	Phe	Ser	Leu	Cys	Ala	Gly	Tyr	Cys	Ile	Gly	Val
		195				200						205			
His	Lys	Pro	Gln	Lys	Arg	Val	Ala	Ser	Ser	Ser	Glu	Pro	Phe	Val	Ile
		210				215					220				
Pro	Glu	Leu	Pro	Gly	Asn	Ile	Val	Ile	Thr	Glu	Glu	Gln	Ile	Ile	Asp
				230						235				240	
Gly	Asp	Gly	Glu	Ser	Asp	Met	Gly	Lys	Phe	Met	Thr	Glu	Val	Arg	Glu
				245					250					255	
Ser	Glu	Val	Lys	Ser	Ser	Gly	Val	Val	Leu	Asn	Ser	Phe	Tyr	Glu	Leu
		260					265						270		
Glu	His	Asp	Tyr	Ala	Asp	Phe	Tyr	Lys	Ser	Cys	Val	Gln	Lys	Arg	Ala
		275					280					285			
Trp	His	Ile	Gly	Pro	Leu	Ser	Val	Tyr	Asn	Arg	Gly	Phe	Glu	Glu	Lys
		290				295					300				
Ala	Glu	Arg	Gly	Lys	Lys	Ala	Asn	Ile	Asp	Xaa	Ala	Glu	Cys	Leu	Lys
		305				310				315				320	
Trp	Leu	Asp	Ser	Lys	Lys	Pro	Asn	Ser	Val	Ile	Tyr	Val	Ser	Phe	Gly
				325					330					335	
Ser	Val	Ala	Phe	Phe	Lys	Asn	Glu	Gln	Leu	Phe	Glu	Ile	Ala	Ala	Gly
		340					345						350		
Leu	Glu	Ala	Ser	Gly	Thr	Ser	Phe	Ile	Trp	Val	Val	Arg	Lys	Thr	Lys
		355					360					365			
Gly	Ile	Glu	Ile	Asp	Val										
															370

(2) INFORMATION FOR SEQ ID NO:36:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..335
 (D) OTHER INFORMATION: / Ceres Seq. ID 1497896
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met	Gly	Ser	Asp	His	His	His	Arg	Lys	Leu	His	Val	Met	Phe	Phe	Pro
1				5					10					15	
Phe	Met	Ala	Tyr	Gly	His	Met	Ile	Pro	Thr	Leu	Asp	Met	Ala	Lys	Leu
		20					25					30			
Phe	Ser	Ser	Arg	Gly	Ala	Lys	Ser	Thr	Ile	Leu	Thr	Thr	Ser	Leu	Asn
		35					40					45			
Ser	Lys	Ile	Leu	Gln	Lys	Pro	Ile	Asp	Thr	Phe	Lys	Asn	Leu	Asn	Pro
		50					55				60				
Gly	Leu	Glu	Ile	Asp	Ile	Gln	Ile	Phe	Asp	Phe	Pro	Cys	Val	Glu	Leu
65					70				75					80	
Gly	Leu	Pro	Glu	Gly	Cys	Glu	Asn	Val	Asp	Phe	Phe	Thr	Ser	Asn	Asn
				85					90					95	
Asn	Asp	Asp	Lys	Asn	Glu	Met	Ile	Val	Lys	Phe	Phe	Phe	Ser	Thr	Arg
			100					105					110		
Phe	Phe	Lys	Asp	Gln	Leu	Glu	Lys	Leu	Leu	Gly	Thr	Thr	Arg	Pro	Asp
		115					120					125			
Cys	Leu	Ile	Ala	Asp	Met	Phe	Phe	Pro	Trp	Ala	Thr	Glu	Ala	Ala	Gly
		130				135					140				
Lys	Phe	Asn	Val	Pro	Arg	Leu	Val	Phe	His	Gly	Thr	Gly	Tyr	Phe	Ser
145					150					155				160	
Leu	Cys	Ala	Gly	Tyr	Cys	Ile	Gly	Val	His	Lys	Pro	Gln	Lys	Arg	Val
			165					170					175		
Ala	Ser	Ser	Ser	Glu	Pro	Phe	Val	Ile	Pro	Glu	Leu	Pro	Gly	Asn	Ile
			180					185					190		
Val	Ile	Thr	Glu	Gln	Ile	Ile	Asp	Gly	Asp	Gly	Glu	Ser	Asp	Met	
		195					200					205			
Gly	Lys	Phe	Met	Thr	Glu	Val	Arg	Glu	Ser	Glu	Val	Lys	Ser	Ser	Gly
		210				215					220				
Val	Val	Leu	Asn	Ser	Phe	Tyr	Glu	Leu	Glu	His	Asp	Tyr	Ala	Asp	Phe
225					230					235				240	
Tyr	Lys	Ser	Cys	Val	Gln	Lys	Arg	Ala	Trp	His	Ile	Gly	Pro	Leu	Ser
			245						250					255	
Val	Tyr	Asn	Arg	Gly	Phe	Glu	Glu	Lys	Ala	Glu	Arg	Gly	Lys	Lys	Ala
		260					265						270		
Asn	Ile	Asp	Xaa	Ala	Glu	Cys	Leu	Lys	Trp	Leu	Asp	Ser	Lys	Lys	Pro
		275					280				285				
Asn	Ser	Val	Ile	Tyr	Val	Ser	Phe	Gly	Ser	Val	Ala	Phe	Phe	Lys	Asn
		290				295					300				
Glu	Gln	Leu	Phe	Glu	Ile	Ala	Ala	Gly	Leu	Glu	Ala	Ser	Gly	Thr	Ser
305					310					315				320	
Phe	Ile	Trp	Val	Val	Arg	Lys	Thr	Lys	Gly	Ile	Glu	Ile	Asp	Val	
			325						330				335		

(2) INFORMATION FOR SEQ ID NO:37:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 323 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..323

(D) OTHER INFORMATION: / Ceres Seq. ID 1497897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met Phe Phe Pro Phe Met Ala Tyr Gly His Met Ile Pro Thr Leu Asp
1 5 10 15
Met Ala Lys Leu Phe Ser Ser Arg Gly Ala Lys Ser Thr Ile Leu Thr
20 25 30
Thr Ser Leu Asn Ser Lys Ile Leu Gln Lys Pro Ile Asp Thr Phe Lys
35 40 45
Asn Leu Asn Pro Gly Leu Glu Ile Asp Ile Gln Ile Phe Asp Phe Pro
50 55 60
Cys Val Glu Leu Gly Leu Pro Glu Gly Cys Glu Asn Val Asp Phe Phe
65 70 75 80
Thr Ser Asn Asn Asn Asp Asp Lys Asn Glu Met Ile Val Lys Phe Phe
85 90 95
Phe Ser Thr Arg Phe Phe Lys Asp Gln Leu Glu Lys Leu Leu Gly Thr
100 105 110
Thr Arg Pro Asp Cys Leu Ile Ala Asp Met Phe Phe Pro Trp Ala Thr
115 120 125
Glu Ala Ala Gly Lys Phe Asn Val Pro Arg Leu Val Phe His Gly Thr
130 135 140
Gly Tyr Phe Ser Leu Cys Ala Gly Tyr Cys Ile Gly Val His Lys Pro
145 150 155 160
Gln Lys Arg Val Ala Ser Ser Ser Glu Pro Phe Val Ile Pro Glu Leu
165 170 175
Pro Gly Asn Ile Val Ile Thr Glu Glu Gln Ile Ile Asp Gly Asp Gly
180 185 190
Glu Ser Asp Met Gly Lys Phe Met Thr Glu Val Arg Glu Ser Glu Val
195 200 205
Lys Ser Ser Gly Val Val Leu Asn Ser Phe Tyr Glu Leu Glu His Asp
210 215 220
Tyr Ala Asp Phe Tyr Lys Ser Cys Val Gln Lys Arg Ala Trp His Ile
225 230 235 240
Gly Pro Leu Ser Val Tyr Asn Arg Gly Phe Glu Glu Lys Ala Glu Arg
245 250 255
Gly Lys Lys Ala Asn Ile Asp Xaa Ala Glu Cys Leu Lys Trp Leu Asp
260 265 270
Ser Lys Lys Pro Asn Ser Val Ile Tyr Val Ser Phe Gly Ser Val Ala
275 280 285
Phe Phe Lys Asn Glu Gln Leu Phe Glu Ile Ala Ala Gly Leu Glu Ala
290 295 300
Ser Gly Thr Ser Phe Ile Trp Val Val Arg Lys Thr Lys Gly Ile Glu
305 310 315 320
Ile Asp Val

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 584 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..584
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

aagtgattaa gcttatgcag agtttccaaat ccaaggagta tggttagggag acaattgcct 60
ggatgcatta ctattgggtt ttgaccaatg aagggatoga gtctttgaga acttatctta 120
atcttcacatc tgatgttggt cctgctactt tgaagaagtc agctaagcct ggtggtgctc 180
catttgggtg cccacctggt gatcgctcaa gaggacctcg ccatgaagga ggagaccgtc 240
ccagggtttg tgaccgtgat gggaccgtg caggtcctcg agctgggtgt gagtttggag 300

gtgaaaaggg	tggagctcct	gcagattacc	agccatcttt	ccaaggaagt	gggcgtgggt	360
ttggccgtgg	tgctggtggc	tacagcgcag	ctgcaccatc	tggttcaggt	ttgccttgaa	420
aaagaaatgt	ctttagggtga	cagtaagacc	atggaggagt	tttcagcttt	aaattttgct	480
tttgaattc	agattccgga	atccttcata	atctctatct	gagtttagtt	ttgttgttga	540
atcaaacatc	cqattttaag	ttatgttcat	tccatcttct	cttc		

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..138
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Val	Ile	Lys	Leu	Met	Gln	Ser	Phe	Lys	Ser	Lys	Glu	Tyr	Val	Arg	Glu
1			5					10					15		
Thr	Ile	Ala	Trp	Met	His	Tyr	Tyr	Trp	Phe	Leu	Thr	Asn	Glu	Gly	Ile
			20					25				30			
Glu	Phe	Leu	Arg	Thr	Tyr	Leu	Asn	Leu	Pro	Ser	Asp	Val	Val	Pro	Ala
			35				40				45				
Thr	Leu	Lys	Lys	Ser	Ala	Lys	Pro	Gly	Gly	Arg	Pro	Phe	Gly	Gly	Pro
			50			55				60					
Pro	Gly	Asp	Arg	Ser	Arg	Gly	Pro	Arg	His	Glu	Gly	Gly	Asp	Arg	Pro
			65			70				75					80
Arg	Phe	Gly	Asp	Arg	Asp	Gly	Tyr	Arg	Ala	Gly	Pro	Arg	Ala	Gly	Gly
						85				90				95	
Glu	Phe	Gly	Gly	Glu	Lys	Gly	Gly	Ala	Pro	Ala	Asp	Tyr	Gln	Pro	Ser
						100				105			110		
Phe	Gln	Gly	Ser	Gly	Arg	Gly	Phe	Gly	Arg	Gly	Ala	Gly	Gly	Tyr	Ser
						115				120			125		
Ala	Ala	Ala	Pro	Ser	Gly	Ser	Gly	Leu	Pro						
						130				135					

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497900

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met	Gln	Ser	Phe	Lys	Ser	Lys	Glu	Tyr	Val	Arg	Glu	Thr	Ile	Ala	Trp
1				5						10				15	
Met	His	Tyr	Tyr	Trp	Phe	Leu	Thr	Asn	Glu	Gly	Ile	Glu	Phe	Leu	Arg
				20				25					30		
Thr	Tyr	Leu	Asn	Leu	Pro	Ser	Asp	Val	Val	Pro	Ala	Thr	Leu	Lys	Lys
				35			40					45			
Ser	Ala	Lys	Pro	Gly	Gly	Arg	Pro	Phe	Gly	Gly	Pro	Pro	Gly	Asp	Arg
				50			55			60					
Ser	Arg	Gly	Pro	Arg	His	Glu	Gly	Gly	Asp	Arg	Pro	Arg	Phe	Gly	Asp
				65			70			75				80	
Arg	Asp	Gly	Tyr	Arg	Ala	Gly	Pro	Arg	Ala	Gly	Gly	Glu	Phe	Gly	Gly
				85						90				95	
Glu	Lys	Gly	Gly	Ala	Pro	Ala	Asp	Tyr	Gln	Pro	Ser	Phe	Gln	Gly	Ser
				100						105				110	

Gly Arg Gly Phe Gly Arg Gly Ala Gly Gly Tyr Ser Ala Ala Ala Pro
115 120 125
Ser Gly Ser Gly Leu Pro
130

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Met His Tyr Tyr Trp Phe Leu Thr Asn Glu Gly Ile Glu Phe Leu Arg
1 5 10 15
Thr Tyr Leu Asn Leu Pro Ser Asp Val Val Pro Ala Thr Leu Lys Lys
20 25 30
Ser Ala Lys Pro Gly Gly Arg Pro Phe Gly Gly Pro Pro Gly Asp Arg
35 40 45
Ser Arg Gly Pro Arg His Glu Gly Gly Asp Arg Pro Arg Phe Gly Asp
50 55 60
Arg Asp Gly Tyr Arg Ala Gly Pro Arg Ala Gly Glu Phe Gly Gly
65 70 75 80
Glu Lys Gly Gly Ala Pro Ala Asp Tyr Gln Pro Ser Phe Gln Gly Ser
85 90 95
Gly Arg Gly Phe Gly Arg Gly Ala Gly Tyr Ser Ala Ala Ala Pro
100 105 110
Ser Gly Ser Gly Leu Pro
115

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1128 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1128
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

acatcccttag tttttctaaa ccacaaaata aaaactttctg ttcatagaat cttatggtaa 60
gttttgagag aaatatccga gtattgcttc agtccgtagc atacgaatca agcgagacga 120
tggtgcagcc tggaaaccgag ataaaaagcaa gcgacctaac cctactagta atcacgatta 180
tactcttcgc aatcttctac gtgtgcttgg smttcggttt gottccgctg gacctctcgc 240
caattttact cacagaatca catcaaccct ttcactgact ccgacgttga atcccgtaac 300
agttattacgg cgggtcgctgg gctcgacgag gctatcatca actcatttcc gacgtttctc 360
tactcgagag tgaaggagcg gagaatcggg ataggtggcg tcgagtgctc agtgtgtatc 420
tgtgtgttcg aagaccatga aacgctccgt ttgatgcctg atgtgctcca cgtgtttcat 480
gctgatttgt taagtgtctg gctctctgat cactccactg gtccactctg tcgtgtggat 540
ctttgcttac aaccgggtga gagaagctac ttgaatccgg aaccggatct tgtagaatct 600
acaaactcgc atttgtttga ttgtgtgacg tggaccaata ggaacagacc gtctcggtca 660
tggtcaacga gattgtctca atgtcgagtc tccagatat taatctcgag atcgatttcg 720
accggacatt ctgtgggtca accgctagat aatttagacc gggttacgct tcggttacca 780
gaagaagtcg ggaggcaact gacgaagaaa acggtggaca acgtggcatt ttctcaaggct 840
aggagctcac ggcgtgttta cagaagcaga agtgcgggaa gcgagaggag tgtcttctcg 900
taccacacgc ggaatgcatt cttctctgat tgtgcatggt ccacctctcg tggcgagaaa 960
cggtggtcgc cgtcaaaaga ttttcgcga atatcagttg aacaatcyca gntagatgat 1020

cgagtgtagt agataggcaa tttcttggt gtgtgttttt tgctaacaac atttggttt 1080
gtctgtttgc tatcatttgc ttttgaaca tgaccaatat tcaagtcc

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..191

(D) OTHER INFORMATION: / Ceres Seq. ID 1497903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Met	Pro	Glu	Cys	Cys	His	Val	Phe	His	Ala	Asp	Cys	Val	Ser	Val	Trp	
1			5						10					15		
Leu	Ser	Asp	His	Ser	Thr	Cys	Pro	Leu	Cys	Arg	Val	Asp	Leu	Cys	Leu	
			20					25					30			
Gln	Pro	Gly	Glu	Arg	Ser	Tyr	Leu	Asn	Pro	Glu	Pro	Asp	Leu	Val	Glu	
			35				40					45				
Ser	Thr	Asn	Ser	His	Leu	Phe	Asp	Gly	Val	Thr	Trp	Thr	Asn	Arg	Asn	
			50			55				60						
Arg	Pro	Ser	Arg	Ser	Trp	Ser	Thr	Arg	Leu	Ser	Gln	Cys	Arg	Val	Ser	
			65			70			75					80		
Gln	Ile	Leu	Ile	Ser	Arg	Ser	His	Ser	Thr	Gly	His	Ser	Val	Val	Gln	
			85						90				95			
Pro	Leu	Asp	Asn	Leu	Asp	Arg	Phe	Thr	Leu	Arg	Leu	Pro	Glu	Glu	Val	
			100				105						110			
Arg	Arg	Gln	Leu	Thr	Lys	Lys	Thr	Val	Asp	Asn	Val	Ala	Phe	Ser	Gln	
			115				120					125				
Ala	Arg	Ser	Ser	Arg	Arg	Gly	Tyr	Arg	Ser	Arg	Ser	Ala	Gly	Ser	Glu	
			130			135					140					
Arg	Ser	Val	Phe	Ser	Tyr	Gln	Arg	Arg	Met	His	Ser	Phe	Ser	Asp	Cys	
			145			150			155					160		
Ala	Trp	Ser	Thr	Ser	Cys	Gly	Gly	Glu	Ala	Val	Ala	Pro	Ser	Lys	Asp	
			165					170					175			
Phe	Arg	Arg	Ile	Ser	Val	Glu	Gln	Xaa	Gln	Xaa	Asp	Asp	Arg	Val		
			180				185						190			

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1208 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1208

(D) OTHER INFORMATION: / Ceres Seq. ID 1497904

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ataacgaagc	ggttggaaga	agatgaaact	gttcgacgcg	cactgtcacc	ttaagagacc	60
gaggattatc	accaaagctc	ctcagataat	cacctccgcc	gttgcttcgc	gcgtctctgc	120
tttcgcgcgc	aatggagctc	ccgagaaaag	ttggagtttg	gtcaaaagaga	tgggagctaa	180
atacctctct	gtgttctctt	gctttgggat	ccatccatgg	tatgtagcag	agaggagctc	240
tcaatggttt	gagacataag	agtttctttg	agaccactcc	tactgtctgt	gttgagagaaa	300
tttggtttga	caaaggggtc	aagggaaggg	agattgattt	ctcagaacac	gttaccgtct	360
tctgcacaac	gcttggaact	gcaaggaagt	tgaagaaacc	tgcgtcagtt	cattgtgttc	420
gtgcatttgg	ggatctactc	gagatattaa	aatctgttag	gccttttctc	tctgggggtca	480
tgtctcaact	gtatttgggt	tytctgtaga	tggttcctga	atttgtctaag	ctcgggtgat	540
atttctcctt	ctccgggttc	cttatgtcca	tgagtggaga	aaaagccaag	aagatgttga	600
aagcagttcc	atctgatagg	atcttattgg	agacggattc	accagatgca	ctaccaaaagg	660

cagatgcagg ttgtctctac ttgttagacg gagatccttc tctacccgaa gaaggaaatt 720
cagctcagga tcttgattct gcttcataatg ataagcctaa tgtgtctagt gactcgatga 780
agttaacaaa ggaacacatt aatcaccogg ctaattattca tatcgctact ggatagttag 840
cgcatgtgtt ggatatgaag aatgaagaac tcgcgggaact aagttatcaa aatgctgttc 900
ggttattctc ttacgaaggt tcaaagatac ttcttgacag aggtactggt gatgtctctg 960
gtcacactca aaaccagtca acaacacatg tatcatgagt tcttacttct taagaaatcg 1020
tagtgtttct catcaactcta ttacgagtct ttgaatttgg actctctctt ttttttttct 1080
tttttttga atgtttgaat ttggaattat tgtactatgt ttatagacaa tcacactttt 1140
ctttgtacaa actacaagg ttctgatttt gtgtgaaaaa taattcagtt aatgatgtga 1200
ttagagcc

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 172 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..172

(D) OTHER INFORMATION: / Ceres Seq. ID 1497905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Met Leu His Ser Tyr Leu Gly Xaa Ala Glu Met Val Pro Glu Phe Ala
1 5 10 15
Lys Leu Gly Ala Tyr Phe Ser Phe Ser Gly Phe Leu Met Ser Met Ser
20 25 30
Glu Lys Lys Ala Lys Lys Met Leu Lys Ala Val Pro Ser Asp Arg Ile
35 40 45
Leu Leu Glu Thr Asp Ser Pro Asp Ala Leu Pro Lys Ala Glu Ser Gly
50 55 60
Cys Leu Tyr Phe Val Asp Gly Asp Pro Ser Leu Pro Glu Glu Gly Asn
65 70 75 80
Ser Ala Gln Asp Leu Asp Ser Ala Ser Tyr Asp Lys Pro Asn Val Ser
85 90 95
Ser Asp Ser Met Lys Leu Thr Lys Glu Thr Leu Asn His Pro Ala Asn
100 105 110
Ile His Ile Val Leu Gly Tyr Val Ala Gln Leu Leu Asp Met Lys Asn
115 120 125
Glu Glu Leu Ala Glu Leu Ser Tyr Gln Asn Ala Val Arg Leu Phe Ser
130 135 140
Tyr Glu Gly Ser Lys Ile Leu Leu Asp Arg Gly Thr Gly Asp Val Ser
145 150 155 160
Gly His Thr Gln Asn Gln Ser Thr Thr His Val Ser
165 170

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1497906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met Val Pro Glu Phe Ala Lys Leu Gly Ala Tyr Phe Ser Phe Ser Gly
1 5 10 15
Phe Leu Met Ser Met Ser Glu Lys Lys Ala Lys Lys Met Leu Lys Ala
20 25 30
Val Pro Ser Asp Arg Ile Leu Leu Glu Thr Asp Ser Pro Asp Ala Leu

35 40 45
Pro Lys Ala Glu Ser Gly Cys Leu Tyr Phe Val Asp Gly Asp Pro Ser
50 55 60
Leu Pro Glu Glu Gly Asn Ser Ala Gln Asp Leu Asp Ser Ala Ser Tyr
65 70 75 80
Asp Lys Pro Asn Val Ser Ser Asp Ser Met Lys Leu Thr Lys Glu Thr
85 90 95
Leu Asn His Pro Ala Asn Ile His Ile Val Leu Gly Tyr Val Ala Gln
100 105 110
Leu Leu Asp Met Lys Asn Glu Glu Leu Ala Glu Leu Ser Tyr Gln Asn
115 120 125
Ala Val Arg Leu Phe Ser Tyr Glu Gly Ser Lys Ile Leu Leu Asp Arg
130 135 140
Gly Thr Gly Asp Val Ser Gly His Thr Gln Asn Gln Ser Thr Thr His
145 150 155 160
Val Ser

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497907

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Met Ser Met Ser Glu Lys Lys Ala Lys Lys Met Leu Lys Ala Val Pro
1 5 10 15
Ser Asp Arg Ile Leu Leu Glu Thr Asp Ser Pro Asp Ala Leu Pro Lys
20 25 30
Ala Glu Ser Gly Cys Leu Tyr Phe Val Asp Gly Asp Pro Ser Leu Pro
35 40 45
Glu Glu Gly Asn Ser Ala Gln Asp Leu Asp Ser Ala Ser Tyr Asp Lys
50 55 60
Pro Asn Val Ser Ser Asp Ser Met Lys Leu Thr Lys Glu Thr Leu Asn
65 70 75 80
His Pro Ala Asn Ile His Ile Val Leu Gly Tyr Val Ala Gln Leu Leu
85 90 95
Asp Met Lys Asn Glu Glu Leu Ala Glu Leu Ser Tyr Gln Asn Ala Val
100 105 110
Arg Leu Phe Ser Tyr Glu Gly Ser Lys Ile Leu Leu Asp Arg Gly Thr
115 120 125
Gly Asp Val Ser Gly His Thr Gln Asn Gln Ser Thr Thr His Val Ser
130 135 140

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 765 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..765
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

gttcgattga	tgaacagact	cttactgctt	ctaaaccggg	aaccgggtgtg	gttattgctg	60
tcaaaaaact	taaccaaagt	ggttgccaag	gtcaccaggga	atggctggcg	gaagtgaatt	120
acttggggcg	gttttcgcac	cctaactctg	tgaaactgat	tggttattgc	ttagaggatg	180
agcatcgctc	tcttgtttat	gagttcatgc	ctcgtgggaag	cttagagaaat	catttgttca	240
gaagaggttc	ttattttcaa	cctttatctt	ggactctccg	gttgaaagtt	gctcttggtg	300
cagcgaaagg	tcttgcgttt	cttcataacg	ccgagactag	tgctatatac	cgcgatttca	360
aaacgtcgaa	tatactgctt	gattcggagt	acaatgctaa	gctttctgat	ttcgggctag	420
ctaaagacgg	tccaacgggt	gataaaagcc	atgtctctac	gcggatcatg	ggtacttacg	480
gatacgcagc	tcctgaatat	cttgcacact	gtcatttaac	aaacaaaagt	gatgtctata	540
gctacgggtg	tgctcttttg	gaggtgttgt	ctggacggag	agctgtagac	aagaaccgtc	600
caccaggaga	gcacaaagcta	gtggaatggg	caagaccgtt	acttgctaac	aaaagggaa	660
ttattccgag	ttatocgataa	cgctctacaa	gatcaatact	caatgggaaga	agcttgtaag	720
tagctactct	tgcgctgaga	tgctcacat	tcgagataag	ctgag		

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..225
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Ser	Ile	Asp	Glu	Gln	Thr	Leu	Thr	Ala	Ser	Lys	Pro	Gly	Thr	Gly	Val
1			5						10					15	
Val	Ile	Ala	Val	Lys	Lys	Leu	Asn	Gln	Asp	Gly	Trp	Gln	Gly	His	Gln
			20						25					30	
Glu	Trp	Leu	Ala	Glu	Val	Asn	Tyr	Leu	Gly	Gln	Phe	Ser	His	Pro	Asn
			35					40					45		
Leu	Val	Lys	Leu	Ile	Gly	Tyr	Cys	Leu	Glu	Asp	Glu	His	Arg	Leu	Leu
			50				55				60				
Val	Tyr	Glu	Phe	Met	Pro	Arg	Gly	Ser	Leu	Glu	Asn	His	Leu	Phe	Arg
						70				75				80	
Arg	Gly	Ser	Tyr	Phe	Gln	Pro	Leu	Ser	Trp	Thr	Leu	Arg	Leu	Lys	Val
						85			90					95	
Ala	Leu	Gly	Ala	Ala	Lys	Gly	Leu	Ala	Phe	Leu	His	Asn	Ala	Glu	Thr
			100				105							110	
Ser	Val	Ile	Tyr	Arg	Asp	Phe	Lys	Thr	Ser	Asn	Ile	Leu	Leu	Asp	Ser
			115				120					125			
Glu	Tyr	Asn	Ala	Lys	Leu	Ser	Asp	Phe	Gly	Leu	Ala	Lys	Asp	Gly	Pro
			130				135					140			
Thr	Gly	Asp	Lys	Ser	His	Val	Ser	Thr	Arg	Ile	Met	Gly	Thr	Tyr	Gly
			145				150				155				160
Tyr	Ala	Ala	Pro	Glu	Tyr	Leu	Ala	Thr	Gly	His	Leu	Thr	Thr	Lys	Ser
						165			170					175	
Asp	Val	Tyr	Ser	Tyr	Gly	Val	Val	Leu	Leu	Glu	Val	Leu	Ser	Gly	Arg
						180			185					190	
Arg	Ala	Val	Asp	Lys	Asn	Arg	Pro	Pro	Gly	Glu	Gln	Lys	Leu	Val	Glu
						195			200				205		
Trp	Ala	Arg	Pro	Leu	Leu	Ala	Asn	Lys	Arg	Xaa	Val	Ile	Pro	Ser	Tyr
						210			215			220			

Arg
225

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..157
 (D) OTHER INFORMATION: / Ceres Seq. ID 1497910
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:
Met Pro Arg Gly Ser Leu Glu Asn His Leu Phe Arg Arg Gly Ser Tyr
1 5 10 15
Phe Gln Pro Leu Ser Trp Thr Leu Arg Leu Lys Val Ala Leu Gly Ala
 20 25 30
Ala Lys Gly Leu Ala Phe Leu His Asn Ala Glu Thr Ser Val Ile Tyr
 35 40 45
Arg Asp Phe Lys Thr Ser Asn Ile Leu Leu Asp Ser Glu Tyr Asn Ala
50 55 60
Lys Leu Ser Asp Phe Gly Leu Ala Lys Asp Gly Pro Thr Gly Asp Lys
65 70 75 80
Ser His Val Ser Thr Arg Ile Met Gly Thr Tyr Gly Tyr Ala Ala Pro
 85 90 95
Glu Tyr Leu Ala Thr Gly His Leu Thr Thr Lys Ser Asp Val Tyr Ser
 100 105 110
Tyr Gly Val Val Leu Leu Glu Val Leu Ser Gly Arg Arg Ala Val Asp
 115 120 125
Lys Asn Arg Pro Pro Gly Glu Gln Lys Leu Val Glu Trp Ala Arg Pro
130 135 140
Leu Leu Ala Asn Lys Arg Xaa Val Ile Pro Ser Tyr Arg
145 150 155

(2) INFORMATION FOR SEQ ID NO:51:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 888 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:

 (A) NAME/KEY: -
 (B) LOCATION: 1..888
 (D) OTHER INFORMATION: / Ceres Seq. ID 1497911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:
atccttataa cctttcttct cctcttctcc ttcttctctc tatgcaaaca tatatttaca 60
taaacacaca catatatata gtaagagaga gagagagaga tctagcaaga tagtgaagac 120
ttcataatca atggaagggg ttgacaacac aaatcctatg ttaaccttag aagaaggcga 180
aaacaacaat ccttttttct ccttagatga caaaacatta atgatgatgg ctcttcgttt 240
aatcttttgg ggcgatgtag ttccatcttc ttcttctgtg actccagcag gttatcatct 300
atctgtcag ctggagaact ttccaggagg tggaggagag atggcaggat tagtgagtaa 360
taatagcaat aatagtgtac ataataagaa ttgcaacaaa ggaaaaggga agagaacttc 420
ggcaatgcag aggatagcct tcatacaag gagtgatgat gatgttcttg atgatggtta 480
tcgttggcga aagatcggtc agaaatctgt caagaacaat gtcataccca ggagctatta 540
tagatgtaca taccacacat gcaacgtgaa gaaacaagt caaagactgg caaaagatcc 600
aaacgttgtc gtaacaacct acgaagggtg tcataatcat gctctctca agagtcttg atctgtaatt 660
gactcttagc cctctcctta agcaacttca gtctctctca agagtcttg atctgtaatt 720
attgaatgtt aattagtgtt gtaatacatt aattatgctt taactctctc attgacccctc 780
aatctccaaa gagacaaagt tatagaataa atctcataac atacatgctt taggtttatt 840
gagacattga tctatgtttt gctttaattt gattcgctta attgtccc

(2) INFORMATION FOR SEQ ID NO:52:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 195 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..195

(D) OTHER INFORMATION: / Ceres Seq. ID 1497912

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met Glu Gly Val Asp Asn Thr Asn Pro Met Leu Thr Leu Glu Glu Gly
1 5 10 15
Glu Asn Asn Asn Pro Phe Ser Ser Leu Asp Lys Thr Leu Met Met
20 25 30
Met Ala Pro Ser Leu Ile Phe Ser Gly Asp Val Gly Pro Ser Ser Ser
35 40 45
Ser Cys Thr Pro Ala Gly Tyr His Leu Ser Ala Gln Leu Glu Asn Phe
50 55 60
Arg Gly Gly Gly Gly Glu Met Ala Gly Leu Val Ser Asn Asn Ser Asn
65 70 75 80
Asn Ser Asp His Asn Lys Asn Cys Asn Lys Gly Lys Gly Lys Arg Thr
85 90 95
Ser Ala Met Gln Arg Ile Ala Phe His Thr Arg Ser Asp Asp Asp Val
100 105 110
Leu Asp Asp Gly Tyr Arg Trp Arg Lys Tyr Gly Gln Lys Ser Val Lys
115 120 125
Asn Asn Ala His Pro Arg Ser Tyr Tyr Arg Cys Thr Tyr His Thr Cys
130 135 140
Asn Val Lys Lys Gln Val Gln Arg Leu Ala Lys Asp Pro Asn Val Val
145 150 155 160
Val Thr Thr Tyr Glu Gly Val His Asn His Pro Cys Glu Lys Leu Met
165 170 175
Glu Thr Leu Ser Pro Leu Leu Lys Gln Leu Gln Phe Leu Ser Arg Val
180 185 190
Ser Asp Leu
195

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..186

(D) OTHER INFORMATION: / Ceres Seq. ID 1497913

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Met Leu Thr Leu Glu Glu Gly Glu Asn Asn Asn Pro Phe Ser Ser Leu
1 5 10 15
Asp Asp Lys Thr Leu Met Met Met Ala Pro Ser Leu Ile Phe Ser Gly
20 25 30
Asp Val Gly Pro Ser Ser Ser Ser Cys Thr Pro Ala Gly Tyr His Leu
35 40 45
Ser Ala Gln Leu Glu Asn Phe Arg Gly Gly Gly Glu Met Ala Gly
50 55 60
Leu Val Ser Asn Asn Ser Asn Asn Ser Asp His Asn Lys Asn Cys Asn
65 70 75 80
Lys Gly Lys Gly Lys Arg Thr Ser Ala Met Gln Arg Ile Ala Phe His
85 90 95
Thr Arg Ser Asp Asp Val Leu Asp Asp Gly Tyr Arg Trp Arg Lys
100 105 110
Tyr Gly Gln Lys Ser Val Lys Asn Asn Ala His Pro Arg Ser Tyr Tyr
115 120 125
Arg Cys Thr Tyr His Thr Cys Asn Val Lys Lys Gln Val Gln Arg Leu
130 135 140
Ala Lys Asp Pro Asn Val Val Val Thr Thr Tyr Glu Gly Val His Asn

145 150 155 160
His Pro Cys Glu Lys Leu Met Glu Thr Leu Ser Pro Leu Leu Lys Gln
165 170 175
Leu Gln Phe Leu Ser Arg Val Ser Asp Leu
180 185

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..165
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497914

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met Met Met Ala Pro Ser Leu Ile Phe Ser Gly Asp Val Gly Pro Ser
1 5 10 15
Ser Ser Ser Cys Thr Pro Ala Gly Tyr His Leu Ser Ala Gln Leu Glu
20 25 30
Asn Phe Arg Gly Gly Gly Gly Glu Met Ala Gly Leu Val Ser Asn Asn
35 40 45
Ser Asn Asn Ser Asp His Asn Lys Asn Cys Asn Lys Gly Lys Gly Lys
50 55 60
Arg Thr Ser Ala Met Gln Arg Ile Ala Phe His Thr Arg Ser Asp Asp
65 70 75 80
Asp Val Leu Asp Asp Gly Tyr Arg Trp Arg Lys Tyr Gly Gln Lys Ser
85 90 95
Val Lys Asn Asn Ala His Pro Arg Ser Tyr Tyr Arg Cys Thr Tyr His
100 105 110
Thr Cys Asn Val Lys Lys Gln Val Gln Arg Leu Ala Lys Asp Pro Asn
115 120 125
Val Val Val Thr Thr Tyr Glu Gly Val His Asn His Pro Cys Glu Lys
130 135 140
Leu Met Glu Thr Leu Ser Pro Leu Leu Lys Gln Leu Phe Leu Ser
145 150 155 160
Arg Val Ser Asp Leu
165

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1257
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497917

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

aaagaaactc aacttttttt ctttatcttt aacatcaaaa aactttatcg atatctttac 60
aaccattaaa caaaaaatttt ggccactaca agttgaaaaa gttttgatta tatctaateg 120
ctgaaatgga ttacaaggtta tcaagaagtgt gggagatagt agaaggagaa gtagaagatt 180
cagaaaagat tgatttacca cctgggtttca gatttcaccc aactgatgaa gaacttataa 240
cacactatct aagaccaaaag gttgtaaaact cttttttctc tgctatagct attggtgaag 300
ttgatctcaa caaagtcgag ccttggggact tgccttggaa ggctaaagctt ggggaaaaaag 360
agtggtaact cttttgcgta agagaccgaa aatacccgac tggtttaaga acgaatcggt 420
ctactaaagc cgggtatttgg aaagctacag ggaaagataa agagatctct aaagggaatt 480
ctctgttggg tatgaagaaa acattgggtt ttacaaaagg aagagctcct aaaggagtta 540
aaacaaaatg ggtcatgcat gattatcgat tagaaggcaa atacggtatc gataatctcc 600

ctaaaaccgc	taagaacgaa	tgtgttatta	gtcgtgtttt	tcataaacgg	actgatggta	660
cgaaggagca	tatgtcogtt	ggtttacctc	cgctgatgga	ttcttctcca	tatctaaaga	720
gtagaggaca	agactcttta	gccgggacca	cccttggtgg	gttgtgtgtc	cacgttacct	780
acttctccga	ccaaacaacc	gatgacaaga	gtcttgtggc	cgattttaaa	actaccatgt	840
ttggttccgg	atcgactaac	tttttaccac	acataggttc	tctactagac	ttcgatccct	900
tggttttaca	aaacaattct	tcagtactaa	agatgttgct	tgacaatgaa	gaaccaacca	960
ttaagaagaa	tcttcacaat	tcagggttcat	cagagagtga	actaacacgc	agttcttggc	1020
aaggtccaaa	ttcttatggg	tcactgtgtc	cagtgaatct	tgattgcggt	tggaatttct	1080
gaatttggaa	aatcgaaaa	ttggatgtta	actagggggg	atatagggtt	tttaaaaaa	1140
gtgtatatat	cggttatgtg	ttagctttag	attctaggat	atacaaat	gacactaata	1200
gattcttata	acattttgtg	aaaaaaaatc	attgtagtga	atactctctt	gccatttt	

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 318 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..318

(D) OTHER INFORMATION: / Ceres Seq. ID 1497918

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Met	Asp	Tyr	Lys	Val	Ser	Arg	Ser	Gly	Glu	Ile	Val	Glu	Gly	Glu	Val
1			5					10					15		
Glu	Asp	Ser	Glu	Lys	Ile	Asp	Leu	Pro	Pro	Gly	Phe	Arg	Phe	His	Pro
			20					25					30		
Thr	Asp	Glu	Glu	Leu	Ile	Thr	His	Tyr	Leu	Arg	Pro	Lys	Val	Val	Asn
			35					40					45		
Ser	Phe	Phe	Ser	Ala	Ile	Ala	Ile	Gly	Glu	Val	Asp	Leu	Asn	Lys	Val
			50					55					60		
Glu	Pro	Trp	Asp	Leu	Pro	Trp	Lys	Ala	Lys	Leu	Gly	Glu	Lys	Glu	Trp
			65					70					75		
Tyr	Phe	Phe	Cys	Val	Arg	Asp	Arg	Lys	Tyr	Pro	Thr	Gly	Leu	Arg	Thr
			85					90					95		
Asn	Arg	Ala	Thr	Lys	Ala	Gly	Tyr	Trp	Lys	Ala	Thr	Gly	Lys	Asp	Lys
			100					105					110		
Glu	Ile	Phe	Lys	Gly	Lys	Ser	Leu	Val	Gly	Met	Lys	Lys	Thr	Leu	Val
			115					120					125		
Phe	Tyr	Lys	Gly	Arg	Ala	Pro	Lys	Gly	Val	Lys	Thr	Asn	Trp	Val	Met
			130					135					140		
His	Glu	Tyr	Arg	Leu	Glu	Gly	Lys	Tyr	Gly	Ile	Asp	Asn	Leu	Pro	Lys
			145					150					155		
Thr	Ala	Lys	Asn	Glu	Cys	Val	Ile	Ser	Arg	Val	Phe	His	Lys	Arg	Thr
			165					170					175		
Asp	Gly	Thr	Lys	Glu	His	Met	Ser	Val	Gly	Leu	Pro	Pro	Leu	Met	Asp
			180					185					190		
Ser	Ser	Pro	Tyr	Leu	Lys	Ser	Arg	Gly	Gln	Asp	Ser	Leu	Ala	Gly	Thr
			195					200					205		
Thr	Leu	Gly	Gly	Leu	Leu	Ser	His	Val	Thr	Tyr	Phe	Ser	Asp	Gln	Thr
			210					215					220		
Thr	Asp	Asp	Lys	Ser	Leu	Val	Ala	Asp	Phe	Lys	Thr	Thr	Met	Phe	Gly
			225					230					235		
Ser	Gly	Ser	Thr	Asn	Phe	Leu	Pro	Asn	Ile	Gly	Ser	Leu	Leu	Asp	Phe
			245					250					255		
Asp	Pro	Leu	Phe	Leu	Gln	Asn	Asn	Ser	Ser	Val	Leu	Lys	Met	Leu	Leu
			260					265					270		
Asp	Asn	Glu	Thr	Gln	Phe	Lys	Lys	Asn	Leu	His	Asn	Ser	Gly	Ser	
			275					280					285		
Ser	Glu	Ser	Glu	Leu	Thr	Ala	Ser	Ser	Trp	Gln	Gly	His	Asn	Ser	Tyr
			290					295					300		

Gly Ser Thr Gly Pro Val Asn Leu Asp Cys Val Trp Lys Phe
305 310 315

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..196
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497919

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Met Lys Lys Thr Leu Val Phe Tyr Lys Gly Arg Ala Pro Lys Gly Val
1 5 10 15
Lys Thr Asn Trp Val Met His Glu Tyr Arg Leu Glu Gly Lys Tyr Gly
20 25 30
Ile Asp Asn Leu Pro Lys Thr Ala Lys Asn Glu Cys Val Ile Ser Arg
35 40 45
Val Phe His Lys Arg Thr Asp Gly Thr Lys Glu His Met Ser Val Gly
50 55 60
Leu Pro Pro Leu Met Asp Ser Ser Pro Tyr Leu Lys Ser Arg Gly Gln
65 70 75 80
Asp Ser Leu Ala Gly Thr Thr Leu Gly Gly Leu Leu Ser His Val Thr
85 90 95
Tyr Phe Ser Asp Gln Thr Thr Asp Asp Lys Ser Leu Val Ala Asp Phe
100 105 110
Lys Thr Thr Met Phe Gly Ser Gly Ser Thr Asn Phe Leu Pro Asn Ile
115 120 125
Gly Ser Leu Leu Asp Phe Asp Pro Leu Phe Leu Gln Asn Asn Ser Ser
130 135 140
Val Leu Lys Met Leu Leu Asp Asn Glu Glu Thr Gln Phe Lys Lys Asn
145 150 155 160
Leu His Asn Ser Gly Ser Ser Glu Ser Glu Leu Thr Ala Ser Ser Trp
165 170 175
Gln Gly His Asn Ser Tyr Gly Ser Thr Gly Pro Val Asn Leu Asp Cys
180 185 190
Val Trp Lys Phe
195

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497920

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Met His Glu Tyr Arg Leu Glu Gly Lys Tyr Gly Ile Asp Asn Leu Pro
1 5 10 15
Lys Thr Ala Lys Asn Glu Cys Val Ile Ser Arg Val Phe His Lys Arg
20 25 30
Thr Asp Gly Thr Lys Glu His Met Ser Val Gly Leu Pro Pro Leu Met
35 40 45
Asp Ser Ser Pro Tyr Leu Lys Ser Arg Gly Gln Asp Ser Leu Ala Gly
50 55 60
Thr Thr Leu Gly Gly Leu Leu Ser His Val Thr Tyr Phe Ser Asp Gln

(A1) SEQUENCE DELTA																			
1	Asn	Gln	Asn	Lys	Thr	Lys	Gln	Lys	Lys	His	Glu	Trp	Lys	Leu	Leu	Asn			
					5					10					15				
1	Lys	Ile	Arg	Lys	Arg	Gly	Arg	Glu	Met	Ala	Thr	Ser	Gly	Thr	Tyr	Val			
					20				25					30					
1	Thr	Glu	Val	Pro	Leu	Lys	Gly	Thr	Val	Glu	Lys	His	Phe	Lys	Arg	Tyr			
					35			40					45						
1	Arg	Asn	Glu	Asn	Tyr	Leu	Phe	Pro	Asp	Thr	Ile	Gly	His	His	Ile	Gln			
		50					55					60							
1	Ser	Val	Thr	Val	His	Asp	Gly	Glu	Trp	Asp	Thr	Gln	Gly	Gly	Ile	Lys			
						70					75					80			
1	Ile	Trp	Asn	Tyr	Thr	Leu	Gly	Asp	Gly	Lys	Glu	Glu	Val	Phe	Lys	Glu			

(2) INFORMATION FOR SEQ ID NO:61:

(A) LENGTH: 152 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..152

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:61:

Ala Thr Ser Gly Thr Tyr Val Thr Glu Val

[illegible]

(2) INFORMATION FOR SEQ ID NO:62:

(A) LENGTH: 591 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

```
(ix) FEATURE:
```

(A) NAME/KEY: -

(B) LOCATION: 1..591

(D) OTHER INFORMATION: / Ceres Seq. ID 1497927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

gtgatctcagt	ttgtgttttg	gaacctaat	ctctctcaag	agattcagct	aagatgagta	60
ctatgaaatt	tfgccgcgaa	tgtaataaca	ttctgtatcc	taaggaggac	aagaacagaa	120
agatctctct	ctatgcttgc	cgtaatctga	attaccaggaa	ggtagctgta	aacagctgtg	180
tgtacagaaa	cgaggttctc	caactgtgtg	gtgacggaac	tcagatctta	acagacgtgg	240

cttctgacbb tactcttccc sgaaccaagg ctgtgcgttg ctctaagtgt cagcataggg 300
aggccgtttt cttccaggct acggttagag gtgaagaagg aatgacactg tcttttgtct 360
gttgcaaccc gaattgtggt catcgctgga gagaataaag agcttttcgg tttcaattgg 420
tgagttctta agagtttttag gagttgatgt agttaccagt aagtgttaata tgtggaatga 480
cgggaaacaac cttctgcccc agtcagagac aaatccgtat tcatgtaatc tgttatgaaa 540
ccataatctc aacttctgtt tcaccaaaaca taaagattgg aacttgtttc t

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..131
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497928

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Asp Ser Val Leu Val Leu Glu Pro Asn Ser Leu Ser Arg Asp Ser Ala
1 5 10 15
Lys Met Ser Thr Met Lys Phe Cys Arg Glu Cys Asn Asn Ile Leu Tyr
20 25 30
Pro Lys Glu Asp Lys Glu Gln Lys Ile Leu Leu Tyr Ala Cys Arg Asn
35 40 45
Cys Asp His Gln Glu Val Ala Asp Asn Ser Cys Val Tyr Arg Asn Glu
50 55 60
Val His His Ser Val Ser Glu Arg Thr Gln Ile Leu Thr Asp Val Ala
65 70 75 80
Ser Asp Xaa Thr Leu Pro Xaa Thr Lys Ala Val Arg Cys Ser Lys Cys
85 90 95
Gln His Arg Glu Ala Val Phe Phe Gln Ala Thr Val Arg Gly Glu Glu
100 105 110
Gly Met Thr Leu Phe Phe Val Cys Cys Asn Pro Asn Cys Gly His Arg
115 120 125
Trp Arg Glu
130

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..114
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497929

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Met Ser Thr Met Lys Phe Cys Arg Glu Cys Asn Asn Ile Leu Tyr Pro
1 5 10 15
Lys Glu Asp Lys Glu Gln Lys Ile Leu Tyr Ala Cys Arg Asn Cys
20 25 30
Asp His Gln Glu Val Ala Asp Asn Ser Cys Val Tyr Arg Asn Glu Val
35 40 45
His His Ser Val Ser Glu Arg Thr Gln Ile Leu Thr Asp Val Ala Ser
50 55 60
Asp Xaa Thr Leu Pro Xaa Thr Lys Ala Val Arg Cys Ser Lys Cys Gln
65 70 75 80
His Arg Glu Ala Val Phe Phe Gln Ala Thr Val Arg Gly Glu Glu Gly
85 90 95
Met Thr Leu Phe Phe Val Cys Cys Asn Pro Asn Cys Gly His Arg Trp

Arg Glu 100 105 110

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1497930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Met	Lys	Phe	Cys	Arg	Glu	Cys	Asn	Asn	Ile	Leu	Tyr	Pro	Lys	Glu	Asp
1			5						10					15	
Lys	Glu	Gln	Lys	Ile	Leu	Leu	Tyr	Ala	Cys	Arg	Asn	Cys	Asp	His	Gln
			20					25					30		
Glu	Val	Ala	Asp	Asn	Ser	Cys	Val	Tyr	Arg	Asn	Glu	Val	His	His	Ser
			35					40				45			
Val	Ser	Glu	Arg	Thr	Gln	Ile	Leu	Thr	Asp	Val	Ala	Ser	Asp	Xaa	Thr
			50				55					60			
Leu	Pro	Xaa	Thr	Lys	Ala	Val	Arg	Cys	Ser	Lys	Cys	Gln	His	Arg	Glu
65				70					75					80	
Ala	Val	Phe	Phe	Gln	Ala	Thr	Val	Arg	Gly	Glu	Glu	Gly	Met	Thr	Leu
				85					90				95		
Phe	Phe	Val	Cys	Cys	Asn	Pro	Asn	Gly	His	Arg	Trp	Arg	Glu		
			100				105						110		

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 568 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..568

(D) OTHER INFORMATION: / Ceres Seq. ID 1497931

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ccttggttag	ccatgggaag	catctctcct	cgttccatgt	tcgatgagct	gaagaaaaa	60
atctccgat	caaccacctc	cacaactcca	aggaacggac	cgggagatac	aggactcaac	120
tggttaatgt	atgagttgct	atggagggat	ttcttcaggt	ttataaccaa	gaaatacacg	180
tcagcgaaga	cgcaggtcga	ggctgggtccg	gctacagcct	gtaccggtgc	ctttgcttaa	240
acatttgaaa	actcttcaggt	gaccggaaaa	gttagaagcg	acctgtttct	ttgccctact	300
ctgggtgatg	gtggattaat	ttgctatccg	gacaggactt	tactgctctc	tttgaaact	360
tgaagtgcag	gagaataaaa	tctaagcttc	tttttttggc	tcaatcaagt	tgctcgttcc	420
ctgttctaaa	catttcggat	actcattcca	taaaaaagtct	ctacaatttg	agacgctctc	480
ctttgtgggt	aagactttgag	aatgtatctt	agaaartaay	cgaagtmgtt	gtgctctatga	540
atattaaatt	caggaatatt	aagatgtc				

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..79

(D) OTHER INFORMATION: / Ceres Seq. ID 1497932

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Pro Trp Leu Ala Met Gly Ser Ile Ser Pro Arg Ser Met Phe Asp Glu
1 5 10 15
Leu Lys Lys Thr Ile Ser Ala Ser Thr Thr Thr Pro Arg Asn
20 25 30
Gly Pro Gly Asp Thr Gly Leu Asn Trp Leu Met Tyr Glu Leu Leu Trp
35 40 45
Arg Asp Phe Phe Arg Phe Ile Thr Lys Lys Tyr Ser Ser Ala Lys Thr
50 55 60
Gln Val Glu Ala Gly Pro Ala Thr Ala Cys Thr Gly Ala Phe Ala
65 70 75

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75

(D) OTHER INFORMATION: / Ceres Seq. ID 1497933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Met Gly Ser Ile Ser Pro Arg Ser Met Phe Asp Glu Leu Lys Lys Thr
1 5 10 15
Ile Ser Ala Ser Thr Thr Ser Thr Thr Pro Arg Asn Gly Pro Gly Asp
20 25 30
Thr Gly Leu Asn Trp Leu Met Tyr Glu Leu Leu Trp Arg Asp Phe Phe
35 40 45
Arg Phe Ile Thr Lys Lys Tyr Ser Ser Ala Lys Thr Gln Val Glu Ala
50 55 60
Gly Pro Ala Thr Ala Cys Thr Gly Ala Phe Ala
65 70 75

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..67

(D) OTHER INFORMATION: / Ceres Seq. ID 1497934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met Phe Asp Glu Leu Lys Lys Thr Ile Ser Ala Ser Thr Thr Ser Thr
1 5 10 15
Thr Pro Arg Asn Gly Pro Gly Asp Thr Gly Leu Asn Trp Leu Met Tyr
20 25 30
Glu Leu Leu Trp Arg Asp Phe Phe Arg Phe Ile Thr Lys Lys Tyr Ser
35 40 45
Ser Ala Lys Thr Gln Val Glu Ala Gly Pro Ala Thr Ala Cys Thr Gly
50 55 60
Ala Phe Ala
65

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1012 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..1012
 (D) OTHER INFORMATION: / Ceres Seq. ID 1497939
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:
acttcagcaa aaccactaca ctttctttat ctctcagatt ttctcaagaa gattgtgtgg 60
aagatgatga gacggaagat ttttcttctt ggtgattcca tcaactgaaga atccctttagt 120
gacggtggct ggggtgcttc tctcgcgcgt ctctccgcc gcaaggctga tatggtgcta 180
cgaggatata tgggataata cactgaggtg gcactgaaa tggtggagag agtttttccg 240
gtggcagaag aagacggcgg agattctccg gcagctgtga ctgttttctt tggagcggaac 300
gacgctgttc ttcgcgagag atgcctgggg ttctcagcatg tgccacttca cgagtacaag 360
cagaatcttc gctctattgt ttcgtttctc aagaatcggt ggccacaaac ggcatttatt 420
cttataactc cgccctcaat agacgaagag gcccgctca gatatactta tatcgaaaaa 480
acaaaggggg tgccggaag aacgaatgaa gtacgaggac gtacgaggac agcatgtata 540
gcagtacgtc aggaatgtca aatttcggtc actgatcttt ggtccaaaat gcagcaaaat 600
scaaatgggs aaacagaatg tctatgggac gggttacatt tgagtcgggt cggtacaaaa 660
gtattgtttg aagaagtagc aaagaagcct aaagaagaag gcattggagc tgaggactta 720
gctgtggatc ttccctctat agaagatggt gaccctaagg atcctctcaa atccctttgat 780
gagttttgat gctttatatt actaccatgc agtttgggtc ttctatcttt gattactctt 840
taatttcgat attaattatg ggaatgtgac attattaggc actttgtgag aatctttttg 900
tgagaatctt tttagctttg aggcacttgt gagagagagg gcactttgcc atcttttttt 960
agaggagatt gaaccaatct gccctgaag tgaatgaaac acaataattt tt
(2) INFORMATION FOR SEQ ID NO:71:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 262 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..262
 (D) OTHER INFORMATION: / Ceres Seq. ID 1497940
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:
Thr Ser Ala Lys Pro Leu His Leu Ser Tyr Leu Ser Asp Phe Leu Lys
1 5 10 15
Lys Ile Val Trp Lys Met Met Arg Arg Lys Ile Phe Leu Phe Gly Asp
20 25 30
Ser Ile Thr Glu Glu Ser Phe Ser Asp Gly Gly Trp Gly Ala Ser Leu
35 40 45
Ala Asp Leu Leu Arg Arg Lys Ala Asp Met Val Leu Arg Gly Tyr Ser
50 55 60
Gly Tyr Asn Thr Arg Trp Ala Leu Lys Val Val Glu Arg Val Phe Pro
65 70 75 80
Val Ala Glu Glu Asp Gly Gly Asp Ser Pro Ala Ala Val Thr Val Phe
85 90 95
Phe Gly Ala Asn Asp Ala Cys Leu Pro Glu Arg Cys Ser Gly Phe Gln
100 105 110
His Val Pro Leu His Glu Tyr Lys Gln Asn Leu Arg Ser Ile Val Ser
115 120 125
Phe Leu Lys Asn Arg Trp Pro Gln Thr Ala Ile Ile Leu Ile Thr Pro
130 135 140
Pro Pro Ile Asp Glu Glu Ala Arg Leu Arg Tyr Pro Tyr Ile Glu Asn
145 150 155 160
Thr Thr Gly Leu Pro Glu Arg Thr Asn Glu Val Ala Gly Leu Tyr Ala
165 170 175
Lys Ala Cys Ile Ala Val Ala Glu Glu Cys Gln Ile Ser Val Thr Asp
180 185 190
Leu Trp Ser Lys Met Gln Gln Xaa Xaa Asn Trp Xaa Thr Glu Cys Leu

195 200 205
Trp Asp Gly Leu His Leu Ser Arg Val Gly Asn Lys Val Leu Phe Glu
210 215 220
Glu Val Ala Lys Lys Leu Lys Glu Glu Gly Ile Gly Ala Glu Asp Leu
225 230 235 240
Ala Val Asp Leu Pro Leu Ile Glu Asp Val Asp Pro Lys Asp Pro Leu
245 250 255
Lys Ser Phe Asp Glu Phe
260

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..241
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Met Met Arg Arg Lys Ile Phe Leu Phe Gly Asp Ser Ile Thr Glu Glu
1 5 10 15
Ser Phe Ser Asp Gly Gly Trp Gly Ala Ser Leu Ala Asp Leu Leu Arg
20 25 30
Arg Lys Ala Asp Met Val Leu Arg Gly Tyr Ser Gly Tyr Asn Thr Arg
35 40 45
Trp Ala Leu Lys Val Val Glu Arg Val Phe Pro Val Ala Glu Glu Asp
50 55 60
Gly Gly Asp Ser Pro Ala Ala Val Thr Val Phe Phe Gly Ala Asn Asp
65 70 75 80
Ala Cys Leu Pro Glu Arg Cys Ser Gly Phe Gln His Val Pro Leu His
85 90 95
Glu Tyr Lys Gln Asn Leu Arg Ser Ile Val Ser Phe Leu Lys Asn Arg
100 105 110
Trp Pro Gln Thr Ala Ile Ile Leu Ile Thr Pro Pro Pro Ile Asp Glu
115 120 125
Glu Ala Arg Leu Arg Tyr Pro Tyr Ile Glu Asn Thr Thr Gly Leu Pro
130 135 140
Glu Arg Thr Asn Glu Val Ala Gly Leu Tyr Ala Lys Ala Cys Ile Ala
145 150 155 160
Val Ala Glu Glu Cys Gln Ile Ser Val Thr Asp Leu Trp Ser Lys Met
165 170 175
Gln Gln Xaa Xaa Asn Trp Xaa Thr Glu Cys Leu Trp Asp Gly Leu His
180 185 190
Leu Ser Arg Val Gly Asn Lys Val Leu Phe Glu Glu Val Ala Lys Lys
195 200 205
Leu Lys Glu Glu Gly Ile Gly Ala Glu Asp Leu Ala Val Asp Leu Pro
210 215 220
Leu Ile Glu Asp Val Asp Pro Lys Asp Pro Leu Lys Ser Phe Asp Glu
225 230 235 240
Phe

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..240
(D) OTHER INFORMATION: / Ceres Seq. ID 1497942
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Met	Arg	Lys	Ile	Phe	Leu	Phe	Gly	Asp	Ser	Ile	Thr	Glu	Glu	Ser
1			5				10					15		
Phe	Ser	Asp	Gly	Trp	Gly	Ala	Ser	Leu	Ala	Asp	Leu	Leu	Arg	Arg
			20				25				30			
Lys	Ala	Asp	Met	Val	Leu	Arg	Gly	Tyr	Ser	Gly	Tyr	Asn	Thr	Arg
			35				40				45			
Ala	Leu	Lys	Val	Val	Glu	Arg	Val	Phe	Pro	Val	Ala	Glu	Glu	Asp
			50				55				60			
Gly	Asp	Ser	Pro	Ala	Ala	Val	Thr	Val	Phe	Phe	Gly	Ala	Asn	Asp
			65				70				75			80
Cys	Leu	Pro	Glu	Arg	Cys	Ser	Gly	Phe	Gln	His	Val	Pro	Leu	His
			85						90			95		
Tyr	Lys	Gln	Asn	Leu	Arg	Ser	Ile	Val	Ser	Phe	Leu	Lys	Asn	Arg
			100						105			110		
Pro	Gln	Thr	Ala	Ile	Ile	Leu	Ile	Thr	Pro	Pro	Pro	Ile	Asp	Glu
			115				120					125		
Ala	Arg	Leu	Arg	Tyr	Pro	Tyr	Ile	Glu	Asn	Thr	Thr	Gly	Leu	Pro
			130				135				140			
Arg	Thr	Asn	Glu	Val	Ala	Gly	Leu	Tyr	Ala	Lys	Ala	Cys	Ile	Ala
			145				150				155			160
Ala	Glu	Glu	Cys	Gln	Ile	Ser	Val	Thr	Asp	Leu	Trp	Ser	Lys	Met
			165						170				175	
Gln	Xaa	Xaa	Asn	Trp	Xaa	Thr	Glu	Cys	Leu	Trp	Asp	Gly	Leu	His
			180						185				190	
Ser	Arg	Val	Gly	Asn	Lys	Val	Leu	Phe	Glu	Glu	Val	Ala	Lys	Lys
			195				200				205			
Lys	Glu	Glu	Gly	Ile	Gly	Ala	Glu	Asp	Leu	Ala	Val	Asp	Leu	Pro
			210				215				220			
Ile	Glu	Asp	Val	Asp	Pro	Lys	Asp	Pro	Leu	Lys	Ser	Phe	Asp	Glu
			225				230				235			240

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1380
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497943

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

atttttatcc	tttctccgct	ataaaaaagcg	atttttttat	tgtagctcga	tttgcgggaa	60
aatcttgcac	ctgcctcaga	aaattttctg	gggagcttcc	accaaatagt	tcttctcgtc	120
ttctctcttc	ttcttgggta	atgtttctac	agattctctc	ctcctaattc	agagacgaca	180
aaacgctata	aacaacattt	ttacagtttg	gaggaggaag	gagaaatgat	aggtttatta	240
actgagagta	gcagcagtc	atgtgttgga	aatgtggatg	gggttgatcg	tccgataccg	300
atgtctccgg	taaatgcgga	gggtgaggag	atgagatcag	agtcgcgcgt	ggttaatgat	360
aaggcgtag	atatttctga	tgatgatcat	gatgatgaga	atgaaccgct	tattgtttct	420
ggtgaaatgc	gtatttcttc	tgatgagtc	cctgttgaga	atcttgagag	cccttgttgc	480
tgcagatgca	gcctaaaaga	tgctcataga	aaatgtgttc	agcggttggt	caatgaaaag	540
aaaaacatta	tatgcgagat	ttgtcaccag	ccttatcaac	ctggatatac	cgctccacca	600
ccctcaactc	agcctgaaga	aacaactatt	gacatttggt	gaggatggac	aatctcaggt	660
ttggatgtgc	atgatctcgc	tgctccttgc	attgtctga	ctgaacgtcg	gtatttagag	720
tctgaatatg	tggaatatata	agcttcaagt	gcaagcgggg	cgcgattctg	tcgctcagct	780

Met	Ile	Gly	Leu	5	Thr	Glu	Ser	Ser	Ser	His	Met	Val	Val	Asn
1				5				10					15	
Val	Asp	Gly	Leu	Met	Arg	Pro	Ile	Pro	Met	Ser	Pro	Val	Asn	Ala
			20					25				30		Glu
Val	Glu	Glu	Met	Arg	Ser	Glu	Ser	Pro	Val	Val	Asn	Asp	Lys	Ala
		35					40				45			Leu
Asp	Ile	Ser	Asp	Asp	Asp	His	Asp	Asp	Glu	Asn	Glu	Pro	Leu	Ile
	50					55				60				Val
Ser	Gly	Glu	Cys	Arg	Ile	Cys	Ser	Asp	Glu	Ser	Pro	Val	Glu	Asn
65					70				75					Leu
Glu	Ser	Pro	Cys	Ala	Cys	Ser	Gly	Ser	Leu	Lys	Tyr	Ala	His	Arg
				85					90					80
Cys	Val	Gln	Arg	Trp	Cys	Asn	Glu	Lys	Lys	Asn	Ile	Ile	Cys	Glu
			100					105				110		Ile
Cys	His	Gln	Pro	Tyr	Gln	Pro	Gly	Tyr	Thr	Ala	Pro	Pro	Pro	Leu
		115					120				125			
Gln	Pro	Glu	Glu	Thr	Thr	Ile	Asp	Ile	Gly	Gly	Gly	Trp	Thr	Ile
		130				135				140				Ser
Gly	Leu	Asp	Val	His	Asp	Pro	Arg	Leu	Leu	Ala	Ile	Ala	Glu	Ala
145					150					155				Glu
Arg	Arg	Tyr	Leu	Glu	Ser	Glu	Tyr	Val	Glu	Tyr	Thr	Ala	Ser	Ser
				165					170					Ala
Ser	Gly	Ala	Ala	Phe	Cys	Arg	Ser	Ala	Ala	Leu	Ile	Leu	Met	Ala
			180					185				190		Leu
Leu	Leu	Leu	Arg	His	Ala	Leu	Thr	Ile	Thr	Asp	Asp	Thr	Asp	Gly
		195					200					205		Glu
Glu	Asp	Asp	Pro	Ser	Ser	Ile	Leu	Ser	Leu	Val	Leu	Leu	Arg	Ala
		210				215					220			Ala
Gly	Phe	Leu	Leu	Pro	Cys	Tyr	Ile	Met	Ala	Xaa	Ala	Ile	Ser	Ile
225					230					235				Leu
Gln	Arg	Arg	Arg	Gln	Arg	Gln	Glu	Ala	Ala	Ala	Leu	Ala	Thr	Gln
				245					250					240
Ala	Phe	Val	Leu	Gln	Ser	Gly	Gln	Pro	Arg	Thr	Val	His	Thr	Val
		260						265				270		
Ser	Pro	Gly	Ile	Ser	Ser	Ser	Ser	Val	Ala	His	Ala	Thr	Ser	Ser
		275					280					285		Thr
Gln	Gln	Gln	His	Asp	Asp	Pro	Val							
		290				295								

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..284
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Met	Val	Val	Asn	Val	Asp	Gly	Leu	Met	Arg	Pro	Ile	Pro	Met	Ser	Pro
1			5					10					15		
Val	Asn	Ala	Glu	Val	Glu	Glu	Met	Arg	Ser	Glu	Ser	Pro	Val	Val	Asn
			20				25						30		
Asp	Lys	Ala	Leu	Asp	Ile	Ser	Asp	Asp	His	Asp	Asp	Glu	Asn	Glu	
			35				40					45			
Pro	Leu	Ile	Val	Ser	Gly	Glu	Cys	Arg	Ile	Cys	Ser	Asp	Glu	Ser	Pro
			50				55				60				
Val	Glu	Asn	Leu	Glu	Ser	Pro	Cys	Ala	Cys	Ser	Gly	Ser	Leu	Lys	Tyr
65							70				75				80
Ala	His	Arg	Lys	Cys	Val	Gln	Arg	Trp	Cys	Asn	Glu	Lys	Lys	Asn	Ile
				85					90					95	
Ile	Cys	Glu	Ile	Cys	His	Gln	Pro	Tyr	Gln	Pro	Gly	Tyr	Thr	Ala	Pro
				100				105					110		
Pro	Pro	Pro	Leu	Gln	Pro	Glu	Glu	Thr	Thr	Ile	Asp	Ile	Gly	Gly	Gly
				115				120					125		
Trp	Thr	Ile	Ser	Gly	Leu	Asp	Val	His	Asp	Pro	Arg	Leu	Leu	Ala	Ile
				130				135				140			
Ala	Glu	Ala	Glu	Arg	Arg	Tyr	Leu	Glu	Ser	Glu	Tyr	Val	Glu	Tyr	Thr
145						150				155					160
Ala	Ser	Ser	Ala	Ser	Gly	Ala	Ala	Phe	Cys	Arg	Ser	Ala	Ala	Leu	Ile
				165					170					175	
Leu	Met	Ala	Leu	Leu	Leu	Arg	His	Ala	Leu	Thr	Ile	Thr	Asp	Asp	
				180				185					190		
Thr	Asp	Gly	Glu	Glu	Asp	Asp	Pro	Ser	Ser	Ile	Leu	Ser	Leu	Val	Leu
				195				200				205			
Leu	Arg	Ala	Ala	Gly	Phe	Leu	Leu	Pro	Cys	Tyr	Ile	Met	Ala	Xaa	Ala
				210				215				220			
Ile	Ser	Ile	Leu	Gln	Arg	Arg	Arg	Gln	Arg	Gln	Glu	Ala	Ala	Ala	Leu
225						230				235					240
Ala	Thr	Gln	Phe	Ala	Phe	Val	Leu	Gln	Ser	Gly	Gln	Pro	Arg	Thr	Val
				245					250					255	
His	Phe	Thr	Val	Ser	Pro	Gly	Ile	Ser	Ser	Ser	Ser	Val	Ala	His	Ala
				260				265					270		
Thr	Thr	Ser	Thr	Gln	Gln	Gln	His	Asp	Asp	Pro	Val				
				275				280							

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..276
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497946

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Met Arg Pro Ile Pro Met Ser Pro Val Asn Ala Glu Val Glu Glu Met

1 5 10 15
Arg Ser Glu Ser Pro Val Val Asn Asp Lys Ala Leu Asp Ile Ser Asp
20 25 30
Asp Asp His Asp Asp Glu Asn Glu Pro Leu Ile Val Ser Gly Glu Cys
35 40 45
Arg Ile Cys Ser Asp Glu Ser Pro Val Glu Asn Leu Glu Ser Pro Cys
50 55 60
Ala Cys Ser Gly Ser Leu Lys Tyr Ala His Arg Lys Cys Val Gln Arg
65 70 75 80
Trp Cys Asn Glu Lys Lys Asn Ile Ile Cys Glu Ile Cys His Gln Pro
85 90 95
Tyr Gln Pro Gly Tyr Thr Ala Pro Pro Pro Pro Leu Gln Pro Glu Glu
100 105 110
Thr Thr Ile Asp Ile Gly Gly Gly Trp Thr Ile Ser Gly Leu Asp Val
115 120 125
His Asp Pro Arg Leu Leu Ala Ile Ala Glu Ala Glu Arg Tyr Leu
130 135 140
Glu Ser Glu Tyr Val Glu Tyr Thr Ala Ser Ser Ala Ser Gly Ala Ala
145 150 155 160
Phe Cys Arg Ser Ala Ala Leu Ile Leu Met Ala Leu Leu Leu Arg
165 170 175
His Ala Leu Thr Ile Thr Asp Asp Thr Asp Gly Glu Glu Asp Asp Pro
180 185 190
Ser Ser Ile Leu Ser Leu Val Leu Leu Arg Ala Ala Gly Phe Leu Leu
195 200 205
Pro Cys Tyr Ile Met Ala Xaa Ala Ile Ser Ile Leu Gln Arg Arg Arg
210 215 220
Gln Arg Gln Glu Ala Ala Ala Leu Ala Thr Gln Phe Ala Phe Val Leu
225 230 235 240
Gln Ser Gly Gln Pro Arg Thr Val His Phe Thr Val Ser Pro Gly Ile
245 250 255
Ser Ser Ser Ser Val Ala His Ala Thr Ser Thr Gln Gln Gln His
260 265 270
Asp Asp Pro Val
275

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1174
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

aaaatttcgc	aaactaat	tttcactt	ttcttcgt	atctctctga	aagcttctct	60
tcttctcttc	accatgtctg	gttatccctc	atcaagccaa	ggttacgggt	acgcggttaa	120
tccacacact	cctcagccac	cgtacggatc	aaccggcaat	aaccctcctc	cgtcgggatc	180
atccggcagc	aatctctctc	ctccgtagcg	atcatcagcc	tcctcaccgt	acgcagttcc	240
ctacggagct	cagcccgctc	cttacgggtg	accaccgta	gcaccgtacg	cgtctctctc	300
aggagaccat	aataaagcgc	acaaagagaa	acctcaccgc	gcctcctacg	gatctccatc	360
tcccgtggcg	tacgggtgct	atccatcgct	tggaccttcc	gactacgggt	gttacggagg	420
agcgcgcgag	cagtcctgac	atggaggagg	ttacggaggg	gcgcgcgcag	agtcctggaa	480
tggaggaggt	tacggagctc	ctctcccgca	agcttcttat	ggaagtcctg	ttgcgtctct	540
ggttccgtgc	gcgtttctct	ccggaaacaga	tccgaacatt	gtggcttggt	tccaagctgc	600
ggatcgggac	aatagtggat	tcacgtgatg	taaggagctt	caaggagctc	tatcttcgta	660
taatcagagc	ttcagcataa	gaactgttca	tctccttatc	tatctattca	ccaacagcaa	720
tgctcaggaa	attggaccac	aaagagttac	ttcacttttc	tkkagctctc	agaattggag	780
gtctatcttt	gagaggtttg	ataaggacag	aagcggtaga	atagatacaa	acgagctgag	840

(2) INFORMATION FOR SEQ ID NO:79:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Lys	Phe	Arg	Lys	Leu	Ile	Phe	Ser	Leu	Ser	Ser	Ser	Leu	Ile	Ser	Leu
1				5				10						15	
Lys	Ala	Ser	Leu	Leu	Leu	Thr	Met	Ser	Gly	Tyr	Pro	Pro	Ser	Ser	
			20				25					30			
Gln	Gly	Tyr	Gly	Tyr	Gly	Gly	Asn	Pro	Pro	Pro	Gln	Pro	Pro	Tyr	
		35					40				45				
Gly	Ser	Thr	Gly	Asn	Asn	Pro	Pro	Cys	Gly	Ser	Ser	Gly	Ser	Asn	
		50				55				60					
Pro	Pro	Pro	Pro	Tyr	Gly	Ser	Ser	Ala	Ser	Ser	Pro	Tyr	Ala	Val	Pro
65					70					75					80
Tyr	Gly	Ala	Gln	Pro	Ala	Pro	Tyr	Gly	Ala	Pro	Pro	Ser	Ala	Pro	Tyr
				85					90					95	
Ala	Ser	Pro	Pro	Gly	Asp	His	Asn	Lys	Pro	His	Lys	Glu	Lys	Pro	His
			100					105					110		
Gly	Ala	Ser	Tyr	Gly	Ser	Pro	Ser	Pro	Gly	Gly	Tyr	Gly	Ala	His	Pro
		115						120				125			
Ser	Ser	Gly	Pro	Ser	Asp	Tyr	Gly	Gly	Tyr	Gly	Gly	Ala	Pro	Gln	Gln
		130				135					140				
Ser	Gly	His	Gly	Gly	Gly	Tyr	Gly	Gly	Ala	Pro	Gln	Gln	Ser	Gly	His
145					150					155					160
Gly	Gly	Gly	Tyr	Gly	Ala	Pro	Pro	Pro	Gln	Ala	Ser	Tyr	Gly	Ser	Pro
				165					170					175	
Phe	Ala	Ser	Leu	Val	Pro	Ser	Ala	Phe	Pro	Pro	Gly	Thr	Asp	Pro	Asn
			180					185					190		
Ile	Val	Ala	Cys	Phe	Gln	Ala	Ala	Asp	Arg	Asp	Asn	Ser	Gly	Phe	Ile
		195					200					205			
Asp	Asp	Lys	Glu	Leu	Gln	Gly	Ala	Leu	Ser	Ser	Tyr	Asn	Gln	Ser	Phe
		210				215					220				
Ser	Ile	Arg	Thr	Val	His	Leu	Leu	Met	Tyr	Leu	Phe	Thr	Asn	Ser	Asn
225					230					235					240
Val	Arg	Lys	Ile	Gly	Pro	Lys	Glu	Phe	Thr	Ser	Leu	Phe	Xaa	Ser	Leu
				245					250					255	
Gln	Asn	Trp	Arg	Ser	Ile	Phe	Glu	Arg	Phe	Asp	Lys	Asp	Arg	Ser	Gly
		260						265					270		
Arg	Ile	Asp	Thr	Asn	Glu	Leu	Arg	Asp	Ala	Leu	Met	Ser	Leu	Gly	Phe
		275					280					285			
Ser	Val	Ser	Pro	Val	Ile	Leu	Asp	Leu	Leu	Val	Ser	Lys	Phe	Asp	Lys
		290				295				300					
Ser	Gly	Gly	Arg	Asn	Arg	Ala	Ile	Glu	Tyr	Asp	Asn	Phe	Ile	Glu	Cys
305				310						315				320	
Cys	Leu	Thr	Val	Lys	Gly	Leu	Thr	Glu	Lys	Phe	Lys	Glu	Lys	Asp	Thr
				325					330					335	
Ala	Leu	Ser	Gly	Ser	Ala	Thr	Phe	Asn	Tyr	Glu	Asn	Phe	Met	Leu	Thr

340 345 350
Val Leu Pro Phe Leu Val Ala
355
(2) INFORMATION FOR SEQ ID NO:80:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 335 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..335
(D) OTHER INFORMATION: / Ceres Seq. ID 1497949
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:
Met Ser Gly Tyr Pro Pro Ser Ser Gln Gly Tyr Gly Tyr Gly Gly Asn
1 5 10 15
Pro Pro Pro Pro Gln Pro Pro Tyr Gly Ser Thr Gly Asn Asn Pro Pro
20 25 30
Pro Cys Gly Ser Ser Gly Ser Asn Pro Pro Pro Tyr Gly Ser Ser
35 40 45
Ala Ser Ser Pro Tyr Ala Val Pro Tyr Gly Ala Gln Pro Ala Pro Tyr
50 55 60
Gly Ala Pro Pro Ser Ala Pro Tyr Ala Ser Pro Pro Gly Asp His Asn
65 70 75 80
Lys Pro His Lys Glu Lys Pro His Gly Ala Ser Tyr Gly Ser Pro Ser
85 90 95
Pro Gly Gly Tyr Gly Ala His Pro Ser Ser Gly Pro Ser Asp Tyr Gly
100 105 110
Gly Tyr Gly Gly Ala Pro Gln Gln Ser Gly His Gly Gly Gly Tyr Gly
115 120 125
Gly Ala Pro Gln Gln Ser Gly His Gly Gly Tyr Gly Ala Pro Pro
130 135 140
Pro Gln Ala Ser Tyr Gly Ser Pro Phe Ala Ser Leu Val Pro Ser Ala
145 150 155 160
Phe Pro Pro Gly Thr Asp Pro Asn Ile Val Ala Cys Phe Gln Ala Ala
165 170 175
Asp Arg Asp Asn Ser Gly Phe Ile Asp Asp Lys Glu Leu Gln Gly Ala
180 185 190
Leu Ser Ser Tyr Asn Gln Ser Phe Ser Ile Arg Thr Val His Leu Leu
195 200 205
Met Tyr Leu Phe Thr Asn Ser Asn Val Arg Lys Ile Gly Pro Lys Glu
210 215 220
Phe Thr Ser Leu Phe Xaa Ser Leu Gln Asn Trp Arg Ser Ile Phe Glu
225 230 235 240
Arg Phe Asp Lys Asp Arg Ser Gly Arg Ile Asp Thr Asn Glu Leu Arg
245 250 255
Asp Ala Leu Met Ser Leu Gly Phe Ser Val Ser Pro Val Ile Leu Asp
260 265 270
Leu Leu Val Ser Lys Phe Asp Lys Ser Gly Gly Arg Asn Arg Ala Ile
275 280 285
Glu Tyr Asp Asn Phe Ile Glu Cys Cys Leu Thr Val Lys Gly Leu Thr
290 295 300
Glu Lys Phe Lys Glu Lys Asp Thr Ala Leu Ser Gly Ser Ala Thr Phe
305 310 315 320
Asn Tyr Glu Asn Phe Met Leu Thr Val Leu Pro Phe Leu Val Ala
325 330 335
(2) INFORMATION FOR SEQ ID NO:81:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 748 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..748
 (D) OTHER INFORMATION: / Ceres Seq. ID 1497953
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:
attagtcatt actctctccg gcgtctccat cgcgctctat atctaatttc gtccctgcgtc 60
gacctgtgga gctactttcag ttccggcgca tcacgcagct ccagttgtat gttttgtggg 120
ttatacaaa atgacaacaa tcgaaacccg tcagaaaaat caaaagtctt ctcccttccgg 180
ttctgtact accgctactg gtacactcaa gcagtcatac gcatcggtta aaagggtggg 240
agggagacac ccggtttgtaa gataatggact tccgatgata tctctcactg tatttggagc 300
cctaggactc ggccaactac ttcaaggcag taaggatatt gcaaaggtaa aagatgacca 360
agaatgggag attatagaaa caagaaaggc actttcgaga acaggacctg tcgatgccta 420
taaacataaa aacacatcca ttgaagatga gctcaaggct atgcaagaga aggtggacat 480
aaacacgtac gagtacaaga aaattccaaa gctaaacgaa agcaagtoga gtttaagaaga 540
gtctttgtat aagattagtc ttcttagatg tgtttcagtt ttaaatgact ctctcagttca 600
cataatcgcc caagtacaaa ttccagtaag ttctgtctgg gcttcctaaa accaagaaca 660
acgagggact tgccaattgk tgataatata tgttgtcgtg ttgatttacg acgtccaaa 720
agatctgaaa gaggtcttat aaccagtt

(2) INFORMATION FOR SEQ ID NO:82:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 76 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..76
 (D) OTHER INFORMATION: / Ceres Seq. ID 1497954
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:
Ile Ser His Tyr Ser Ser Arg Arg Leu His Arg Arg Leu Tyr Leu Ile
1 5 10 15
Ser Ser Cys Val Asp Leu Val Ser Tyr Phe Ser Phe Arg Pro Ser Arg
20 25 30
Ser Ser Ser Cys Met Phe Cys Gly Leu Tyr Lys Asp Asp Asn Asn Arg
35 40 45
Asn Arg Ser Glu Asn Ser Lys Val Phe Ser Phe Arg Phe Cys Tyr Tyr
50 55 60
Arg Tyr Trp Tyr Thr Gln Ala Val Ile Ser Ile Val
65 70 75

(2) INFORMATION FOR SEQ ID NO:83:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 134 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..134
 (D) OTHER INFORMATION: / Ceres Seq. ID 1497955
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:
Met Thr Thr Ile Glu Thr Gly Gln Lys Thr Gln Lys Ser Ser Pro Ser
1 5 10 15
Gly Ser Ala Thr Thr Ala Thr Gly Thr Leu Lys Gln Ser Ser Ala Ser
20 25 30
Phe Lys Arg Trp Gly Gly Arg His Pro Phe Val Arg Tyr Gly Leu Pro
35 40 45

Met Ile Ser Leu Thr Val Phe Gly Ala Leu Gly Leu Gly Gln Leu Leu
50 55 60
Gln Gly Ser Lys Asp Ile Ala Lys Val Lys Asp Asp Gln Glu Trp Glu
65 70 75 80
Ile Ile Glu Thr Arg Lys Ala Leu Ser Arg Thr Gly Pro Val Asp Ala
85 90 95
Tyr Lys Pro Lys Asn Thr Ser Ile Glu Asp Glu Leu Lys Ala Met Gln
100 105 110
Glu Lys Val Asp Ile Asn Thr Tyr Glu Tyr Lys Lys Ile Pro Lys Leu
115 120 125
Asn Glu Ser Lys Ser Ser
130

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 86 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..86

(D) OTHER INFORMATION: / Ceres Seq. ID 1497956

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Met Ile Ser Leu Thr Val Phe Gly Ala Leu Gly Leu Gly Gln Leu Leu
1 5 10 15
Gln Gly Ser Lys Asp Ile Ala Lys Val Lys Asp Asp Gln Glu Trp Glu
20 25 30
Ile Ile Glu Thr Arg Lys Ala Leu Ser Arg Thr Gly Pro Val Asp Ala
35 40 45
Tyr Lys Pro Lys Asn Thr Ser Ile Glu Asp Glu Leu Lys Ala Met Gln
50 55 60
Glu Lys Val Asp Ile Asn Thr Tyr Glu Tyr Lys Lys Ile Pro Lys Leu
65 70 75 80
Asn Glu Ser Lys Ser Ser
85

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 563 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..563

(D) OTHER INFORMATION: / Ceres Seq. ID 1497957

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

attcaccaga	gaaatggctg	tcgctgacta	ctaaccagag	ccatcggtgg	ttgatttcgc	60
gatttcgagc	tcatttccta	cttgtctcac	cttaatctcc	ggcgatcgaa	tttcacgggt	120
ccggttaaat	aattctctcc	tggccatgga	caaagaagtt	acaaagattg	aaagtgatga	180
caattcatcg	gtggagatca	aagtgttgtt	attcgccaga	gcacgagagc	tcacaggtgt	240
gcttgatcta	acactgaaga	tgscatgagg	tagtacaaca	cagaaatgcc	tggatgagtt	300
ggtgcttaag	tttccaagct	tggaaagaggt	acgtagctgt	gtgttctctg	ctttgaacga	360
ggaatataca	accgattccg	ccattgttca	acatagagat	gagttagcca	tcataacctc	420
gataagcggc	ggctaatagc	tcgacacttc	ttaaatccct	ttaactcggg	gattgtatct	480
catggcgat	gatccaaaaa	tgaacttttg	tcataataac	acagaaatat	ctgtctttta	540
taatggaaaag	aaaaatgttac	atc				

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..30
(D) OTHER INFORMATION: / Ceres Seq. ID 1497958
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:
Ser Pro Glu Lys Trp Ser Ser Leu Thr Thr Asn Gln Ser His Arg Trp
1 5 10 15
Leu Ile Ser Arg Phe Arg Ala Pro Phe Leu Leu Val Ser Pro
20 25 30

(2) INFORMATION FOR SEQ ID NO:87:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..40
(D) OTHER INFORMATION: / Ceres Seq. ID 1497959
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:
Met Asp Lys Glu Val Thr Lys Ile Glu Ser Asp Asp Thr Ser Ser Val
1 5 10 15
Glu Ile Lys Val Leu Leu Phe Ala Arg Ala Arg Glu Leu Thr Gly Val
20 25 30
Pro Asp Leu Thr Leu Lys Met Xaa
35 40

(2) INFORMATION FOR SEQ ID NO:88:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 933 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..933
(D) OTHER INFORMATION: / Ceres Seq. ID 1497963
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:
acaattcaga tttaatttc tcmaaaatsc ttaaaaactt tchctcaatt ctctckaggc 60
ttcgtgrtca ggtatgcaga tcttlygttya agacgtctsa cyggaaarac tatcacyyts 120
gaggtggava gytctgacac catygayaac gtkaargcca agatccaggga yaargarggt 180
atycwcwccg aycagcagag gmttgatctt cgcyggaag caasttgar gatgmgama 240
ckttggctga ytaacaacaty cagaaggagt ccacacttca cttggtcttg cgtctgcgtg 300
gaggtatgca gatctctgk aagactctva ccgaaaagac catcaactyk gaggtgraga 360
gctctgacac cattgacaac gtgaaggcca agatccaggga taagggaagt atccctccgg 420
accagcagag gttgatcttt gccgaaaac aattggagga yggcagaact ttrcggaatt 480
acaacatcca gaaggagtct acccttcaact tggctcttg tctbcttgga ggtatgcaga 540
tcttygttaa gactttgacc ggvaagacca tcactcttga agtggagagc tcygacacca 600
ttgacacagt gaagcgyaag atccaggaya aggaaggwat cctccggac cagcagagst 660
ctsatcttsg cksgaaaacca gcttgaggat ggacgtacat tggccgacta caacatccag 720
aaggagtcta ccttcaactt ggtctccgt ctctgtggag gtttctaaat ctctgtctgt 780
ttatgcttta agaagttcaa tgtctcgttt ctgttaaaac tttggtggct tgtgttttgg 840
ggccttgat aatccctga tgaataattg ttccaactat gtttccattc ctgttatctc 900

(2) INFORMATION FOR SEQ ID NO:89:
(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..127
(D) OTHER INFORMATION: / Ceres Seq. ID 1497964
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:
Thr Ile Gln Ile Ser Ile Ser Xaa Lys Xaa Leu Lys Thr Phe Xaa Gln
1 5 10 15
Phe Ser Xaa Gly Phe Val Xaa Arg Tyr Ala Asp Leu Xaa Xaa Arg Arg
20 25 30
Xaa Xaa Gly Xaa Thr Ile Xaa Xaa Glu Val Xaa Xaa Ser Asp Thr Xaa
35 40 45
Xaa Asn Xaa Xaa Ala Lys Ile Gln Xaa Xaa Xaa Gly Xaa Xaa Pro Xaa
50 55 60
Gln Gln Arg Xaa Asp Leu Arg Xaa Lys Ala Xaa Trp Xaa Met Xaa Xaa
65 70 75 80
Xaa Trp Leu Xaa Thr Thr Xaa Arg Arg Ser Pro His Phe Thr Trp Ser
85 90 95
Cys Val Cys Val Glu Val Cys Arg Ser Ser Xaa Arg Leu Xaa Pro Glu
100 105 110
Arg Pro Ser Xaa Xaa Arg Xaa Arg Ala Leu Thr Pro Leu Thr Thr
115 120 125
(2) INFORMATION FOR SEQ ID NO:90:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..126
(D) OTHER INFORMATION: / Ceres Seq. ID 1497965
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:
Met Gln Ile Phe Xaa Lys Thr Xaa Thr Gly Lys Thr Ile Thr Xaa Glu
1 5 10 15
Xaa Glu Ser Ser Asp Thr Ile Asp Asn Val Lys Ala Lys Ile Gln Asp
20 25 30
Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala Gly Lys
35 40 45
Gln Leu Glu Xaa Gly Arg Thr Xaa Ala Asp Tyr Asn Ile Gln Lys Glu
50 55 60
Ser Thr Leu His Leu Val Leu Arg Xaa Arg Gly Gly Met Gln Ile Xaa
65 70 75 80
Val Lys Thr Leu Thr Xaa Lys Thr Ile Thr Leu Glu Val Glu Ser Xaa
85 90 95
Asp Thr Ile Asp Asn Val Lys Xaa Lys Ile Gln Xaa Lys Glu Xaa Ile
100 105 110
Pro Pro Asp Gln Gln Xaa Ser Xaa Leu Xaa Xaa Lys Ala Ala
115 120 125
(2) INFORMATION FOR SEQ ID NO:91:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1251 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1251

(D) OTHER INFORMATION: / Ceres Seq. ID 1497966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

acgcaggcaaa	atgtctcgtg	atttaactcta	tagaagaaac	agagctctct	gttttgtttt	60
aatcttggtc	tgcttccctt	accggtttgg	cgctagaaac	acgcgggagg	cggancaatc	120
cacagcaaaa	gcaactcaaa	taatacacgt	cagcaattcc	acgtggcgat	atttctctcg	180
ttctgtagat	gtccaaatag	gtagccacgt	cagcggcgta	tcagagctca	aaagataacc	240
ccacagattc	ggttacgtca	aggatggctc	cgaaatat	tcgcacgtgt	tcgatgggtc	300
ttctggaatc	gcaatctctc	tgatcaacga	aaatctcggt	ttaccaataa	ccggaaagat	360
cgacacgagt	acagttactc	tcattgtcgt	accgagatgt	ggcgcttagg	atcacgacat	420
gaccatcaac	aacgatttcc	tcacacacaa	ggcgcatatt	acgtatttca	acggtaaaac	480
gaaatggaac	cgtgatcacg	taacctaacg	tatctccaaa	actcacaaac	tcgattacct	540
gacgtcagaa	gacgtcaaaa	ccgttttccg	gcgagctttt	tcacagtggt	caagcgtgat	600
tcgggtgagt	ttcgaggaag	tcgacgattt	cacgacggct	gatttaaaga	tcggattcta	660
cgctgggtg	cacggtgacg	ggcttcacgt	tgacgggtga	cttggaacct	tagcacacgc	720
ttttgcgcc	gagaacggga	ggcttcacgt	cgacggcgcg	gagacgtgga	tcgtcgacga	780
tgacttgaaa	ggatctctca	agggtggcgt	tgacttgga	tcgttgggcg	ctcaccagat	840
cggtcacatt	ttgggattag	gacatagctc	gcaggagctg	gcggttatgt	atcccgagct	900
ccgacggagg	accnagaaga	ttgatcttac	ggttgatgac	gtggcaggtg	tacttaagct	960
atatggtccg	aatcctaacc	tacggttgga	ttcactaacg	cagtcggaag	attctattaa	1020
aaacgcgacc	gtatcacata	gattcttgct	ggggaatttt	atcggttatg	ttctgttggt	1080
tggttggttt	attctttttc	tataggttta	taggcataaa	aaataactgt	tttatttcatt	1140
tatttttaat	taaatgtaca	tatatatttc	aactatgtga	atgtaatgat	atagttgaac	1200
aaaaaaagat	gtacatatat	agttaggctt	ataattaggt	ttatggtctt	g	

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 367 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..367

(D) OTHER INFORMATION: / Ceres Seq. ID 1497967

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Arg	Arg	Gln	Met	Ser	Arg	Asn	Leu	Ile	Tyr	Arg	Arg	Asn	Arg	Ala	Leu	
1				5				10							15	
Cys	Phe	Val	Leu	Ile	Leu	Phe	Cys	Phe	Pro	Tyr	Arg	Phe	Gly	Ala	Arg	
			20					25					30			
Asn	Thr	Pro	Glu	Ala	Xaa	Gln	Ser	Thr	Ala	Lys	Ala	Thr	Gln	Ile	Ile	
			35				40					45				
His	Val	Ser	Asn	Ser	Thr	Trp	His	Asp	Phe	Ser	Arg	Leu	Val	Asp	Val	
			50				55				60					
Gln	Ile	Gly	Ser	His	Val	Ser	Gly	Val	Ser	Glu	Leu	Lys	Arg	Tyr	Leu	
			65				70			75				80		
His	Arg	Phe	Gly	Tyr	Val	Lys	Asp	Gly	Ser	Glu	Ile	Phe	Ser	Asp	Val	
			85					90						95		
Phe	Asp	Gly	Pro	Leu	Glu	Ser	Ala	Ile	Ser	Leu	Tyr	Gln	Glu	Asn	Leu	
			100					105						110		
Gly	Leu	Pro	Ile	Thr	Gly	Arg	Leu	Asp	Thr	Ser	Thr	Val	Thr	Leu	Met	
			115				120					125				
Ser	Leu	Pro	Arg	Cys	Gly	Val	Xaa	Asp	Thr	His	Met	Thr	Ile	Asn	Asn	
			130				135				140					
Asp	Phe	Leu	His	Thr	Thr	Ala	His	Tyr	Thr	Tyr	Phe	Asn	Gly	Lys	Pro	
			145				150			155				160		
Lys	Trp	Asn	Arg	Asp	Thr	Leu	Thr	Tyr	Ala	Ile	Ser	Lys	Thr	His	Lys	
			165					170						175		
Leu	Asp	Tyr	Leu	Thr	Ser	Glu	Asp	Val	Lys	Thr	Val	Phe	Arg	Arg	Ala	

180 185 190
Phe Ser Gln Trp Ser Ser Val Ile Pro Val Ser Phe Glu Glu Val Asp
195 200 205
Asp Phe Thr Thr Ala Asp Leu Lys Ile Gly Phe Tyr Ala Gly Asp His
210 215 220
Gly Asp Gly Leu Pro Phe Asp Gly Val Leu Gly Thr Leu Ala His Ala
225 230 235 240
Phe Ala Pro Glu Asn Gly Arg Leu His Leu Asp Ala Ala Glu Thr Trp
245 250 255
Ile Val Asp Asp Asp Leu Lys Gly Ser Ser Glu Val Ala Val Asp Leu
260 265 270
Glu Ser Val Ala Thr His Glu Ile Gly His Leu Leu Gly Leu Gly His
275 280 285
Ser Ser Gln Glu Ser Ala Val Met Tyr Pro Ser Leu Arg Pro Arg Thr
290 295 300
Lys Lys Val Asp Leu Thr Val Asp Asp Val Ala Gly Val Leu Lys Leu
305 310 315 320
Tyr Gly Pro Asn Pro Lys Leu Arg Leu Asp Ser Leu Thr Gln Ser Glu
325 330 335
Asp Ser Ile Lys Asn Gly Thr Val Ser His Arg Phe Leu Ser Gly Asn
340 345 350
Phe Ile Gly Tyr Val Leu Leu Val Val Gly Leu Ile Leu Phe Leu
355 360 365

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..364
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497968

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Met Ser Arg Asn Leu Ile Tyr Arg Arg Asn Arg Ala Leu Cys Phe Val
1 5 10 15
Leu Ile Leu Phe Cys Phe Pro Tyr Arg Phe Gly Ala Arg Asn Thr Pro
20 25 30
Glu Ala Xaa Gln Ser Thr Ala Lys Ala Thr Gln Ile Ile His Val Ser
35 40 45
Asn Ser Thr Trp His Asp Phe Ser Arg Leu Val Asp Val Gln Ile Gly
50 55 60
Ser His Val Ser Gly Val Ser Glu Leu Lys Arg Tyr Leu His Arg Phe
65 70 75 80
Gly Tyr Val Lys Asp Gly Ser Glu Ile Phe Ser Asp Val Phe Asp Gly
85 90 95
Pro Leu Glu Ser Ala Ile Ser Leu Tyr Gln Glu Asn Leu Gly Leu Pro
100 105 110
Ile Thr Gly Arg Leu Asp Thr Ser Thr Val Thr Leu Met Ser Leu Pro
115 120 125
Arg Cys Gly Val Xaa Asp Thr His Met Thr Ile Asn Asn Asp Phe Leu
130 135 140
His Thr Thr Ala His Tyr Thr Tyr Phe Asn Gly Lys Pro Lys Trp Asn
145 150 155 160
Arg Asp Thr Leu Thr Tyr Ala Ile Ser Lys Thr His Lys Leu Asp Tyr
165 170 175
Leu Thr Ser Glu Asp Val Lys Thr Val Phe Arg Arg Ala Phe Ser Gln
180 185 190
Trp Ser Ser Val Ile Pro Val Ser Phe Glu Glu Val Asp Asp Phe Thr
195 200 205

Thr Ala Asp Leu Lys Ile Gly Phe Tyr Ala Gly Asp His Gly Asp Gly
210 215 220
Leu Pro Phe Asp Gly Val Leu Gly Thr Leu Ala His Ala Phe Ala Pro
225 230 235 240
Glu Asn Gly Arg Leu His Leu Asp Ala Ala Glu Thr Trp Ile Val Asp
245 250 255
Asp Asp Leu Lys Gly Ser Ser Glu Val Ala Val Asp Leu Glu Ser Val
260 265 270
Ala Thr His Glu Ile Gly His Leu Leu Gly Leu Gly His Ser Ser Gln
275 280 285
Glu Ser Ala Val Met Tyr Pro Ser Leu Arg Pro Arg Thr Lys Lys Val
290 295 300
Asp Leu Thr Val Asp Asp Val Ala Gly Val Leu Lys Leu Tyr Gly Pro
305 310 315 320
Asn Pro Lys Leu Arg Leu Asp Ser Leu Thr Gln Ser Glu Asp Ser Ile
325 330 335
Lys Asn Gly Thr Val Ser His Arg Phe Leu Ser Gly Asn Phe Ile Gly
340 345 350
Tyr Val Leu Leu Val Val Gly Leu Ile Leu Phe Leu
355 360

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..240
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497969

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Met Ser Leu Pro Arg Cys Gly Val Xaa Asp Thr His Met Thr Ile Asn
1 5 10 15
Asn Asp Phe Leu His Thr Thr Ala His Tyr Thr Tyr Phe Asn Gly Lys
20 25 30
Pro Lys Trp Asn Arg Asp Thr Leu Thr Tyr Ala Ile Ser Lys Thr His
35 40 45
Lys Leu Asp Tyr Leu Thr Ser Glu Asp Val Lys Thr Val Phe Arg Arg
50 55 60
Ala Phe Ser Gln Trp Ser Ser Val Ile Pro Val Ser Phe Glu Glu Val
65 70 75 80
Asp Asp Phe Thr Thr Ala Asp Leu Lys Ile Gly Phe Tyr Ala Gly Asp
85 90 95
His Gly Asp Gly Leu Pro Phe Asp Gly Val Leu Gly Thr Leu Ala His
100 105 110
Ala Phe Ala Pro Glu Asn Gly Arg Leu His Leu Asp Ala Ala Glu Thr
115 120 125
Trp Ile Val Asp Asp Asp Leu Lys Gly Ser Ser Glu Val Ala Val Asp
130 135 140
Leu Glu Ser Val Ala Thr His Glu Ile Gly His Leu Leu Gly Leu Gly
145 150 155 160
His Ser Ser Gln Glu Ser Ala Val Met Tyr Pro Ser Leu Arg Pro Arg
165 170 175
Thr Lys Lys Val Asp Leu Thr Val Asp Asp Val Ala Gly Val Leu Lys
180 185 190
Leu Tyr Gly Pro Asn Pro Lys Leu Arg Leu Asp Ser Leu Thr Gln Ser
195 200 205
Glu Asp Ser Ile Lys Asn Gly Thr Val Ser His Arg Phe Leu Ser Gly
210 215 220
Asn Phe Ile Gly Tyr Val Leu Leu Val Val Gly Leu Ile Leu Phe Leu

225

230

235

240

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1457 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1457
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

gattgggtcaaa aaaaattgaa gggcggaaga aacagagtgt tacaaatcag cttctcgccg 60
tgaatcagc ttcggcgaag acttttagcc agttagccgc ggagacaggt ctaaccaacg 120
tatacgtagc tcaagctctc cgtcgtcaag ctacagctcaa accggacaca gtcccaaacg 180
ttaaggaagc ttaccagcgt ctgaccgatg aactaatcgg agatatgatg tctccaccgt 240
ggagatccta cgatccataa ctcatccaa gaaacactat ctacaggttg aatgaagcag 300
tgatgcattt tggtagaggt ataaaggaga ttatcaatga agattttgga gatggcatca 360
tgtcggcgat agatttctat tgctctgtcg acaaaatcaa aggagtggat ggtaacaatc 420
gcgtgggtgt gacgcttgat ggaagatmtc ttctgcattc cgaacagagg acggagaata 480
tggtctcaag gctaaatctc aaggaggagta caagcgaatg ataagaaagc ctttacgtat 540
ccatgaagcg cttattgtaa gtggtaacgt tgaataacct atgtgtttgt ttatctgtaa 600
tatatgcaac ttacagatct agattaaaaa ctgtttcagg ttgaataaca gtgaataaac 660
aaaactttata aaacctttct atgtttatct tcaaaaaaaa aaaaaaaa cggcacgaga 720
agcttttttt tttttttttt tattaatact ctcttttatg tgtttggttg ctttgacacg 780
ttgagaggtc taacttggtg aaattagccc ctggttggtc ccttggttagg ttgttgattt 840
ggactaaagt tgccttttag aagcttgaat ctatctatgg ctggtttgag aaacatcag 900
agaagaagaa gggttacgtc ttgcctcgtg cgaagatggt gaatgctgat ctgtcagga 960
tttataactc cgatgaggta cagagtgtgg tgaaccgatg taaggatggt tccaagagag 1020
cggttctgaa gaagaatcca ttgaagaacc ttaatgtgat gttcaagttg aatccttatg 1080
ctaagaccgc aaagagaatg tctctgttgg ctgaagcttc aagggttaag gctaagaagg 1140
agaagctcga gaagaagagg aaagtgtcga ctaaggagga ggcccaagcg atcaaaagcag 1200
caggcaagcg ttggtatcag actatgattt cagacagtga ctacaccgag ttcgataact 1260
tcaccaagtg gcttggcgct agtcagtaat gatgcctcgc tcatcgcaaa gtctcttata 1320
tctagccaaa gattttggtt ttctgattta tgttctctgt ttgtatttga ttatcttggg 1380
attttatggt gttgagtttg taagacgatt ttaagaact atgatggtgt ttttcaact 1440
cttttcaatc tgtttcc

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..172
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497971

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Leu Val Lys Lys Met Glu Ala Ala Lys Lys Gln Ser Val Thr Asn Gln 5 10 15
Leu Leu Ala Val Lys Ser Ala Ser Gly Lys Thr Phe Ser Gln Leu Ala 20 25 30
Ala Glu Thr Gly Leu Thr Asn Val Tyr Val Ala Gln Leu Leu Arg Arg 35 40 45
Gln Ala Gln Leu Lys Pro Asp Thr Val Pro Lys Leu Lys Glu Ala Leu 50 55 60
Pro Ala Leu Thr Asp Glu Leu Ile Gly Asp Met Met Ser Pro Pro Trp

65 70 75 80
Arg Ser Tyr Asp Pro Asn Leu Ile Gln Glu Pro Thr Ile Tyr Arg Leu
85 90 95
Asn Glu Ala Val Met His Phe Gly Glu Ser Ile Lys Glu Ile Ile Asn
100 105 110
Glu Asp Phe Gly Asp Gly Ile Met Ser Ala Ile Asp Phe Tyr Cys Ser
115 120 125
Val Asp Lys Ile Lys Gly Val Asp Gly Asn Asn Arg Val Val Val Thr
130 135 140
Leu Asp Gly Lys Xaa Leu Ser His Ser Glu Gln Arg Thr Glu Asn Met
145 150 155 160
Val Ser Arg Leu Asn Leu Lys Gly Gly Thr Ser Glu
165 170

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..168

(D) OTHER INFORMATION: / Ceres Seq. ID 1497972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Met Glu Ala Ala Lys Lys Gln Ser Val Thr Asn Gln Leu Leu Ala Val
1 5 10 15
Lys Ser Ala Ser Gly Lys Thr Phe Ser Gln Leu Ala Ala Glu Thr Gly
20 25 30
Leu Thr Asn Val Tyr Val Ala Gln Leu Leu Arg Arg Gln Ala Gln Leu
35 40 45
Lys Pro Asp Thr Val Pro Lys Leu Lys Glu Ala Leu Pro Ala Leu Thr
50 55 60
Asp Glu Leu Ile Gly Asp Met Met Ser Pro Pro Trp Arg Ser Tyr Asp
65 70 75 80
Pro Asn Leu Ile Gln Glu Pro Thr Ile Tyr Arg Leu Asn Glu Ala Val
85 90 95
Met His Phe Gly Glu Ser Ile Lys Glu Ile Ile Asn Glu Asp Phe Gly
100 105 110
Asp Gly Ile Met Ser Ala Ile Asp Phe Tyr Cys Ser Val Asp Lys Ile
115 120 125
Lys Gly Val Asp Gly Asn Asn Arg Val Val Val Thr Leu Asp Gly Lys
130 135 140
Xaa Leu Ser His Ser Glu Gln Arg Thr Glu Asn Met Val Ser Arg Leu
145 150 155 160
Asn Leu Lys Gly Gly Thr Ser Glu
165

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1497973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Met Val Asn Ala Asp Leu Ala Arg Ile Ile Asn Ser Asp Glu Val Gln
1 5 10 15

Ser Val Val Asn Pro Ile Lys Asp Gly Ser Lys Arg Ala Val Leu Lys
20 25 30
Lys Asn Pro Leu Lys Asn Leu Asn Val Met Phe Lys Leu Asn Pro Tyr
35 40 45
Ala Lys Thr Ala Lys Arg Met Ser Leu Leu Ala Glu Ala Ser Arg Val
50 55 60
Lys Ala Lys Lys Glu Lys Leu Glu Lys Lys Arg Lys Val Val Thr Lys
65 70 75 80
Glu Glu Ala Gln Ala Ile Lys Ala Ala Gly Lys Ala Trp Tyr Gln Thr
85 90 95
Met Ile Ser Asp Ser Asp Tyr Thr Glu Phe Asp Asn Phe Thr Lys Trp
100 105 110
Leu Gly Ala Ser Gln
115

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..732

(D) OTHER INFORMATION: / Ceres Seq. ID 1497974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

agaaacagtt	ccgtgtaggc	aaccattagg	aaaaccctaa	ctaaattcca	ttattaattt	60
cttttataat	ccctttctct	tgacattgac	ttctctctct	cgattctctt	tctccagttt	120
caatcaaaat	caattttctt	tcaacgaacc	ctaatttcca	acaaatcgga	ttcagtttct	180
tcttcggaga	ctaattcgaa	cgcaatggct	aagagttcct	tcaagatctc	taaccctctc	240
gaggcagagg	tgagtgaaat	ttctcgaatc	agagagaagt	accctgacag	aattcccgtg	300
attgtggaga	aggctggaca	aagtgatgtt	cctgacattg	acaagaagaa	gtatcktgtta	360
ccagctgac	taacagtggt	acaatttgta	tacgtgtgtc	gtaaaagaat	caagcttgga	420
gctgagaaag	ctatttttgt	ctttgttaag	aacacattgc	ctccaactgc	tgcatctgatg	480
tctgcgatct	atgaasaaca	caaagatgag	gatgggttcc	tctacatgac	ttacagtgga	540
gagaacactt	ttggatctct	taccgttgct	tgaataaaaa	tcgatctttg	gatgactttg	600
atgtacatac	ataaatcagg	aagataaaga	tgatattgct	ttccttcttt	tctctggctt	660
ttaaactttg	tttggatgtt	tggtatcttt	tccttttggg	tttattaatc	gtcagaagaa	720
ttctcttttc	tt					

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1497975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Met Ala Lys Ser Ser Phe Lys Ile Ser Asn Pro Leu Glu Ala Arg Met	
1 5 10 15	
Ser Glu Ser Ser Arg Ile Arg Glu Lys Tyr Pro Asp Arg Ile Pro Val	
20 25 30	
Ile Val Glu Lys Ala Gly Gln Ser Asp Val Pro Asp Ile Asp Lys Lys	
35 40 45	
Lys Tyr Xaa Val Pro Ala Asp Leu Thr Val Gly Gln Phe Val Tyr Val	
50 55 60	
Val Arg Lys Arg Ile Lys Leu Gly Ala Glu Lys Ala Ile Phe Val Phe	
65 70 75 80	

Val Lys Asn Thr Leu Pro Pro Thr Ala Ala Leu Met Ser Ala Ile Tyr
85 90 95
Glu Xaa His Lys Asp Glu Asp Gly Phe Leu Tyr Met Thr Tyr Ser Gly
100 105 110
Glu Asn Thr Phe Gly Ser Leu Thr Val Ala
115 120

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..107

- (D) OTHER INFORMATION: / Ceres Seq. ID 1497976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Met Ser Glu Ser Ser Arg Ile Arg Glu Lys Tyr Pro Asp Arg Ile Pro
1 5 10 15
Val Ile Val Glu Lys Ala Gly Gln Ser Asp Val Pro Asp Ile Asp Lys
20 25 30
Lys Lys Tyr Xaa Val Pro Ala Asp Leu Thr Val Gly Gln Phe Val Tyr
35 40 45
Val Val Arg Lys Arg Ile Lys Leu Gly Ala Glu Lys Ala Ile Phe Val
50 55 60
Phe Val Lys Asn Thr Leu Pro Pro Thr Ala Ala Leu Met Ser Ala Ile
65 70 75 80
Tyr Glu Xaa His Lys Asp Glu Asp Gly Phe Leu Tyr Met Thr Tyr Ser
85 90 95
Gly Glu Asn Thr Phe Gly Ser Leu Thr Val Ala
100 105

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..494

- (D) OTHER INFORMATION: / Ceres Seq. ID 1497977

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

taacattgtg gtactaatg gagggaggat agtagaggaa ggtacacatg attcctttagc 60
agcaaaaaat ggggtgtatg tacgtttgat gcaaccacac tttggtaaag gtctacagcca 120
acatogactg atatagagtt ttgaggctoc atcaatgata atgattttgg catctctgat 180
caatgattct ccggaggatt acaagatggt caaaaaaac cctatacaac caccggtagt 240
tcctcagcag atagggsctg tagatgtaga ttcccatagt cttcgagctg cttattcttt 300
ttttggagac gaagcatcag aagtaggtca tggtcattgc ttgcgtctcc aaagtatatc 360
gattttgtct attgaatctg aatatatttag gaggttggtt aatcattttg gaggcgtgtt 420
attgccttt cctttatatg tgcctgtgct ggtttgttct tgcaaaaaca tggatgatgt 480
atgtaaaagt taag

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..44
(D) OTHER INFORMATION: / Ceres Seq. ID 1497978
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:
Asn Ile Val Val Leu Asn Gly Gly Arg Ile Val Glu Glu Gly Thr His
1 5 10 15
Asp Ser Leu Ala Ala Lys Asn Gly Leu Tyr Val Arg Leu Met Gln Pro
20 25 30
His Phe Gly Lys Gly Leu Arg Gln His Arg Leu Ile
35 40

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..30
(D) OTHER INFORMATION: / Ceres Seq. ID 1497979

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:
Met Ile Met Ile Leu Ala Ser Leu Ile Asn Asp Ser Pro Glu Asp Tyr
1 5 10 15
Lys Met Phe Lys Lys Asn Pro Ile Gln Pro Arg Val Val Leu
20 25 30

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1592 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1592
(D) OTHER INFORMATION: / Ceres Seq. ID 1497987
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

aagactctct	ctgctttcga	ccmaaaaac	ttctcctctc	ctctgggaga	tctccatctt	60
cttcgcttct	tcgcttcccc	gcctgaaaca	attactcgat	ctcgccggcg	gaacaagctc	120
tcogtttctc	tttccggcag	atcgattctt	ccaattctct	attcctttct	aggtcttctc	180
taagaaaccc	ttacttttct	caaaatctgc	atttatggcg	attagggtta	ccttcaceta	240
ctccagctat	gttgctagga	gcattgtctc	atccgcggcg	actcgtgtcg	gtaccggcga	300
cgtagagtaa	tgcttcgaaa	catgggttgc	tcccagggtc	tgccggccaca	atcagatacc	360
agatatgttt	gataaatctc	ccggatccaa	cacatggggt	ccaagctcag	gccctcgtgc	420
tcgaccagct	tcatcaatgt	atagaccocat	tgccagggaa	atccctcgaag	aaggctgcga	480
gagttccact	gtcttgggta	tgatctctct	catgaatttg	actggagctc	cacagttttc	540
gggtgtgacc	ggtctcggga	tctctccctt	taagaacttt	tctgtcatcc	cgttccttag	600
gggttccaaag	tggatgcctt	gtagttattc	ggcgacgtta	gagttgagtg	ataaagtctc	660
tgatagagga	ggaagggttc	tgatccttaa	agtgaaagtg	gttgaaatct	tgctcggagg	720
gaatggtgga	aacgggatgg	tttaataagct	gttgaaatct	gtctcggagg	atgcctcctc	780
tgctttcacg	gcggtttact	tttctctctc	tttccgacg	gctttggccg	aggctcctcc	840
tataccttca	acatctatgc	ttcctactct	cgatgtgggt	gatcgtgtta	tagccgagaa	900
ggtctcatac	tttttcagga	agccagaggt	ttcagacata	gttatcttca	aggtcctctc	960
tatttttggt	gaacatgggt	acagttgtgc	tgatgttttc	ataaaaagga	tagttgctag	1020
cgaagggtgac	tgsggttgag	tttgtgatgg	aaagctctta	gtaaatgaca	ctgttcaagc	1080
agaggatttt	gtcttagagc	caattgacta	tgaaatggaa	ccaatgtttg	tcctcgaagg	1140
ttagtctctc	gtcttagagc	acaaacgcga	caaaagcttt	gattctcata	actgggggtc	1200
atttccaata	aagaacatca	tagggagatc	tgtgtttcgc	tattggccac	caagcgaagt	1260
gtcagacata	atacacatg	atacaagttg	ccaaaagaga	gctgtttgag	tatcttgacc	1320
aacgcagatg	gtatcttagg	attaagcaga	aaatttgatt	agatgagctg	tgccatgcca	1380

accatttttg cgctgaaggc aacagagcaa ttcttttctt ctgtctaggc ttgatggcgg 1440
acatggaatg cactgggaaa tccatataaa aagaacaaga aaattgatat ttttgctttg 1500
atttttttg atgtgttgaa acctaaatgc atccagtga attggcagta gctgtcaaac 1560
ataaaagggt aaacttttct ttttgagtat tt

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 367 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..367

(D) OTHER INFORMATION: / Ceres Seq. ID 1497988

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Met Ala Ile Arg Val Thr Phe Thr Tyr Ser Ser Tyr Val Ala Arg Ser
1 5 10 15
Ile Ala Ser Ser Ala Gly Thr Arg Val Gly Thr Gly Asp Val Arg Ser
20 25 30
Cys Phe Glu Thr Trp Val Arg Pro Arg Phe Cys Gly His Asn Gln Ile
35 40 45
Pro Asp Ile Val Asp Lys Ser Pro Gly Ser Asn Thr Trp Gly Pro Ser
50 55 60
Ser Gly Pro Arg Ala Arg Pro Ala Ser Ser Met Tyr Ser Thr Ile Ala
65 70 75 80
Arg Glu Ile Leu Glu Gly Cys Lys Ser Pro Leu Val Leu Gly Met
85 90 95
Ile Ser Leu Met Asn Leu Thr Gly Ala Pro Gln Phe Ser Gly Val Thr
100 105 110
Gly Leu Gly Ile Ser Pro Phe Lys Thr Ser Ser Val Ile Pro Phe Leu
115 120 125
Arg Gly Ser Lys Trp Met Pro Cys Ser Ile Pro Ala Thr Leu Ser Thr
130 135 140
Asp Ile Ala Glu Val Asp Arg Gly Gly Lys Val Cys Asp Pro Lys Val
145 150 155 160
Lys Leu Glu Leu Ser Asp Lys Val Ser Asn Gly Gly Asn Gly Trp Val
165 170 175
Asn Lys Leu Leu Asn Ile Cys Ser Glu Asp Ala Lys Ala Ala Phe Thr
180 185 190
Ala Val Thr Phe Ser Leu Leu Phe Arg Ser Ala Leu Ala Glu Pro Lys
195 200 205
Ser Ile Pro Ser Thr Ser Met Leu Pro Thr Leu Asp Val Gly Asp Arg
210 215 220
Val Ile Ala Glu Lys Val Ser Tyr Phe Phe Arg Lys Pro Glu Val Ser
225 230 235 240
Asp Ile Val Ile Phe Lys Ala Pro Pro Ile Leu Val Glu His Gly Tyr
245 250 255
Ser Cys Ala Asp Val Phe Ile Lys Arg Ile Val Ala Ser Glu Gly Asp
260 265 270
Trp Val Glu Val Cys Asp Gly Lys Leu Leu Val Asn Asp Thr Val Gln
275 280 285
Ala Glu Asp Phe Val Leu Glu Pro Ile Asp Tyr Glu Met Glu Pro Met
290 295 300
Phe Val Pro Glu Gly Tyr Val Phe Val Leu Gly Asp Asn Arg Asn Lys
305 310 315 320
Ser Phe Asp Ser His Asn Trp Gly Pro Leu Pro Ile Lys Asn Ile Ile
325 330 335
Gly Arg Ser Val Phe Arg Tyr Trp Pro Pro Ser Lys Val Ser Asp Ile
340 345 350
Ile His His Glu Gln Val Ser Gln Lys Arg Ala Val Asp Val Ser

355 360 365

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 293 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..293

(D) OTHER INFORMATION: / Ceres Seq. ID 1497989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

Met	Tyr	Ser	Thr	Ile	Ala	Arg	Glu	Ile	Leu	Glu	Gly	Cys	Lys	Ser
1				5				10					15	
Pro	Leu	Val	Leu	Gly	Met	Ile	Ser	Leu	Met	Asn	Leu	Thr	Gly	Ala
			20					25					30	Pro
Gln	Phe	Ser	Gly	Val	Thr	Gly	Leu	Gly	Ile	Ser	Pro	Phe	Lys	Thr
			35				40					45		Ser
Ser	Val	Ile	Pro	Phe	Leu	Arg	Gly	Ser	Lys	Trp	Met	Pro	Cys	Ser
			50			55				60				Ile
Pro	Ala	Thr	Leu	Ser	Thr	Asp	Ile	Ala	Glu	Val	Asp	Arg	Gly	Gly
65					70				75					Lys
Val	Cys	Asp	Pro	Lys	Val	Lys	Leu	Glu	Leu	Ser	Asp	Lys	Val	Ser
				85					90				95	Asn
Gly	Gly	Asn	Gly	Trp	Val	Asn	Lys	Leu	Leu	Asn	Ile	Cys	Ser	Glu
			100					105					110	Asp
Ala	Lys	Ala	Ala	Phe	Thr	Ala	Val	Thr	Phe	Ser	Leu	Leu	Phe	Arg
			115				120					125		Ser
Ala	Leu	Ala	Glu	Pro	Lys	Ser	Ile	Pro	Ser	Thr	Ser	Met	Leu	Pro
			130			135					140			Thr
Leu	Asp	Val	Gly	Asp	Arg	Val	Ile	Ala	Glu	Lys	Val	Ser	Tyr	Phe
145				150					155					Phe
Arg	Lys	Pro	Glu	Val	Ser	Asp	Ile	Val	Ile	Phe	Lys	Ala	Pro	Pro
			165					170					175	Ile
Leu	Val	Glu	His	Gly	Tyr	Ser	Cys	Ala	Asp	Val	Phe	Ile	Lys	Arg
			180					185				190		Ile
Val	Ala	Ser	Glu	Gly	Asp	Trp	Val	Glu	Val	Cys	Asp	Gly	Lys	Leu
			195				200					205		Leu
Val	Asn	Asp	Thr	Val	Gln	Ala	Glu	Asp	Phe	Val	Leu	Glu	Pro	Ile
			210			215					220			Asp
Tyr	Glu	Met	Glu	Pro	Met	Phe	Val	Pro	Glu	Gly	Tyr	Val	Phe	Val
225					230					235				Leu
Gly	Asp	Asn	Arg	Asn	Lys	Ser	Phe	Asp	Ser	His	Asn	Trp	Gly	Pro
				245					250				255	Leu
Pro	Ile	Lys	Asn	Ile	Ile	Gly	Arg	Ser	Val	Phe	Arg	Tyr	Trp	Pro
			260				265						270	Pro
Ser	Lys	Val	Ser	Asp	Ile	Ile	His	His	Glu	Gln	Val	Ser	Gln	Lys
			275				280					285		Arg
Ala	Val	Asp	Val	Ser										
			290											

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 272 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..272

(D) OTHER INFORMATION: / Ceres Seq. ID 1497990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Met Ile Ser Leu Met Asn Leu Thr Gly Ala Pro Gln Phe Ser Gly Val
1 5 10 15
Thr Gly Leu Gly Ile Ser Pro Phe Lys Thr Ser Ser Val Ile Pro Phe
20 25 30
Leu Arg Gly Ser Lys Trp Met Pro Cys Ser Ile Pro Ala Thr Leu Ser
35 40 45
Thr Asp Ile Ala Glu Val Asp Arg Gly Gly Lys Val Cys Asp Pro Lys
50 55 60
Val Lys Leu Glu Leu Ser Asp Lys Val Ser Asn Gly Gly Asn Gly Trp
65 70 75 80
Val Asn Lys Leu Leu Asn Ile Cys Ser Glu Asp Ala Lys Ala Ala Phe
85 90 95
Thr Ala Val Thr Phe Ser Leu Leu Phe Arg Ser Ala Leu Ala Glu Pro
100 105 110
Lys Ser Ile Pro Ser Thr Ser Met Leu Pro Thr Leu Asp Val Gly Asp
115 120 125
Arg Val Ile Ala Glu Lys Val Ser Tyr Phe Phe Arg Lys Pro Glu Val
130 135 140
Ser Asp Ile Val Ile Phe Lys Ala Pro Pro Ile Leu Val Glu His Gly
145 150 155 160
Tyr Ser Cys Ala Asp Val Phe Ile Lys Arg Ile Val Ala Ser Glu Gly
165 170 175
Asp Trp Val Glu Val Cys Asp Gly Lys Leu Leu Val Asn Asp Thr Val
180 185 190
Gln Ala Glu Asp Phe Val Leu Glu Pro Ile Asp Tyr Glu Met Glu Pro
195 200 205
Met Phe Val Pro Glu Gly Tyr Val Phe Val Leu Gly Asp Asn Arg Asn
210 215 220
Lys Ser Phe Asp Ser His Asn Trp Gly Pro Leu Pro Ile Lys Asn Ile
225 230 235 240
Ile Gly Arg Ser Val Phe Arg Tyr Trp Pro Pro Ser Lys Val Ser Asp
245 250 255
Ile Ile His His Glu Gln Val Ser Gln Lys Arg Ala Val Asp Val Ser
260 265 270

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..591

(D) OTHER INFORMATION: / Ceres Seq. ID 1497991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

aatttcacat ctttctcacc caaatctact cttaaccgta cttcttcttc tacagacatc 60
aatttctctc gagataaaact aaatcttcgc tgaaaaaatg tcgggtcgtg gaaagggagg 120
aaaaggtttg ggtaaaggag gagccaacgc tcacaggaag gttctgagag acaacatcca 180
aggaatcacc aagcctgcga ttogaagatt ggctcgtaga ggtggagatca agcgtatcac 240
tggtctcacc tacgaggaga ctgcgtggcgt cctcaagatc tttctcgaga acgtgattcg 300
tgatgctgtc acttacaccg agcacgctag gaggaagact gtgaccgccca tggatgttgt 360
ctacgctctc aaaggagcaag gaaggactct ttacggattc ggtgggttaat tagagttttt 420
cagatccgcg ttgtgtttt ctgggtttct cacttaagcg totgcgtttt acttttgtat 480
tgggtttggc gtttagtag ttgcggttagc gttcttgtta tggtaataa cgctttttct 540
tcttgcttca gcagtttgg ttgaaatata aatcgaatca agtttcactt c

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 103 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..103
 (D) OTHER INFORMATION: / Ceres Seq. ID 1497992
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:
Met Ser Gly Arg Gly Lys Gly Lys Gly Leu Gly Lys Gly Ala
1 5 10 15
Lys Arg His Arg Lys Val Leu Arg Asp Asn Ile Gln Gly Ile Thr Lys
 20 25 30
Pro Ala Ile Arg Arg Leu Ala Arg Arg Gly Gly Val Lys Arg Ile Ser
 35 40 45
Gly Leu Ile Tyr Glu Glu Thr Arg Gly Val Leu Lys Ile Phe Leu Glu
 50 55 60
Asn Val Ile Arg Asp Ala Val Thr Tyr Thr Glu His Ala Arg Arg Lys
65 70 75 80
Thr Val Thr Ala Met Asp Val Val Tyr Ala Leu Lys Arg Gln Gly Arg
 85 90 95
Thr Leu Tyr Gly Phe Gly Gly
 100
(2) INFORMATION FOR SEQ ID NO:111:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1508 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..1508
 (D) OTHER INFORMATION: / Ceres Seq. ID 1497993
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:
gcncnagncc nttncskggg nsggcnnkrr ksggrrrrrk srsghkkkkk gatcactttt 60
tttggttttt ttccgcgaagc caaaaaaa caagacaaaa agaaataaac gacgaggctt 120
ttgttttatt tataaagctc cttcacccgtt aaaagccttg gtccctcatga aaccgggaag 180
cccaagtact tacttccacc atcaaatcgt caaacattt gcaaccatcg atgggtggtca 240
tgtcacagagt aagcttctac tcttctttct tgcactactc gttagaggtc gtgtgcgtca 300
gcagcgagtt tgatgatgag aagaacatcg ttccagtcct ccaaggctat aatcatgato 360
gtactcgtta gtgtttttct cgcacttgga tgtatctccg tctacatgag gaggtgtctc 420
cagcacgctc tggggatgga cagcggtggt gggtccaggaa actggcttaa cgtgaggcaa 480
acgacggagc ctgggctaga cgcgtctggt atagaaacgt ttccaacggt tcttactct 540
acagtgaaga cgttgaggat cgttaagaaa gctttggagt gtcccgtttg tctcaacgag 600
ttcgaggacg acgaaacgct cgcgttgatt cctcagtggt gtcacgtggt tcatctcggt 660
tgcattgatg cctggctccg ttctcagacc acatgtctct tttgccgagc caatctcggt 720
cctgtaccgg gtgagtcctt ttcttcggag ataccgggt tagctagaga aaccggtcag 780
aactctctca gaacgccgat tgatgataac cggaaaaagg ttttaacctc aacctgacga 840
cggttgattg actcagtggt ttggacgggt tggcctagtt caccgggcca accggaggag 900
acaggttgga aactagctga atgtacacg ccgcctagtt caccgggcca accggaggag 960
aatctcgacc ggtatacgtc gaggttaccac caagagatac atgaccagct tgtgaactcc 1020
agcctgggaa agcaaggctc aaaaggccaa ctggccttac ctcaagaagc gagctcggtt 1080
agaggggttc gaaccgggag cctagggaat gaataagaat ttgaacggtt 1140
gatcaagagc gtcggttgga ccggagacca ttttctataa ctctccataa ccataccggg 1200
tcgatacagt ctcggatgga gattatcaac gctagtggta attatcaga tctgtctggt 1260
tcacctaaag gtttgcttct agcaataaag tcaccgtttg atcggttatt taactgggaag 1320
ataaatgcgc gtgagcgctt gtaacctcaa tcggcgcatg cgagccctgt ctaggcgaaat 1380
tactactatt ggggttatta gaaatatctt gaataaaga aaatctgtat atgtattttc 1440

ttttcttag tttcttatg ttatatgaga aattcaattc cttaccaat ataattgcatc 1500
tgttactg

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..353
- (D) OTHER INFORMATION: / Ceres Seq. ID 1497994

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Met Met Arg Arg Thr Ser Phe Ser Pro Thr Thr Ala Ile Ile Met Ile
1 5 10 15
Val Leu Val Ser Val Phe Phe Ala Leu Gly Cys Ile Ser Val Tyr Met
20 25 30
Arg Arg Cys Leu Gln His Ala Leu Gly Met Asp Ser Gly Gly Gly Pro
35 40 45
Gly Asn Trp Leu Asn Val Arg Gln Thr Thr Glu Pro Gly Leu Asp Ala
50 55 60
Ser Val Ile Glu Thr Phe Pro Thr Phe Pro Tyr Ser Thr Val Lys Thr
65 70 75 80
Leu Arg Ile Gly Lys Glu Ala Leu Glu Cys Pro Val Cys Leu Asn Glu
85 90 95
Phe Glu Asp Asp Glu Thr Leu Arg Leu Ile Pro Gln Cys Cys His Val
100 105 110
Phe His Pro Gly Cys Ile Asp Ala Trp Leu Arg Ser Gln Thr Thr Cys
115 120 125
Pro Leu Cys Arg Ala Asn Leu Val Pro Val Pro Gly Glu Ser Val Ser
130 135 140
Ser Glu Ile Pro Gly Leu Ala Arg Glu Thr Gly Gln Asn Ser Leu Arg
145 150 155 160
Thr Pro Ile Asp Asp Asn Arg Lys Arg Val Leu Thr Ser Pro Asp Glu
165 170 175
Arg Leu Ile Asp Ser Val Ala Trp Thr Gly Asn Gln Ser Met Pro Arg
180 185 190
Lys Ser Met Ser Thr Gly Trp Lys Leu Ala Glu Leu Tyr Ser Pro Ala
195 200 205
Ser Ser Pro Gly Gln Pro Glu Asn Leu Asp Arg Tyr Thr Leu Arg
210 215 220
Leu Pro Gln Glu Ile His Asp Gln Leu Val Asn Ser Ser Leu Gly Lys
225 230 235 240
Gln Gly Ser Lys Gly Gln Leu Ala Leu Pro Gln Glu Arg Ser Ser Val
245 250 255
Arg Gly Phe Arg Thr Gly Ser Leu Gly Thr Glu Lys Asn Tyr Phe Tyr
260 265 270
Phe Glu Arg Phe Asp Gln Asp Gly Arg Leu Asp Arg Arg Pro Phe Ser
275 280 285
Ile Thr Pro Pro Tyr His Thr Arg Ser Ile Gln Ser Pro Asp Glu Ile
290 295 300
Ile Asn Ala Ser Gly Asn Tyr Gln Asp Arg Ala Gly Ser Pro Lys Gly
305 310 315 320
Leu Leu Leu Ala Ile Arg Ser Pro Phe Asp Arg Leu Phe Thr Gly Lys
325 330 335
Lys Asn Ala Gly Glu Arg Ser Tyr Leu Gln Ser Gly Asp Ala Ser Pro
340 345 350
Val

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 352 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..352
 (D) OTHER INFORMATION: / Ceres Seq. ID 1497995

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Met	Arg	Arg	Thr	Ser	Phe	Ser	Pro	Thr	Thr	Ala	Ile	Ile	Met	Ile	Val
1				5					10					15	
Leu	Val	Ser	Val	Phe	Phe	Ala	Leu	Gly	Cys	Ile	Ser	Val	Tyr	Met	Arg
			20					25					30		
Arg	Cys	Leu	Gln	His	Ala	Leu	Gly	Met	Asp	Ser	Gly	Gly	Gly	Pro	Gly
		35					40					45			
Asn	Trp	Leu	Asn	Val	Arg	Gln	Thr	Thr	Glu	Pro	Gly	Leu	Asp	Ala	Ser
		50				55					60				
Val	Ile	Glu	Thr	Phe	Pro	Thr	Phe	Pro	Tyr	Ser	Thr	Val	Lys	Thr	Leu
65				70					75					80	
Arg	Ile	Gly	Lys	Glu	Ala	Leu	Glu	Cys	Pro	Val	Cys	Leu	Asn	Glu	Phe
			85					90					95		
Glu	Asp	Asp	Glu	Thr	Leu	Arg	Leu	Ile	Pro	Gln	Cys	Cys	His	Val	Phe
			100				105						110		
His	Pro	Gly	Cys	Ile	Asp	Ala	Trp	Leu	Arg	Ser	Gln	Thr	Thr	Cys	Pro
		115					120				125				
Leu	Cys	Arg	Ala	Asn	Leu	Val	Pro	Val	Pro	Gly	Glu	Ser	Val	Ser	Ser
		130			135						140				
Glu	Ile	Pro	Gly	Leu	Ala	Arg	Glu	Thr	Gly	Gln	Asn	Ser	Leu	Arg	Thr
145				150					155					160	
Pro	Ile	Asp	Asp	Asn	Arg	Lys	Arg	Val	Leu	Thr	Ser	Pro	Asp	Glu	Arg
			165					170					175		
Leu	Ile	Asp	Ser	Val	Ala	Trp	Thr	Gly	Asn	Gln	Ser	Met	Pro	Arg	Lys
			180					185					190		
Ser	Met	Ser	Thr	Gly	Trp	Lys	Leu	Ala	Glu	Leu	Tyr	Ser	Pro	Ala	Ser
		195					200					205			
Ser	Pro	Gly	Gln	Pro	Glu	Glu	Asn	Leu	Asp	Arg	Tyr	Thr	Leu	Arg	Leu
		210			215						220				
Pro	Gln	Glu	Ile	His	Asp	Gln	Leu	Val	Asn	Ser	Ser	Leu	Gly	Lys	Gln
225				230						235					240
Gly	Ser	Lys	Gly	Gln	Leu	Ala	Leu	Pro	Gln	Glu	Arg	Ser	Ser	Val	Arg
			245						250					255	
Gly	Phe	Arg	Thr	Gly	Ser	Leu	Gly	Thr	Glu	Lys	Asn	Tyr	Phe	Tyr	Phe
			260				265						270		
Glu	Arg	Phe	Asp	Gln	Asp	Gly	Arg	Leu	Asp	Arg	Arg	Pro	Phe	Ser	Ile
		275					280					285			
Thr	Pro	Pro	Tyr	His	Thr	Arg	Ser	Ile	Gln	Ser	Pro	Asp	Glu	Ile	Ile
		290					295					300			
Asn	Ala	Ser	Gly	Asn	Tyr	Gln	Asp	Arg	Ala	Gly	Ser	Pro	Lys	Gly	Leu
305				310						315					320
Leu	Leu	Ala	Ile	Arg	Ser	Pro	Phe	Asp	Arg	Leu	Phe	Thr	Gly	Lys	Lys
			325						330					335	
Asn	Ala	Gly	Glu	Arg	Ser	Tyr	Leu	Gln	Ser	Gly	Asp	Ala	Ser	Pro	Val
			340					345					350		

- (2) INFORMATION FOR SEQ ID NO:114:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 339 amino acids
 (B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..339
 (D) OTHER INFORMATION: / Ceres Seq. ID 1497996
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Met Ile Val Leu Val Ser Val Phe Phe Ala Leu Gly Cys Ile Ser Val
1 5 10 15
Tyr Met Arg Arg Cys Leu Gln His Ala Leu Gly Met Asp Ser Gly Gly
20 25 30
Gly Pro Gly Asn Trp Leu Asn Val Arg Gln Thr Thr Glu Pro Gly Leu
35 40 45
Asp Ala Ser Val Ile Glu Thr Phe Pro Thr Phe Pro Tyr Ser Thr Val
50 55 60
Lys Thr Leu Arg Ile Gly Lys Glu Ala Leu Glu Cys Pro Val Cys Leu
65 70 75 80
Asn Glu Phe Glu Asp Asp Glu Thr Leu Arg Leu Ile Pro Gln Cys Cys
85 90 95
His Val Phe His Pro Gly Cys Ile Asp Ala Trp Leu Arg Ser Gln Thr
100 105 110
Thr Cys Pro Leu Cys Arg Ala Asn Leu Val Pro Val Pro Gly Glu Ser
115 120 125
Val Ser Ser Glu Ile Pro Gly Leu Ala Arg Glu Thr Gly Gln Asn Ser
130 135 140
Leu Arg Thr Pro Ile Asp Asp Asn Arg Lys Arg Val Leu Thr Ser Pro
145 150 155 160
Asp Glu Arg Leu Ile Asp Ser Val Ala Trp Thr Gly Asn Gln Ser Met
165 170 175
Pro Arg Lys Ser Met Ser Thr Gly Trp Lys Leu Ala Glu Leu Tyr Ser
180 185 190
Pro Ala Ser Ser Pro Gly Gln Pro Glu Glu Asn Leu Asp Arg Tyr Thr
195 200 205
Leu Arg Leu Pro Gln Glu Ile His Asp Gln Leu Val Asn Ser Ser Leu
210 215 220
Gly Lys Gln Gly Ser Lys Gly Gln Leu Ala Leu Pro Gln Glu Arg Ser
225 230 235 240
Ser Val Arg Gly Phe Arg Thr Gly Ser Leu Gly Thr Glu Lys Asn Tyr
245 250 255
Phe Tyr Phe Glu Arg Phe Asp Gln Asp Gly Arg Leu Asp Arg Arg Pro
260 265 270
Phe Ser Ile Thr Pro Pro Tyr His Thr Arg Ser Ile Gln Ser Pro Asp
275 280 285
Glu Ile Ile Asn Ala Ser Gly Asn Tyr Gln Asp Arg Ala Gly Ser Pro
290 295 300
Lys Gly Leu Leu Leu Ala Ile Arg Ser Pro Phe Asp Arg Leu Phe Thr
305 310 315 320
Gly Lys Lys Asn Ala Gly Glu Arg Ser Tyr Leu Gln Ser Gly Asp Ala
325 330 335
Ser Pro Val

- (2) INFORMATION FOR SEQ ID NO:115:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 842 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -

(B) LOCATION: 1..842

(D) OTHER INFORMATION: / Ceres Seq. ID 1497997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

[illegible]

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..116

(D) OTHER INFORMATION

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:
Leu Val Tyr Asp Met Thr Ile Arg Glu Ser P

[illegible]

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

{B) LOCATION: 1..11]

(D) OTHER INFORMATION

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Thr Ile Arg Glu Ser Phe Glu His Ile Pro G

Leu Arg Val His Ala Asp Lys Asn Ile Val Ile Ile Leu Ile Gly Asn

(X) SEQUENCE ALIGNMENT

Lys	Lys	Gly	Thr	Lys	Gly	Asp	Val	Thr	Ala	Leu	Lys	Pro	Thr	Ile	Met
1				5				10						15	
Thr	Ala	Val	Pro	Ala	Ile	Leu	Asp	Arg	Val	Arg	Asp	Gly	Val	Arg	Lys
			20				25					30			

Lys Val Asp Ala Lys Gly Gly Leu Ser Lys Lys Leu Phe Asp Phe Ala
35 40 45
Tyr Ala Arg Arg Leu Ser Ala Ile Asn Gly Ser Trp Phe Gly Ala Trp
50 55 60
Gly Leu Glu Lys Leu Leu Trp Asp Val Leu Val Phe Arg Lys Ile Arg
65 70 75 80
Ala Val Leu Gly Gly Gln Ile Arg Tyr Leu Leu Ser Gly Gly Ala Pro
85 90 95
Leu Ser Gly Asp Thr Gln Arg Phe Ile Asn Ile Cys Val Gly Ala Pro
100 105 110
Ile Gly Gln Gly Tyr Gly Leu Thr Glu Thr Cys Ala Gly Gly Thr Phe
115 120 125
Ser Glu Phe Glu Asp Thr Ser Val Gly Arg Val Gly Ala Pro Leu Pro
130 135 140
Cys Ser Phe Val Lys Leu Val Asp Trp Ala Glu Gly Gly Tyr Leu Thr
145 150 155 160
Ser Asp Lys Pro Met Pro Arg Gly Glu Ile Val Ile Gly Gly Ser Asn
165 170 175
Ile Thr Leu Gly Tyr Phe Lys Asn Glu Glu Lys Thr Lys Glu Val Tyr
180 185 190
Lys Val Asp Glu Lys Gly Met Arg Trp Phe Tyr Thr Gly Asp Ile Gly
195 200 205
Arg Phe His Pro Asp Gly Cys Leu Glu Ile Ile Asp Arg Lys Lys Asp
210 215 220
Ile Val Lys Leu Gln His Gly Glu Tyr Val Ser Leu Gly Lys Val Glu
225 230 235 240
Ala Ala Leu Ser Ile Ser Pro Tyr Val Glu Asn Ile Met Val His Ala
245 250 255
Asp Ser Phe Tyr Ser Tyr Cys Val Ala Leu Val Val Ala Ser Gln His
260 265 270
Thr Val Glu Gly Trp Ala Ser Lys Xaa Gly Ile Xaa Phe Ala Asn Phe
275 280 285
Glu Glu Leu Cys Thr Lys Glu Gln Ala Val Lys Glu Val Tyr Ala Tyr
290 295 300
Leu Val Lys Ala Ala Lys Gln Ser Arg Leu Glu Lys Phe Glu Ile Xaa
305 310 315 320
Ala Lys Ile Lys Leu Leu Ala Ser Pro Trp Thr Pro Glu Ser Gly Leu
325 330 335
Val Thr Ala Ala Leu Lys Leu Lys Arg Asp Val Ile Arg Arg Glu Phe
340 345 350
Ser Glu Asp Leu Thr Lys Leu Tyr Ala
355 360

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..346
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Met Thr Ala Val Pro Ala Ile Leu Asp Arg Val Arg Asp Gly Val Arg
1 5 10 15
Lys Lys Val Asp Ala Lys Gly Gly Leu Ser Lys Lys Leu Phe Asp Phe
20 25 30
Ala Tyr Ala Arg Arg Leu Ser Ala Ile Asn Gly Ser Trp Phe Gly Ala
35 40 45
Trp Gly Leu Glu Lys Leu Leu Trp Asp Val Leu Val Phe Arg Lys Ile

50	55	60
Arg Ala Val Leu Gly Gly Gln Ile Arg Tyr Leu Leu Ser Gly Gly Ala		
65	70	75
Pro Leu Ser Gly Asp Thr Gln Arg Phe Ile Asn Ile Cys Val Gly Ala		80
	85	90
Pro Ile Gly Gln Gly Tyr Gly Leu Thr Glu Thr Cys Ala Gly Gly Thr		95
	100	105
Phe Ser Glu Phe Glu Asp Thr Ser Val Gly Arg Val Gly Ala Pro Leu		110
	115	120
Pro Cys Ser Phe Val Lys Leu Val Asp Trp Ala Glu Gly Gly Tyr Leu		125
	130	135
Thr Ser Asp Lys Pro Met Pro Arg Gly Glu Ile Val Ile Gly Gly Ser		140
	145	150
Asn Ile Thr Leu Gly Tyr Phe Lys Asn Glu Glu Lys Thr Lys Glu Val		155
	160	165
Tyr Lys Val Asp Glu Lys Gly Met Arg Trp Phe Tyr Thr Gly Asp Ile		170
	175	180
Gly Arg Phe His Pro Asp Gly Cys Leu Glu Ile Ile Asp Arg Lys Lys		185
	190	195
Asp Ile Val Lys Leu Gln His Gly Glu Tyr Val Ser Leu Gly Lys Val		200
	205	210
Glu Ala Ala Leu Ser Ile Ser Pro Tyr Val Glu Asn Ile Met Val His		215
	220	225
Ala Asp Ser Phe Tyr Ser Tyr Cys Val Ala Leu Val Val Ala Ser Gln		230
	235	240
His Thr Val Glu Gly Trp Ala Ser Lys Xaa Gly Ile Xaa Phe Ala Asn		245
	250	255
Phe Glu Glu Leu Cys Thr Lys Glu Gln Ala Val Lys Glu Val Tyr Ala		260
	265	270
Tyr Leu Val Lys Ala Ala Lys Gln Ser Arg Leu Glu Lys Phe Glu Ile		275
	280	285
Xaa Ala Lys Ile Lys Leu Leu Ala Ser Pro Trp Thr Pro Glu Ser Gly		290
	295	300
Leu Val Thr Ala Ala Leu Lys Leu Lys Arg Asp Val Ile Arg Arg Glu		305
	310	315
Phe Ser Glu Asp Leu Thr Lys Leu Tyr Ala		320
	325	330
	335	340
	345	

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..197

(D) OTHER INFORMATION: / Ceres Seq. ID 1498003

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Met Pro Arg Gly Glu Ile Val Ile Gly Gly Ser Asn Ile Thr Leu Gly		
1	5	10
Tyr Phe Lys Asn Glu Glu Lys Thr Lys Glu Val Tyr Lys Val Asp Glu		15
	20	25
Lys Gly Met Arg Trp Phe Tyr Thr Gly Asp Ile Gly Arg Phe His Pro		30
	35	40
Asp Gly Cys Leu Glu Ile Ile Asp Arg Lys Lys Asp Ile Val Lys Leu		45
	50	55
Gln His Gly Glu Tyr Val Ser Leu Gly Lys Val Glu Ala Ala Leu Ser		60
	65	70
Ile Ser Pro Tyr Val Glu Asn Ile Met Val His Ala Asp Ser Phe Tyr		75
	80	85
	90	95

Ser Tyr Cys Val Ala Leu Val Val Ala Ser Gln His Thr Val Glu Gly
100 105 110
Trp Ala Ser Lys Xaa Gly Ile Xaa Phe Ala Asn Phe Glu Glu Leu Cys
115 120 125
Thr Lys Glu Gln Ala Val Lys Glu Val Tyr Ala Tyr Leu Val Lys Ala
130 135 140
Ala Lys Gln Ser Arg Leu Glu Lys Phe Glu Ile Xaa Ala Lys Ile Lys
145 150 155 160
Leu Leu Ala Ser Pro Trp Thr Pro Glu Ser Gly Leu Val Thr Ala Ala
165 170 175
Leu Lys Leu Lys Arg Asp Val Ile Arg Arg Glu Phe Ser Glu Asp Leu
180 185 190
Thr Lys Leu Tyr Ala
195

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 764 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..764

(D) OTHER INFORMATION: / Ceres Seq. ID 1498006

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

ctaattcgaaa	aatcatcact	ttcacaatct	tcttcacgca	ttctctctct	ccaaaatctcc	60
caaaagatgt	cgaaccctag	agttttctct	gacatgagtc	tcagcgggtac	tcaccatcgga	120
cggatcgaga	tggagctttt	cgctgatata	accccaaaaca	cgcgcgagaa	tttcggtgct	180
ctctgtaccg	cgagagaaag	aatgggaaag	ctaggttaagc	cacttcaact	caaaaggatcg	240
atcttcacac	gtgtgattcc	cggattcatg	tgtaaggag	gtgatttcac	cgccaagaac	300
ggaaccgggt	gtgaatcgat	ctacgggtgc	aagttcaagg	acgagaactt	tatcaagaag	360
catacaggag	ctgggattct	ctcaatggct	aactctggct	ctaacactaa	cggatctcag	420
ttcttcactt	gtaccgataa	gacgtcgtgg	ttagatggta	agcacgttgt	gtttggacaa	480
gttgtaaag	gcttggacgt	cgtgaaggcg	attgagaaag	ttggatctga	ttctggaaa	540
acttccaaag	tcgttaccat	cactgattgt	ggtcagcttt	cttagatcta	agtgagaaa	600
tgagagactt	tgatctttat	gagtaataat	gggtctcttt	gctttcgggt	gttcttcctc	660
ttaccttaat	ggattattct	gtttagggtt	tgagttttcg	tttcagagtt	tgtaacaaaa	720
ccctttttgt	ttttctgggg	tttgaaataa	ttatgagctt	actc		

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..194

(D) OTHER INFORMATION: / Ceres Seq. ID 1498007

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Leu	Ile	Glu	Lys	Ser	Ser	Leu	Ser	Gln	Ser	Ser	Ser	Ile	Ser	Leu
1			5					10				15		
Phe	Gln	Ile	Ser	Gln	Lys	Met	Ser	Asn	Pro	Arg	Val	Phe	Phe	Asp Met
			20					25				30		
Ser	Leu	Ser	Gly	Thr	Pro	Ile	Gly	Arg	Ile	Glu	Met	Glu	Leu	Phe Ala
			35				40					45		
Asp	Thr	Thr	Pro	Asn	Thr	Ala	Glu	Asn	Phe	Arg	Ala	Leu	Cys	Thr Gly
			50				55				60			
Glu	Lys	Gly	Met	Gly	Lys	Leu	Gly	Lys	Pro	Leu	His	Phe	Lys	Gly Ser
65					70					75				80

Ile Phe His Arg Val Ile Pro Gly Phe Met Cys Gln Gly Gly Asp Phe
85 90 95
Thr Ala Lys Asn Gly Thr Gly Gly Glu Ser Ile Tyr Gly Ala Lys Phe
100 105 110
Lys Asp Glu Asn Phe Ile Lys Lys His Thr Gly Ala Gly Ile Leu Ser
115 120 125
Met Ala Asn Ser Gly Pro Asn Thr Asn Gly Ser Gln Phe Phe Ile Cys
130 135 140
Thr Asp Lys Thr Ser Trp Leu Asp Gly Lys His Val Val Phe Gly Gln
145 150 155 160
Val Val Lys Gly Leu Asp Val Val Lys Ala Ile Glu Lys Val Gly Ser
165 170 175
Asp Ser Gly Lys Thr Ser Lys Val Val Thr Ile Thr Asp Cys Gly Gln
180 185 190
Leu Ser

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..172

(D) OTHER INFORMATION: / Ceres Seq. ID 1498008

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Met Ser Asn Pro Arg Val Phe Phe Asp Met Ser Leu Ser Gly Thr Pro
1 5 10 15
Ile Gly Arg Ile Glu Met Glu Leu Phe Ala Asp Thr Thr Pro Asn Thr
20 25 30
Ala Glu Asn Phe Arg Ala Leu Cys Thr Gly Glu Lys Gly Met Gly Lys
35 40 45
Leu Gly Lys Pro Leu His Phe Lys Gly Ser Ile Phe His Arg Val Ile
50 55 60
Pro Gly Phe Met Cys Gln Gly Gly Asp Phe Thr Ala Lys Asn Gly Thr
65 70 75 80
Gly Gly Glu Ser Ile Tyr Gly Ala Lys Phe Lys Asp Glu Asn Phe Ile
85 90 95
Lys Lys His Thr Gly Ala Gly Ile Leu Ser Met Ala Asn Ser Gly Pro
100 105 110
Asn Thr Asn Gly Ser Gln Phe Phe Ile Cys Thr Asp Lys Thr Ser Trp
115 120 125
Leu Asp Gly Lys His Val Val Phe Gly Gln Val Val Lys Gly Leu Asp
130 135 140
Val Val Lys Ala Ile Glu Lys Val Gly Ser Asp Ser Gly Lys Thr Ser
145 150 155 160
Lys Val Val Thr Ile Thr Asp Cys Gly Gln Leu Ser
165 170

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..163

(D) OTHER INFORMATION: / Ceres Seq. ID 1498009

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:
Met Ser Leu Ser Gly Thr Pro Ile Gly Arg Ile Glu Met Glu Leu Phe
1 5 10 15
Ala Asp Thr Thr Pro Asn Thr Ala Glu Asn Phe Arg Ala Leu Cys Thr
20 25 30
Gly Glu Lys Gly Met Gly Lys Leu Gly Lys Pro Leu His Phe Lys Gly
35 40 45
Ser Ile Phe His Arg Val Ile Pro Gly Phe Met Cys Gln Gly Gly Asp
50 55 60
Phe Thr Ala Lys Asn Gly Thr Gly Gly Glu Ser Ile Tyr Gly Ala Lys
65 70 75 80
Phe Lys Asp Glu Asn Phe Ile Lys Lys His Thr Gly Ala Gly Ile Leu
85 90 95
Ser Met Ala Asn Ser Gly Pro Asn Thr Asn Gly Ser Gln Phe Phe Ile
100 105 110
Cys Thr Asp Lys Thr Ser Trp Leu Asp Gly Lys His Val Val Phe Gly
115 120 125
Gln Val Val Lys Gly Leu Asp Val Val Lys Ala Ile Glu Lys Val Gly
130 135 140
Ser Asp Ser Gly Lys Thr Ser Lys Val Val Thr Ile Thr Asp Cys Gly
145 150 155 160
Gln Leu Ser

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1231
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

aacaaaaga	atcacgacat	tgaatcttct	ttcatttctc	tcctcaagac	atagtagcat	60
aagamaatga	agatatcatc	actaggaatg	gtcttagtcc	ttatcttcat	ctctattacc	120
attgttttga	gtgcaccagc	acctaaacct	cctaaacctt	agcctgcacc	agcacctaca	180
ctctctaaac	ctaagcccac	accagcacct	acacctccta	aacctaaacc	caaacaccga	240
ctctacacct	ctaaacctaa	gccacaccca	gcacctacac	ctctctaaacc	taagcctgca	300
ccagcaccag	caccagcacc	aacaccagca	cggaaacctt	aacctgcacc	taaacccagca	360
ccaggtggag	aagttgagga	cgaacccgag	tttagctacg	agacgaaagg	aaacaagggg	420
ccagcgaaat	ggggaaacct	acatgcagag	tggaataatg	gtggaatagg	caaaatgc aa	480
ttctctattg	atcttcggga	caaaaatgtg	gtagttagta	ataaatttgg	attgcttcgt	540
agccagtatc	tgctttctaa	taccaccatt	aagaacagag	gtcatgatat	catgttgaaa	600
ttcaaagag	gcaataaagg	tattggtgtc	actatccgtg	gtactagata	tcaacttc aa	660
caacttcatt	ggcactctcc	ttccgaacat	acaaatcaatg	gcaaaagggt	tcgcctagag	720
gaacacttgg	ttcatgagag	taaagatava	cgctacgctg	ttgtcgcgtt	cttatacaat	780
ctcggagcat	ctgacccctt	tctcttttgc	ttggaaaacc	aattgaagaa	gataactgat	840
acacatgcgt	ccgagggaaca	tgtcggaaatc	atgatoccca	aaaaactcag	ttttgaatca	900
aaacattatt	atagatatct	cggatcactt	actgctctct	catgttctga	aaatgtttat	960
tggtcgtttt	ccaaagagat	tcgcaactgt	tcaagtaaac	aagtgaagct	tcttcgtgtg	1020
gctgtacacg	atgcttcaga	ttcaaatgcc	agggccgctt	aagcagtc aa	taagcgcaag	1080
gtatatattt	acaaaccaaa	ggttaagtta	atgaagaat	actgtaatat	aagtctttac	1140
tagtaattct	taattcttta	tatatgtaca	ttatgaattg	tacactaaaa	tgatgttttt	1200
agggataaac	tgatgacttg	tgtttgttat	t			

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..358
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498011
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:
Met Lys Ile Ser Ser Leu Gly Trp Val Leu Val Leu Ile Phe Ile Ser
1 5 10 15
Ile Thr Ile Val Ser Ser Ala Pro Ala Pro Lys Pro Pro Lys Pro Lys
20 25 30
Pro Ala Pro Ala Pro Thr Pro Pro Lys Pro Lys Pro Thr Pro Ala Pro
35 40 45
Thr Pro Pro Lys Pro Lys Pro Lys Pro Ala Pro Thr Pro Pro Lys Pro
50 55 60
Lys Pro Thr Pro Ala Pro Thr Pro Pro Lys Pro Lys Pro Ala Pro Ala
65 70 75 80
Pro Ala Pro Ala Pro Thr Pro Ala Pro Lys Pro Lys Pro Ala Pro Lys
85 90 95
Pro Ala Pro Gly Gly Glu Val Glu Asp Glu Thr Glu Phe Ser Tyr Glu
100 105 110
Thr Lys Gly Asn Lys Gly Pro Ala Lys Trp Gly Thr Leu His Ala Glu
115 120 125
Trp Lys Met Cys Gly Ile Gly Lys Met Gln Ser Pro Ile Asp Leu Arg
130 135 140
Asp Lys Asn Val Val Val Ser Asn Lys Phe Gly Leu Leu Arg Ser Gln
145 150 155 160
Tyr Leu Pro Ser Asn Thr Thr Ile Lys Asn Arg Gly His Asp Ile Met
165 170 175
Leu Lys Phe Lys Gly Gly Asn Lys Gly Ile Gly Val Thr Ile Arg Gly
180 185 190
Thr Arg Tyr Gln Leu Gln Leu His Trp His Ser Pro Ser Glu His
195 200 205
Thr Ile Asn Gly Lys Arg Phe Ala Leu Glu Glu His Leu Val His Glu
210 215 220
Ser Lys Asp Xaa Arg Tyr Ala Val Val Ala Phe Leu Tyr Asn Leu Gly
225 230 235 240
Ala Ser Asp Pro Phe Leu Phe Ser Leu Glu Lys Gln Leu Lys Ile
245 250 255
Thr Asp Thr His Ala Ser Glu Glu His Val Gly Ile Ile Asp Pro Lys
260 265 270
Lys Leu Ser Phe Glu Ser Lys His Tyr Tyr Arg Tyr Ser Gly Ser Leu
275 280 285
Thr Ala Pro Pro Cys Ser Glu Asn Val Ile Trp Ser Val Ser Lys Glu
290 295 300
Ile Arg Thr Val Ser Ser Lys Gln Val Lys Leu Leu Arg Val Ala Val
305 310 315 320
His Asp Ala Ser Asp Ser Asn Ala Arg Pro Leu Gln Ala Val Asn Lys
325 330 335
Arg Lys Val Tyr Leu Tyr Lys Pro Lys Val Lys Leu Met Lys Lys Tyr
340 345 350
Cys Asn Ile Ser Ser Tyr
355

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..228
(D) OTHER INFORMATION: / Ceres Seq. ID 1498012

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:
Met Cys Gly Ile Gly Lys Met Gln Ser Pro Ile Asp Leu Arg Asp Lys
1 5 10 15
Asn Val Val Val Ser Asn Lys Phe Gly Leu Leu Arg Ser Gln Tyr Leu
20 25 30
Pro Ser Asn Thr Thr Ile Lys Asn Arg Gly His Asp Ile Met Leu Lys
35 40 45
Phe Lys Gly Gly Asn Lys Gly Ile Gly Val Thr Ile Arg Gly Thr Arg
50 55 60
Tyr Gln Leu Gln Gln Leu His Trp His Ser Pro Ser Glu His Thr Ile
65 70 75 80
Asn Gly Lys Arg Phe Ala Leu Glu Glu His Leu Val His Glu Ser Lys
85 90 95
Asp Xaa Arg Tyr Ala Val Val Ala Phe Leu Tyr Asn Leu Gly Ala Ser
100 105 110
Asp Pro Phe Leu Phe Ser Leu Glu Lys Gln Leu Lys Lys Ile Thr Asp
115 120 125
Thr His Ala Ser Glu Glu His Val Gly Ile Ile Asp Pro Lys Lys Leu
130 135 140
Ser Phe Glu Ser Lys His Tyr Tyr Arg Tyr Ser Gly Ser Leu Thr Ala
145 150 155 160
Pro Pro Cys Ser Glu Asn Val Ile Trp Ser Val Ser Lys Glu Ile Arg
165 170 175
Thr Val Ser Ser Lys Gln Val Lys Leu Arg Val Ala Val His Asp
180 185 190
Ala Ser Asp Ser Asn Ala Arg Pro Leu Gln Ala Val Asn Lys Arg Lys
195 200 205
Val Tyr Leu Tyr Lys Pro Lys Val Lys Leu Met Lys Lys Tyr Cys Asn
210 215 220
Ile Ser Ser Tyr
225

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..222
(D) OTHER INFORMATION: / Ceres Seq. ID 1498013

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:
Met Gln Ser Pro Ile Asp Leu Arg Asp Lys Asn Val Val Val Ser Asn
1 5 10 15
Lys Phe Gly Leu Leu Arg Ser Gln Tyr Leu Pro Ser Asn Thr Thr Ile
20 25 30
Lys Asn Arg Gly His Asp Ile Met Leu Lys Phe Lys Gly Gly Asn Lys
35 40 45
Gly Ile Gly Val Thr Ile Arg Gly Thr Arg Tyr Gln Leu Gln Gln Leu
50 55 60
His Trp His Ser Pro Ser Glu His Thr Ile Asn Gly Lys Arg Phe Ala
65 70 75 80
Leu Glu Glu His Leu Val His Glu Ser Lys Asp Xaa Arg Tyr Ala Val
85 90 95
Val Ala Phe Leu Tyr Asn Leu Gly Ala Ser Asp Pro Phe Leu Phe Ser
100 105 110
Leu Glu Lys Gln Leu Lys Lys Ile Thr Asp Thr His Ala Ser Glu Glu

115	120	125
His Val Gly Ile Ile Asp Pro Lys Lys Leu Ser Phe Glu Ser Lys His		
130	135	140
Tyr Tyr Arg Tyr Ser Gly Ser Leu Thr Ala Pro Pro Cys Ser Glu Asn		
145	150	155
Val Ile Trp Ser Val Ser Lys Glu Ile Arg Thr Val Ser Ser Lys Gln		
165	170	175
Val Lys Leu Leu Arg Val Ala Val His Asp Ala Ser Asp Ser Asn Ala		
180	185	190
Arg Pro Leu Gln Ala Val Asn Lys Arg Lys Val Tyr Leu Tyr Lys Pro		
195	200	205
Lys Val Lys Leu Met Lys Lys Tyr Cys Asn Ile Ser Ser Tyr		
210	215	220

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1084 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1084
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498018

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

aaatttcaac	ccctggttgc	tttgtttgat	ccctagattt	tcgccgtgtt	atagaagaat	60
ctcatttttt	gccgtctgaa	tcgaaatttc	gtgtcgagaa	ctctccact	ctctccactt	120
tcgttttttc	tttttaattt	attttactct	attgtgacca	ttttgagcgt	tattgagaac	180
tcaaaagctca	agaatgcgtg	caccattctt	gcttgcaaaa	tgcttgccgg	gtttgtctgcc	240
tcaagaccga	ggsggtgtgt	ctgcrttatc	agagaaggat	ttgcagcttc	caacaccagg	300
tggttgagat	atacctctta	agacagtagc	tcatacagag	tattcagggg	agaattctaga	360
tgccgtcggt	ttacaagttt	tcaagggaag	agtaagtgtt	gctgatatca	ttgggctctc	420
tggttcagaa	actgctcctt	taaaaaatga	aggttctttg	aaaagtggg	aaagctctgt	480
tgttcttgtt	aatgtcctta	aaaacgagat	ccgtgatgga	cagcttagct	tcaggggcaca	540
aagggtctct	gagctaggct	gtccatcacg	gatctcgttt	taaaggacnt	taaagagwac	600
aagcaactgt	atgctgaaat	ccacaggaac	tacatctacg	gtggccatct	ctcaaaactac	660
atgaagctgt	tgggggaaga	tgagccggag	aagttgcaaa	ctcacttcag	tgcttaacatt	720
aaagaaggag	ttgaagctga	gagcatcgag	gagatgtaca	agaaggttca	cgcagctatc	780
cgagcagaac	ccaaccataa	gaaaaccgag	aaatctgctc	ccamsgaaca	caagaggtac	840
aacttgaaga	aactgactta	cgaagagagg	aagaacaagt	tgatcgagag	agtggaaggca	900
ttaaaccggag	cagggttggtg	tgatgatgat	gaggatgatg	aagagttaaa	acccaatcaa	960
gcctctcttg	tctcatgcct	ctagtagctt	tttacttatt	tattttcaga	ctaaaacact	1020
cagtttttgt	tttcaacatt	tagttggtgt	tgaagatttt	gaattcgagg	atatgttttg	1080

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..156
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498019

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Met Arg Ala Pro Ser Leu Leu Ala Gln Cys Leu Pro Gly Leu Leu Pro	
1	5
Gln Asp Arg Xaa Gly Val Ser Xaa Leu Ser Glu Lys Asp Leu Gln Leu	
20	25
Pro Thr Pro Ala Val Glu Ile Ile Pro Ser Lys Thr Val Ala His His	
	30

ctttaaacttc	aaatctccc	atgttatgaa	tcttcgagtt	accacaaaca	aaaaaaactct	60
ctctttatttc	agttttctctt	tacaaacacct	ttatctctct	tctgtatccat	ctctgtgaacc	120
accggcattaa	gaaataattga	caattctgctt	aacgatcggg	ggaaacaggtt	tttcgggctc	180
accaggagctg	tcgtttttctc	catcatctctc	tcgtttctga	tacaaaaaca	cgagaagaaga	240
gaacacacgaag	atgctcaaca	ctgcataaagt	cgtttgtctt	tctctatctc	ctgtataatga	300
tcogthtaag	acctcttaaga	tccgaccgga	ttcatcttgaa	tacagggtcta	agaaagagctg	360
cgagacaactc	gctcaaaaagg	tttgacctctt	tggtttagctc	aatcatctcta	gatctcgggtt	420
tttaaaattt	gacatctcttc	tgatcgattt	tggtttgatt	gttcgagtat	catctctgatg	480
tttgttagagg	aagcaattgct	gggggtacatt	ttcagacaact	tacaaagaagt	tacagtgtaa	540
cgctgtgagct	ttgaaagcta	acctgtctctt	ttggttaact	taaacacagat	tgaaaattcgc	600

ttttgtaagt aaaattgatc tctttgtttt ttttctttg aagattgtgt tgaagg

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..82
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Met	Thr	Ile	Ala	Leu	Thr	Ile	Gly	Gly	Asn	Gly	Phe	Ser	Gly	Leu	Pro
1				5					10					15	
Gly	Ser	Ser	Phe	Ser	Ser	Ser	Ser	Ser	Ser	Phe	Arg	Leu	Lys	Asn	Ser
			20						25					30	
Arg	Arg	Lys	Asn	Thr	Lys	Met	Leu	Asn	Arg	Ser	Lys	Val	Val	Cys	Ser
			35					40						45	
Ser	Ser	Ser	Ser	Val	Met	Asp	Pro	Xaa	Lys	Thr	Leu	Lys	Ile	Arg	Pro
			50			55			60						
Asp	Ser	Ser	Glu	Tyr	Glu	Val	Lys	Lys	Ala	Phe	Arg	Gln	Leu	Ala	Lys
65					70				75					80	
Lys	Val														

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..44
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Met	Leu	Asn	Arg	Ser	Lys	Val	Val	Cys	Ser	Ser	Ser	Ser	Ser	Val	Met
1				5					10					15	
Asp	Pro	Xaa	Lys	Thr	Leu	Lys	Ile	Arg	Pro	Asp	Ser	Ser	Glu	Tyr	Glu
			20					25					30		
Val	Lys	Lys	Ala	Phe	Arg	Gln	Leu	Ala	Lys	Lys	Val				
			35				40								

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1135
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498033

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

actcaccaaa	gcatacacata	acactcacac	acacactttc	tcttctctta	ttttctcagt	60
tcttttaact	cttttctctta	octatatatca	aatggccacc	gtcagagggtg	aacaagtgc	120
tccagtagca	gctgagaaca	togaggtgccc	accaccaaa	gctgtggagt	cggaggaagt	180
caccaccgtc	tccaggtctc	tccagctcc	ggtaacagaa	tctcagcgc	ctgtcgaagt	240
aacaactaaa	gatttggctg	tggagagac	agagaaacca	atcgaagaaa	cagaggaagc	300
tcaagtggaa	actccggagg	ttgtggagat	caagaaagat	gaagaaagctc	cggttgaaac	360

tccgggtggt	gtggaggatg	agagcaaaac	agagggaagt	gtaggaggga	agaagaggga	420
agaagtagaa	gaaagaaga	cagagggaagc	tccagtgggt	gtggagggaag	agaagaagcc	480
agaggcagag	gaggagaaac	ccggcggtgt	tacctccccc	gctcaagcca	ccatgggtcg	540
tccattccac	gggttgaagt	catccgcttc	tttcccggtc	accgcgaag	ccaacaacga	600
cattacttcc	atcacaagca	acggagggaag	agttagctgc	atgaaggtgt	ggccaccaat	660
cggaagaag	aagtttagac	tctatcttac	ctccctgacc	ttagtgcagt	tgaattggct	720
aagggaagtt	actaccttct	ccgcaacaag	tggattccct	gtgttgatt	cgagttggag	780
cacgattttg	tgtaccgtga	gcacggaaac	actcccgat	actatgatgg	acggtactgg	840
acaatttgga	agcttccatt	gttcggatgc	accgactccg	ctcaagtgtt	gaaggaaagt	900
gaagaatgca	agaaggagta	ccctggcgcc	ttcattagga	tcactggatt	gcacaacacc	960
cgctcaagtc	aatgcacatc	tttcattgoc	tacaagcccc	caagctctac	cgaagcttaa	1020
tccctttctt	ggaatatcca	cggttgatta	ttctggaacc	catttctatg	tgttcaatgc	1080
aaattttaaga	aattattttg	cgaacttaaaa	gttgaggaaac	tattgtttga	aagtc	

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 296 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..296

(D) OTHER INFORMATION: / Ceres Seq. ID 1498034

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Leu	Thr	Lys	Ala	Ser	His	Asn	Thr	His	Thr	His	Thr	Phe	Ser	Ser	Leu
1			5					10					15		
Ile	Phe	Ser	Val	Leu	Leu	Thr	Leu	Phe	Ser	Thr	Tyr	Ile	Gln	Met	Ala
			20					25					30		
Thr	Val	Glu	Val	Glu	Gln	Val	Thr	Pro	Val	Ala	Ala	Glu	Asn	Ile	Glu
			35					40				45			
Val	Pro	Pro	Pro	Lys	Ala	Val	Glu	Ser	Glu	Glu	Val	Thr	Thr	Val	Ser
						55					60				
Glu	Ser	Leu	Pro	Ala	Pro	Val	Thr	Glu	Ser	Gln	Ala	Pro	Val	Glu	Val
						70				75				80	
Thr	Thr	Lys	Asp	Leu	Val	Val	Glu	Glu	Thr	Glu	Lys	Pro	Ile	Glu	Glu
						85				90				95	
Thr	Glu	Glu	Ala	Gln	Val	Glu	Thr	Pro	Glu	Val	Val	Glu	Ile	Lys	Lys
						100				105				110	
Asp	Glu	Glu	Ala	Pro	Val	Glu	Thr	Pro	Val	Val	Val	Glu	Asp	Glu	Ser
						115								125	
Lys	Thr	Glu	Glu	Val	Val	Glu	Ala	Lys	Lys	Glu	Glu	Glu	Val	Glu	Glu
						130				135				140	
Lys	Lys	Thr	Glu	Glu	Ala	Pro	Val	Val	Val	Glu	Glu	Glu	Lys	Lys	Pro
						145				150				155	
Glu	Ala	Glu	Glu	Glu	Lys	Pro	Ala	Val	Val	Thr	Ser	Pro	Ala	Gln	Ala
						165				170				175	
Thr	Met	Val	Ala	Pro	Phe	Thr	Gly	Leu	Lys	Ser	Ser	Ala	Ser	Phe	Pro
						180				185				190	
Val	Thr	Arg	Lys	Ala	Asn	Asn	Asp	Ile	Thr	Ser	Ile	Thr	Ser	Asn	Gly
						195				200				205	
Gly	Arg	Val	Ser	Cys	Met	Lys	Val	Trp	Pro	Pro	Ile	Gly	Lys	Lys	Lys
						210				215				220	
Phe	Arg	Leu	Tyr	Leu	Thr	Ser	Leu	Thr	Leu	Val	Thr	Leu	Asn	Trp	Leu
						225				230				235	
Arg	Lys	Leu	Thr	Thr	Phe	Ser	Ala	Thr	Ser	Gly	Phe	Leu	Val	Leu	Asn
						245				250				255	
Ser	Ser	Trp	Ser	Thr	Asp	Leu	Cys	Thr	Val	Ser	Thr	Glu	Thr	Leu	Pro
						260				265				270	
Asp	Thr	Met	Met	Asp	Gly	Thr	Gly	Gln	Cys	Gly	Ser	Phe	His	Cys	Ser
						275				280				285	

Asp Ala Pro Thr Pro Leu Lys Cys
290 295

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..266
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Met Ala Thr Val Glu Val Glu Gln Val Thr Pro Val Ala Ala Glu Asn
1 5 10 15
Ile Glu Val Pro Pro Pro Lys Ala Val Glu Ser Glu Glu Val Thr Thr
20 25 30
Val Ser Glu Ser Leu Pro Ala Pro Val Thr Glu Ser Gln Ala Pro Val
35 40 45
Glu Val Thr Thr Lys Asp Leu Val Val Glu Glu Thr Glu Lys Pro Ile
50 55 60
Glu Glu Thr Glu Glu Ala Gln Val Glu Thr Pro Glu Val Val Glu Ile
65 70 75 80
Lys Lys Asp Glu Glu Ala Pro Val Glu Thr Pro Val Val Val Glu Asp
85 90 95
Glu Ser Lys Thr Glu Glu Val Val Glu Ala Lys Lys Glu Glu Val
100 105 110
Glu Glu Lys Lys Thr Glu Glu Ala Pro Val Val Val Glu Glu Lys
115 120 125
Lys Pro Glu Ala Glu Glu Glu Lys Pro Ala Val Val Thr Ser Pro Ala
130 135 140
Gln Ala Thr Met Val Ala Pro Phe Thr Gly Leu Lys Ser Ser Ala Ser
145 150 155 160
Phe Pro Val Thr Arg Lys Ala Asn Asn Asp Ile Thr Ser Ile Thr Ser
165 170 175
Asn Gly Gly Arg Val Ser Cys Met Lys Val Trp Pro Pro Ile Gly Lys
180 185 190
Lys Lys Phe Arg Leu Tyr Leu Thr Ser Leu Thr Leu Val Thr Leu Asn
195 200 205
Trp Leu Arg Lys Leu Thr Thr Phe Ser Ala Thr Ser Gly Phe Leu Val
210 215 220
Leu Asn Ser Ser Trp Ser Thr Asp Leu Cys Thr Val Ser Thr Glu Thr
225 230 235 240
Leu Pro Asp Thr Met Met Asp Gly Thr Gly Gln Cys Gly Ser Phe His
245 250 255
Cys Ser Asp Ala Pro Thr Pro Leu Lys Cys
260 265

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..427
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498036

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

gtctcattagg gttttctcatc tacgacggcg tgggtgttccct ccttctgtgt ctgaaaaatg

gcgaagagaa	cgaagaaggt	tggaatcgtc	ggcaaatcac	gaacacgtta	tggtgcgagt	120
atcaggaagc	agattaagaa	gatggaggtc	agccagcaca	gcaagtactt	ctgtgagttg	180
tatctggggt	tgaaggatt	tgggcaaggt	caaggcaggt	ggtgcttaca	caatgaacac	240
cgccagtgcg	gtcactgtta	gaagcacgat	cagaaggttg	aggagacaga	tcgaggggta	300
aaagtctgct	ggctttttat	atttggtttc	cttggtttga	caatttaagt	tttgcaaaact	360
ctatgcttgt	gattttgaat	caagacttat	acattgagca	gttttaagcag	gttttttatt	420
ttttgttg						

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..99
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498037

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Leu	Ile	Arg	Val	Ser	His	Leu	Arg	Arg	Arg	Gly	Val	Pro	Pro	Ser	Cys	
1			5						10					15		
Ser	Glu	Lys	Trp	Arg	Arg	Glu	Arg	Arg	Leu	Glu	Ser	Ser	Ala	Asn		
			20					25				30				
Thr	Glu	His	Val	Met	Val	Arg	Val	Ser	Gly	Ser	Arg	Leu	Arg	Arg	Trp	
		35					40					45				
Arg	Ser	Ala	Ser	Thr	Ala	Ser	Thr	Ser	Val	Ser	Cys	Ile	Trp	Gly	Cys	
		50				55					60					
Lys	Asp	Cys	Gly	Lys	Val	Lys	Ala	Gly	Gly	Ala	Tyr	Thr	Met	Asn	Thr	
		65				70				75					80	
Ala	Ser	Ala	Val	Thr	Val	Arg	Ser	Thr	Ile	Arg	Arg	Leu	Arg	Glu	Gln	
			85						90					95		
Ile	Glu	Gly														

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..67
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

Met	Ala	Lys	Arg	Thr	Lys	Lys	Val	Gly	Ile	Val	Gly	Lys	Tyr	Gly	Thr	
1			5						10				15			
Arg	Tyr	Gly	Ala	Ser	Ile	Arg	Lys	Gln	Ile	Lys	Lys	Met	Glu	Val	Ser	
			20					25					30			
Gln	His	Ser	Lys	Tyr	Phe	Cys	Glu	Leu	Tyr	Leu	Gly	Leu	Gln	Gly	Leu	
		35					40					45				
Trp	Gln	Gly	Gln	Gly	Arg	Trp	Cys	Leu	His	Asn	Glu	His	Arg	Gln	Cys	
		50				55				60						
Gly	His	Cys														
		65														

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..63

(D) OTHER INFORMATION: / Ceres Seq. ID 1498039

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Met	Val	Arg	Val	Ser	Gly	Ser	Arg	Leu	Arg	Trp	Arg	Ser	Ala	Ser
1			5					10				15		
Thr	Ala	Ser	Thr	Ser	Val	Ser	Cys	Ile	Trp	Gly	Cys	Lys	Asp	Cys
			20				25					30		
Lys	Val	Lys	Ala	Gly	Gly	Ala	Tyr	Thr	Met	Asn	Thr	Ala	Ser	Ala
			35				40					45		
Thr	Val	Arg	Ser	Thr	Ile	Arg	Arg	Leu	Arg	Glu	Gln	Ile	Glu	Gly
			50				55					60		

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2253 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..2253

(D) OTHER INFORMATION: / Ceres Seq. ID 1498043

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

aaaaccacac	acacagcttc	ttaactgaga	gcttttttct	agggttttct	tctttgtttc	60
ttacaatgag	actctttctc	acaccgtcaa	tgtccaatct	ctccatatct	ttctcgattc	120
ttctctcttc	ttctctcttc	ccgtcaatcg	gagatctcgc	cgccgacaaa	tcgcctcttc	180
ttctcttttc	ttccgcgcgt	gggtgtcgta	cattactctg	ggacgtcaag	caaacctcac	240
catgcaactg	gacccgcgtc	ttatgcgacg	gtggctgtgt	tactgctctt	cgtcttcccg	300
gtgaaagcgt	ctccggtcat	ataccggagg	gtatttttgg	taatttaact	cagctcccgga	360
gccttagtct	ccgtctcaat	ggctcttact	gttctctctc	tttggatctc	ggaagatgct	420
ccgactcttc	gcgtttgtac	ctgcagggtt	acagattctc	cggtgagatt	ccggaggttt	480
tgtttagtgt	tagtaacctt	gttaggttga	atctagctga	gaatgaattt	agtggagaga	540
ttctcgtcag	gtttaaaaac	cttactaggc	tttaagactct	gtacctggag	aataacaagc	600
ttctctggctc	ttcttttagac	ttggatttgt	ctttggatca	gttcaacggt	tctaataact	660
gtttgcaacg	atctataact	aagagtttgc	agaagtttga	ttctgattcg	tttgtgggaa	720
cttctctctg	cgcccaaacg	cttgttgtct	gctctaatag	gggaactgtg	ccaagccagc	780
caatttctgt	ttggcaaatat	cccggaaact	ttgaaggacg	tgaggagaga	aggaanaagg	840
agaagctttc	ttggtggagct	atagctggaa	tagtgatttg	atgtgttggt	ggtttgtccc	900
tgattgttat	gatttttgat	gttctcttta	ggaaaaaggg	gaacgagaga	acaagggcca	960
ttgaccttgc	aaccataca	cccatgaa	ttgaaattcc	ttggcgagaa	cgccgctgtg	1020
aagcaccgga	gaatgagagc	tatgtaaat	agtactctcc	gtctgcagtg	aaagctgtgg	1080
aagtgaacag	ttcagggtag	aagaagttag	gttttttttg	gaatgcgaca	aaagttctcg	1140
atcttgagga	ttgttgtaga	gcttcaacgg	aggttctgtg	gaaggaacg	ttcgggacag	1200
cttataaagc	ggtgtgtgac	gcggtgacat	tggttgctgt	gaagagactg	aagatgttaa	1260
cgatggcgga	caagagagtt	aaggagaaga	ttgagggttg	ttggggcgatg	gatcatgaga	1320
actgtgtgcc	cttgagagcg	tactattaca	gtggagacga	gaagctgtct	gtctatgact	1380
ttcagctcat	gggaagctta	tcagctctct	tacacggaaa	caaaagtgtga	ggccgctctc	1440
cattgaactg	ggaagtacga	tcaggcatcg	cccttgaggc	tgctcgtggc	ttagactata	1500
ttactcaaca	agaccacact	agctctcacg	gaacacgtca	gtcctccaat	actctcttaa	1560
caaacctccc	tgacgcacga	gtgtctgatt	tcggcctggc	tcagcttgtga	agcgctctat	1620
ccacaacccc	aaaccggggc	actgggtacc	gtgcggccaga	agtaactgac	ccgagcgctg	1680
ttctcacagaa	agcggcagtg	tacagctttg	gtgtggtgtt	gctagagtgt	ctcaccggaa	1740
aagctccgtc	taactcgtgt	atgaacgagg	aaggaatgaa	tttggcgagg	ttgggtgcatt	1800
cagtggtcag	agaggagtgg	aggaatgagg	tttttgactc	ggagctgatg	agtatcgaga	1860
cagttgtctc	gggtgaagaa	gagatggcgg	aaatgctgtca	gctgggcatc	gactgtacag	1920
agacaccccc	agacaaagcg	ccagttatgg	tggaggttgt	gagaagagtc	caggagtgtgc	1980
gcacatcggt	tcagatcggt	gtggggtaag	accatcagat	gaaaggagac	ttgagacatg	2040
agctgtgttc	atgatctgaa	gcggcgacgt	tttcagtgtt	tagtttttaag	aataaggcgg	2100

gaattagagt tggggctggt aattagatgt ttttaatttt ttttttttgt ttttttgggt 2160
tctttcatgt gtgggcactg atgatgagga gtttcgtggt ggttgtaatt attagtgcct 2220
ttaactttaa cttttatttc aattattggtt ttc

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 668 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..668
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498044

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Asn	His	Thr	His	Ser	Phe	Phe	Thr	Glu	Ser	Phe	Phe	Leu	Gly	Phe	Leu	5	10	15
Ser	Leu	Phe	Leu	Thr	Met	Arg	Leu	Phe	Thr	Pro	Ser	Met	Ser	Asn	20	25	30	
Leu	Ser	Ile	Phe	Phe	Ser	Ile	Leu	Leu	Ser	Leu	Pro	Leu	Pro	Ser	35	40	45	
Ile	Gly	Asp	Leu	Ala	Ala	Asp	Lys	Ser	Ala	Leu	Leu	Ser	Phe	Arg	Ser	50	55	60
Ala	Val	Gly	Gly	Arg	Thr	Leu	Leu	Trp	Asp	Val	Lys	Gln	Thr	Ser	Pro	65	70	75
Cys	Asn	Trp	Thr	Gly	Val	Leu	Cys	Asp	Gly	Gly	Arg	Val	Thr	Ala	Leu	85	90	95
Arg	Leu	Pro	Gly	Glu	Thr	Leu	Ser	Gly	His	Ile	Pro	Glu	Gly	Ile	Phe	100	105	110
Gly	Asn	Leu	Thr	Gln	Leu	Arg	Thr	Leu	Ser	Leu	Arg	Leu	Asn	Gly	Leu	115	120	125
Thr	Gly	Ser	Leu	Pro	Leu	Asp	Leu	Gly	Arg	Cys	Ser	Asp	Leu	Arg	Arg	130	135	140
Leu	Tyr	Leu	Gln	Gly	Asn	Arg	Phe	Ser	Gly	Glu	Ile	Pro	Glu	Val	Leu	145	150	155
Phe	Ser	Leu	Ser	Asn	Leu	Val	Arg	Leu	Asn	Leu	Ala	Glu	Asn	Glu	Phe	165	170	175
Ser	Gly	Glu	Ile	Ser	Ser	Gly	Phe	Lys	Asn	Leu	Thr	Arg	Leu	Lys	Thr	180	185	190
Leu	Tyr	Leu	Glu	Asn	Asn	Lys	Leu	Ser	Gly	Ser	Leu	Leu	Asp	Leu	Asp	195	200	205
Leu	Ser	Leu	Asp	Gln	Phe	Asn	Val	Ser	Asn	Asn	Leu	Leu	Asn	Gly	Ser	210	215	220
Ile	Pro	Lys	Ser	Leu	Gln	Lys	Phe	Asp	Ser	Asp	Ser	Phe	Val	Gly	Thr	225	230	235
Ser	Leu	Cys	Gly	Lys	Pro	Leu	Val	Val	Cys	Ser	Asn	Glu	Gly	Thr	Val	245	250	255
Pro	Ser	Gln	Pro	Ile	Ser	Val	Gly	Asn	Ile	Pro	Gly	Thr	Val	Glu	Gly	260	265	270
Arg	Glu	Glu	Lys	Lys	Lys	Arg	Lys	Lys	Leu	Ser	Gly	Gly	Ala	Ile	Ala	275	280	285
Gly	Ile	Val	Ile	Gly	Cys	Val	Val	Gly	Leu	Ser	Leu	Ile	Val	Met	Ile	290	295	300
Leu	Met	Val	Leu	Phe	Arg	Lys	Lys	Gly	Asn	Glu	Arg	Thr	Arg	Ala	Ile	305	310	315
Asp	Leu	Ala	Thr	Ile	Lys	His	His	Glu	Val	Glu	Ile	Pro	Gly	Glu	Lys	325	330	335
Ala	Ala	Val	Glu	Ala	Pro	Glu	Asn	Arg	Ser	Tyr	Val	Asn	Glu	Tyr	Ser	340	345	350
Pro	Ser	Ala	Val	Lys	Ala	Val	Glu	Val	Asn	Ser	Ser	Gly	Met	Lys	Lys	355	360	365

Leu Val Phe Phe Gly Asn Ala Thr Lys Val Phe Asp Leu Glu Asp Leu
370 375 380
Leu Arg Ala Ser Ala Glu Val Leu Gly Lys Gly Thr Phe Gly Thr Ala
385 390 395 400
Tyr Lys Ala Val Leu Asp Ala Val Thr Leu Val Ala Val Lys Arg Leu
405 410 415
Lys Asp Val Thr Met Ala Asp Arg Glu Lys Glu Lys Ile Glu Val
420 425 430
Val Gly Ala Met Asp His Glu Asn Leu Val Pro Leu Arg Ala Tyr Tyr
435 440 445
Tyr Ser Gly Asp Glu Lys Leu Leu Val Tyr Asp Phe Met Pro Met Gly
450 455 460
Ser Leu Ser Ala Leu Leu His Gly Asn Lys Gly Ala Gly Arg Pro Pro
465 470 475 480
Leu Asn Trp Glu Val Arg Ser Gly Ile Ala Leu Gly Ala Ala Arg Gly
485 490 495
Leu Asp Tyr Leu His Ser Gln Asp Pro Leu Ser Ser His Gly Asn Val
500 505 510
Lys Ser Ser Asn Ile Leu Leu Thr Asn Ser His Asp Ala Arg Val Ser
515 520 525
Asp Phe Gly Leu Ala Gln Leu Val Ser Ala Ser Ser Thr Thr Pro Asn
530 535 540
Arg Ala Thr Gly Tyr Arg Ala Pro Glu Val Thr Asp Pro Arg Arg Val
545 550 555 560
Ser Gln Lys Ala Asp Val Tyr Ser Phe Gly Val Val Leu Leu Glu Leu
565 570 575
Leu Thr Gly Lys Ala Pro Ser Asn Ser Val Met Asn Glu Glu Gly Met
580 585 590
Asp Leu Ala Arg Trp Val His Ser Val Ala Arg Glu Glu Trp Arg Asn
595 600 605
Glu Val Phe Asp Ser Glu Leu Met Ser Ile Glu Thr Val Val Ser Val
610 615 620
Glu Glu Glu Met Ala Glu Met Leu Gln Leu Gly Ile Asp Cys Thr Glu
625 630 635 640
Gln His Pro Asp Lys Arg Pro Val Met Val Glu Val Val Arg Arg Ile
645 650 655
Gln Glu Leu Arg Gln Ser Gly Ala Asp Arg Val Gly
660 665

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 647 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..647
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498045

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

Met Arg Leu Phe Phe Thr Pro Ser Met Ser Asn Leu Ser Ile Phe Phe
1 5 10 15
Ser Ile Leu Leu Leu Ser Leu Pro Leu Pro Ser Ile Gly Asp Leu Ala
20 25 30
Ala Asp Lys Ser Ala Leu Leu Ser Phe Arg Ser Ala Val Gly Gly Arg
35 40 45
Thr Leu Leu Trp Asp Val Lys Gln Thr Ser Pro Cys Asn Trp Thr Gly
50 55 60
Val Leu Cys Asp Gly Gly Arg Val Thr Ala Leu Arg Leu Pro Gly Glu
65 70 75 80
Thr Leu Ser Gly His Ile Pro Glu Gly Ile Phe Gly Asn Leu Thr Gln

	85		90		95
Leu Arg Thr	Leu Ser	Leu Arg	Leu Asn	Gly Leu Thr	Gly Ser Leu Pro
	100		105		110
Leu Asp Leu	Gly Arg	Cys Ser	Asp Leu	Arg Arg Leu Tyr	Leu Gln Gly
	115		120		125
Asn Arg Phe	Ser Gly	Glu Ile	Pro Glu	Val Leu Phe	Ser Leu Ser Asn
	130		135		140
Leu Val Arg	Leu Asn	Leu Ala	Glu Asn	Glu Phe	Ser Gly Glu Ile Ser
	145		150		155
Ser Gly Phe	Lys Asn	Leu Thr	Arg Leu	Lys Thr	Leu Tyr Leu Glu Asn
	165		170		175
Asn Lys Leu	Ser Gly	Ser Leu	Leu Asp	Leu Asp	Leu Ser Leu Asp Gln
	180		185		190
Phe Asn Val	Ser Asn	Asn Leu	Leu Asn	Gly Ser	Ile Pro Lys Ser Leu
	195		200		205
Gln Lys Phe	Asp Ser	Asp Ser	Phe Val	Gly Thr	Ser Leu Cys Gly Lys
	210		215		220
Pro Leu Val	Val Cys	Ser Asn	Glu Gly	Thr Val	Pro Ser Gln Pro Ile
	225		230		235
Ser Val Gly	Asn Ile	Pro Gly	Thr Val	Glu Gly	Arg Glu Glu Lys Lys
	245		250		255
Lys Arg Lys	Lys Leu	Ser Gly	Gly Ala	Ile Ala	Gly Ile Val Ile Gly
	260		265		270
Cys Val Val	Gly Leu	Ser Leu	Ile Val	Met Ile	Leu Met Val Leu Phe
	275		280		285
Arg Lys Lys	Gly Asn	Glu Arg	Thr Arg	Ala Ile	Asp Leu Ala Thr Ile
	290		295		300
Lys His His	Glu Val	Glu Ile	Pro Gly	Glu Lys	Ala Ala Val Glu Ala
	305		310		315
Pro Glu Asn	Arg Ser	Tyr Val	Asn Glu	Tyr Ser	Pro Ser Ala Val Lys
	325		330		335
Ala Val Glu	Val Asn	Ser Ser	Gly Met	Lys Lys	Leu Val Phe Phe Gly
	340		345		350
Asn Ala Thr	Lys Val	Phe Asp	Leu Glu	Asp Leu	Leu Arg Ala Ser Ala
	355		360		365
Glu Val Leu	Gly Lys	Gly Thr	Phe Gly	Thr Ala	Tyr Lys Ala Val Leu
	370		375		380
Asp Ala Val	Thr Leu	Val Ala	Val Lys	Arg Leu	Lys Asp Val Thr Met
	385		390		395
Ala Asp Arg	Glu Phe	Lys Glu	Lys Ile	Glu Val	Val Gly Ala Met Asp
	405		410		415
His Glu Asn	Leu Val	Pro Leu	Arg Ala	Tyr Tyr	Tyr Ser Gly Asp Glu
	420		425		430
Lys Leu Leu	Val Tyr	Asp Phe	Met Pro	Met Gly	Ser Leu Ser Ala Leu
	435		440		445
Leu His Gly	Asn Lys	Gly Ala	Gly Arg	Pro Pro	Leu Asn Trp Glu Val
	450		455		460
Arg Ser Gly	Ile Ala	Leu Gly	Ala Ala	Arg Gly	Leu Asp Tyr Leu His
	465		470		475
Ser Gln Asp	Pro Leu	Ser Ser	His Gly	Asn Val	Lys Ser Ser Asn Ile
	485		490		495
Leu Leu Thr	Asn Ser	His Asp	Ala Arg	Val Ser	Asp Phe Gly Leu Ala
	500		505		510
Gln Leu Val	Ser Ala	Ser Ser	Thr Thr	Pro Asn	Arg Ala Thr Gly Tyr
	515		520		525
Arg Ala Pro	Glu Val	Thr Asp	Pro Arg	Arg Val	Ser Gln Lys Ala Asp
	530		535		540
Val Tyr Ser	Phe Gly	Val Val	Leu Leu	Glu Leu	Leu Thr Gly Lys Ala
	545		550		555
Pro Ser Asn	Ser Val	Met Asn	Glu Glu	Gly Met	Asp Leu Ala Arg Trp
	565		570		575

Val His Ser Val Ala Arg Glu Glu Trp Arg Asn Glu Val Phe Asp Ser
580 585 590
Glu Leu Met Ser Ile Glu Thr Val Val Ser Val Glu Glu Glu Met Ala
595 600 605
Glu Met Leu Gln Leu Gly Ile Asp Cys Thr Glu Gln His Pro Asp Lys
610 615 620
Arg Pro Val Met Val Glu Val Val Arg Arg Ile Gln Glu Leu Arg Gln
625 630 635 640
Ser Gly Ala Asp Arg Val Gly
645

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 639 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..639

(D) OTHER INFORMATION: / Ceres Seq. ID 1498046

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Met Ser Asn Leu Ser Ile Phe Phe Ser Ile Leu Leu Leu Ser Leu Pro
1 5 10 15
Leu Pro Ser Ile Gly Asp Leu Ala Ala Asp Lys Ser Ala Leu Leu Ser
20 25 30
Phe Arg Ser Ala Val Gly Gly Arg Thr Leu Leu Trp Asp Val Lys Gln
35 40 45
Thr Ser Pro Cys Asn Trp Thr Gly Val Leu Cys Asp Gly Gly Arg Val
50 55 60
Thr Ala Leu Arg Leu Pro Gly Glu Thr Leu Ser Gly His Ile Pro Glu
65 70 75 80
Gly Ile Phe Gly Asn Leu Thr Gln Leu Arg Thr Leu Ser Leu Arg Leu
85 90 95
Asn Gly Leu Thr Gly Ser Leu Pro Leu Asp Leu Gly Arg Cys Ser Asp
100 105 110
Leu Arg Arg Leu Tyr Leu Gln Gly Asn Arg Phe Ser Gly Glu Ile Pro
115 120 125
Glu Val Leu Phe Ser Leu Ser Asn Leu Val Arg Leu Asn Leu Ala Glu
130 135 140
Asn Glu Phe Ser Gly Glu Ile Ser Ser Gly Phe Lys Asn Leu Thr Arg
145 150 155 160
Leu Lys Thr Leu Tyr Leu Glu Asn Asn Lys Leu Ser Gly Ser Leu Leu
165 170 175
Asp Leu Asp Leu Ser Leu Asp Gln Phe Asn Val Ser Asn Asn Leu Leu
180 185 190
Asn Gly Ser Ile Pro Lys Ser Leu Gln Lys Phe Asp Ser Asp Ser Phe
195 200 205
Val Gly Thr Ser Leu Cys Gly Lys Pro Leu Val Val Cys Ser Asn Glu
210 215 220
Gly Thr Val Pro Ser Gln Pro Ile Ser Val Gly Asn Ile Pro Gly Thr
225 230 235 240
Val Glu Gly Arg Glu Glu Lys Lys Lys Arg Lys Lys Leu Ser Gly Gly
245 250 255
Ala Ile Ala Gly Ile Val Ile Gly Cys Val Val Gly Leu Ser Leu Ile
260 265 270
Val Met Ile Leu Met Val Leu Phe Arg Lys Lys Gly Asn Glu Arg Thr
275 280 285
Arg Ala Ile Asp Leu Ala Thr Ile Lys His His Glu Val Glu Ile Pro
290 295 300
Gly Glu Lys Ala Ala Val Glu Ala Pro Glu Asn Arg Ser Tyr Val Asn

305 310 315 320
Glu Tyr Ser Pro Ser Ala Val Lys Ala Val Glu Val Asn Ser Ser Gly
325 330 335
Met Lys Lys Leu Val Phe Phe Gly Asn Ala Thr Lys Val Phe Asp Leu
340 345 350
Glu Asp Leu Leu Arg Ala Ser Ala Glu Val Leu Gly Lys Gly Thr Phe
355 360 365
Gly Thr Ala Tyr Lys Ala Val Leu Asp Ala Val Thr Leu Val Ala Val
370 375 380
Lys Arg Leu Lys Asp Val Thr Met Ala Asp Arg Glu Phe Lys Glu Lys
385 390 395 400
Ile Glu Val Val Gly Ala Met Asp His Glu Asn Leu Val Pro Leu Arg
405 410 415
Ala Tyr Tyr Tyr Ser Gly Asp Glu Lys Leu Val Tyr Asp Phe Met
420 425 430
Pro Met Gly Ser Leu Ser Ala Leu Leu His Gly Asn Lys Gly Ala Gly
435 440 445
Arg Pro Pro Leu Asn Trp Glu Val Arg Ser Gly Ile Ala Leu Gly Ala
450 455 460
Ala Arg Gly Leu Asp Tyr Leu His Ser Gln Asp Pro Leu Ser Ser His
465 470 475 480
Gly Asn Val Lys Ser Ser Asn Ile Leu Leu Thr Asn Ser His Asp Ala
485 490 495
Arg Val Ser Asp Phe Gly Leu Ala Gln Leu Val Ser Ala Ser Ser Thr
500 505 510
Thr Pro Asn Arg Ala Thr Gly Tyr Arg Ala Pro Glu Val Thr Asp Pro
515 520 525
Arg Arg Val Ser Gln Lys Ala Asp Val Tyr Ser Phe Gly Val Val Leu
530 535 540
Leu Glu Leu Leu Thr Gly Lys Ala Pro Ser Asn Ser Val Met Asn Glu
545 550 555 560
Glu Gly Met Asp Leu Ala Arg Trp Val His Ser Val Ala Arg Glu Glu
565 570 575
Trp Arg Asn Glu Val Phe Asp Ser Glu Leu Met Ser Ile Glu Thr Val
580 585 590
Val Ser Val Glu Glu Glu Met Ala Glu Met Leu Gln Leu Gly Ile Asp
595 600 605
Cys Thr Glu Gln His Pro Asp Lys Arg Pro Val Met Val Glu Val Val
610 615 620
Arg Arg Ile Gln Glu Leu Arg Gln Ser Gly Ala Asp Arg Val Gly
625 630 635

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 852 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..852
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

acaccatcca	ctctactcaa	catggactcc	tccaaactct	catctctctc	tcctttgctc	60
ttcctcattt	gcattatcta	tctcccccaa	cattctctcg	catgoggctc	ttgcaaccca	120
cgggaaggcg	gaaagcactc	ccctaagccc	cctaagctac	cagttctccc	ggtgaccgtc	180
cctaagctac	cagttctctc	ggtagccgtc	cctaagctac	cagtcctccc	ggtagccgtc	240
cctaagctac	ccgttctctc	tgtgamcatc	cctaagctac	ccgttccacc	agtgactgtg	300
cctaagctac	ccgttctctc	tgtgaccgtc	cccaagctac	ccgttctccc	agtgaccgtc	360
cccaaggagg	aacgggtagc	ttaggtacag	tcactggtgg	aacgggtagc	ttaggggtgg	420
tcacggagkg	ggaggaggcc	acggacatgg	aggacacaac	ggaggagggg	gccacggact	480

tgacggatac	ggaggagggtg	gaggacacta	tggaggagggt	ggaggacact	acggaggagg	540
tggaggacac	tacgaaggag	gtgaggacac	tacggaggag	gtggtggagg	acacggagggt	600
ggaggacact	acggagggtg	tggaggaggga	tacggagggtg	gaggaggaga	ccacggaggga	660
ggaggccacg	ggctaaacga	acctgttcag	actaagccgg	gtgttataaa	ctatataata	720
ycttcactac	catgcatgat	tgcatatata	tatatacgt	tatgtattat	ctatagcct	780
ataaataaac	catggtgagt	ttgtaacgca	gtgccttcag	aatgttcgg	aataaaattt	840
cataatatta	gt					

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..127
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498048

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Thr	Pro	Ser	Thr	Leu	Leu	Asn	Met	Asp	Ser	Ser	Lys	Leu	Ser	Ser	Leu
1			5					10					15		
Ser	Leu	Cys	Leu	Phe	Leu	Ile	Cys	Ile	Tyr	Leu	Pro	Gln	His	Ser	
			20				25					30			
Leu	Ala	Cys	Gly	Ser	Cys	Asn	Pro	Arg	Lys	Gly	Gly	Lys	His	Ser	Pro
		35					40				45				
Lys	Ala	Pro	Lys	Leu	Pro	Val	Pro	Pro	Val	Thr	Val	Pro	Lys	Leu	Pro
		50				55					60				
Val	Pro	Pro	Val	Thr	Val	Pro	Lys	Leu	Pro	Val	Pro	Pro	Val	Thr	Val
		65				70				75				80	
Pro	Lys	Leu	Pro	Val	Pro	Pro	Val	Xaa	Ile	Pro	Lys	Leu	Pro	Val	Pro
			85					90					95		
Pro	Val	Thr	Val	Pro	Lys	Leu	Pro	Val	Pro	Pro	Val	Thr	Val	Pro	Lys
			100				105						110		
Leu	Pro	Val	Pro	Pro	Val	Thr	Val	Pro	Lys	Glu	Glu	Arg	Val	Ala	
		115					120					125			

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498049

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

Met	Asp	Ser	Ser	Lys	Leu	Ser	Ser	Leu	Ser	Leu	Cys	Leu	Phe	Leu	Ile
1				5				10					15		
Cys	Ile	Ile	Tyr	Leu	Pro	Gln	His	Ser	Leu	Ala	Cys	Gly	Ser	Cys	Asn
			20				25					30			
Pro	Arg	Lys	Gly	Gly	Lys	His	Ser	Pro	Lys	Ala	Pro	Lys	Leu	Pro	Val
		35				40					45				
Pro	Pro	Val	Thr	Val	Pro	Lys	Leu	Pro	Val	Pro	Pro	Val	Thr	Val	Pro
		50				55					60				
Lys	Leu	Pro	Val	Pro	Pro	Val	Thr	Val	Pro	Lys	Leu	Pro	Val	Pro	Pro
		65				70				75				80	
Val	Xaa	Ile	Pro	Lys	Leu	Pro	Val	Pro	Pro	Val	Thr	Val	Pro	Lys	Leu
			85					90					95		
Pro	Val	Pro	Pro	Val	Thr	Val	Pro	Lys	Leu	Pro	Val	Pro	Pro	Val	Thr
			100				105						110		

Val Pro Lys Glu Glu Arg Val Ala
115 120

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..82
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Met Glu Asp Thr Thr Glu Glu Gly Ala Thr Asp Leu Thr Asp Thr Glu
1 5 10 15
Glu Val Glu Asp Thr Met Glu Glu Val Glu Asp Thr Thr Glu Glu Val
20 25 30
Glu Asp Thr Thr Lys Glu Val Arg Thr Leu Arg Arg Arg Trp Trp Arg
35 40 45
Thr Arg Arg Trp Arg Thr Leu Arg Arg Trp Trp Arg Arg Ile Arg Arg
50 55 60
Trp Arg Arg Thr Pro Arg Arg Arg Pro Arg Ala Lys Arg Thr Cys
65 70 75 80
Ser Asp

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1095 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1095
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498051

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

gtagatcttt ttctgctctt tctctctctc tctctctctc tctctctctc tctctcttgt 60
attattttcta tctccccgc cgtcgaaaga gaaacgtcga tcggagaacc ttgaaatgt 120
cgactggtat agatatgtct ctcgacgaca tgatcgccaa gaaccgtaag tctcgtggtg 180
gagccggccc cgctcgtgga accggatccg gatccggacc gggctccgact cgcgcgaaca 240
accctaotcg gaaatcaaac cgatctgctc cataccaatc agccaaggcg ccggagtcca 300
cctggggctca cgacatgttc tcgatagat ctgaagatca ccgattcgga cgttctctcg 360
ccggaatcga aactggaacc aagctctaca ttccaattt ggattaccgt gtcattgaacg 420
aagacatcaa ggaactgttt gctgaagtgt gagaacttaa acgctacaca gtctattttg 480
atagaagtgg aagatcaaa ggaactgctg aagtagtgtt ttctcggcgt ggcatggcac 540
tcgcagctgt gaagaagtat aatgatgttc agctggatgg aaaacccatg aagatagaga 600
tttggggcac taattctcaa actgctgcag ccccgctcgg tagacctgcg atgggaaact 660
ccaatggtgc tccatggaga ggaggacaag ggagaggagg tcaacgaggt ggtggacgag 720
gaggcgggtg ccgaggtggt ggtggtcgtg gttagcgctc ttgtaagta cctggaagaga 780
agattttctg ggaagatctt gatcgcgatc ttgataagta coattctgga gatatggaga 840
caaactaagg aactgactgt atcttctcaa accggtaggg gttttaggag gaagagaatc 900
gagaaaatgt ttgccagagg ctttaccact tagcgctctt ttggctgtgt tgttcatttg 960
tttcattaga atgactttac agaattgaga atatgtgtta tttaaagtgt ttgtctatct 1020
taataccctc aagtgaagg cagaggaagg aataccaatt tcgtttacag atcatatgca 1080
ggcaaaagag ttttc

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..281
(D) OTHER INFORMATION: / Ceres Seq. ID 1498052
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Arg	Ser	Phe	Ser	Ala	Leu	Ser	Leu	Ser	Leu	Ser	Leu	Ser	Leu	1
1			5					10					15	
Ser	Leu	Leu	Tyr	Tyr	Phe	Tyr	Leu	Pro	Arg	Arg	Arg	Lys	Arg	Val
			20					25				30		
Asp	Arg	Arg	Thr	Phe	Glu	Met	Ser	Thr	Gly	Leu	Asp	Met	Ser	Leu
			35				40				45			Asp
Asp	Met	Ile	Ala	Lys	Asn	Arg	Lys	Ser	Arg	Gly	Gly	Ala	Gly	Pro
	50					55				60				Ala
Arg	Gly	Thr	Gly	Ser	Gly	Ser	Gly	Pro	Gly	Pro	Thr	Arg	Arg	Asn
	65				70				75					Asn
Pro	Asn	Arg	Lys	Ser	Thr	Arg	Ser	Ala	Pro	Tyr	Gln	Ser	Ala	Lys
			85						90				95	Ala
Pro	Glu	Ser	Thr	Trp	Gly	His	Asp	Met	Phe	Ser	Asp	Arg	Ser	Glu
			100				105						110	Asp
His	Arg	Ser	Gly	Arg	Ser	Ser	Ala	Gly	Ile	Glu	Thr	Gly	Thr	Lys
			115				120					125		Leu
Tyr	Ile	Ser	Asn	Leu	Asp	Tyr	Gly	Val	Met	Asn	Glu	Asp	Ile	Lys
	130					135					140			Glu
Leu	Phe	Ala	Glu	Val	Gly	Glu	Leu	Lys	Arg	Tyr	Thr	Val	His	Phe
	145				150				155					Asp
Arg	Ser	Gly	Arg	Ser	Lys	Gly	Thr	Ala	Glu	Val	Val	Tyr	Ser	Arg
				165					170					Arg
Gly	Asp	Ala	Leu	Ala	Ala	Val	Lys	Lys	Tyr	Asn	Asp	Val	Gln	Leu
			180				185						190	Asp
Gly	Lys	Pro	Met	Lys	Ile	Glu	Ile	Val	Gly	Thr	Asn	Leu	Gln	Thr
		195					200				205			Ala
Ala	Ala	Pro	Ser	Gly	Arg	Pro	Ala	Asn	Gly	Asn	Ser	Asn	Gly	Ala
	210					215					220			Pro
Trp	Arg	Gly	Gly	Gln	Gly	Arg	Gly	Gly	Gln	Arg	Gly	Gly	Gly	Arg
	225				230					235				Gly
Gly	Gly	Gly	Arg	Gly	Gly	Gly	Gly	Arg	Gly	Arg	Pro	Gly	Lys	Gly
				245					250				255	
Pro	Ala	Glu	Lys	Ile	Ser	Ala	Glu	Asp	Leu	Asp	Ala	Asp	Leu	Lys
			260					265					270	
Tyr	His	Ser	Gly	Asp	Met	Glu	Thr	Asn						
			275				280							

(2) INFORMATION FOR SEQ ID NO:153:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 243 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..243
(D) OTHER INFORMATION: / Ceres Seq. ID 1498053
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Met	Ser	Thr	Gly	Leu	Asp	Met	Ser	Leu	Asp	Asp	Met	Ile	Ala	Lys	Asn
1				5					10					15	
Arg	Lys	Ser	Arg	Gly	Gly	Ala	Gly	Pro	Ala	Arg	Gly	Thr	Gly	Ser	Gly
				20				25				30			
Ser	Gly	Pro	Gly	Pro	Thr	Arg	Arg	Asn	Asn	Pro	Asn	Arg	Lys	Ser	Thr

35	40	45
Arg Ser Ala Pro Tyr Gln Ser Ala Lys Ala Pro Glu Ser Thr Trp Gly		
50	55	60
His Asp Met Phe Ser Asp Arg Ser Glu Asp His Arg Ser Gly Arg Ser		
65	70	75
Ser Ala Gly Ile Glu Thr Gly Thr Lys Leu Tyr Ile Ser Asn Leu Asp		80
	85	90
Tyr Gly Val Met Asn Glu Asp Ile Lys Glu Leu Phe Ala Glu Val Gly		95
	100	105
Glu Leu Lys Arg Tyr Thr Val His Phe Asp Arg Ser Gly Arg Ser Lys		110
	115	120
Gly Thr Ala Glu Val Val Tyr Ser Arg Arg Gly Asp Ala Leu Ala Ala		125
	130	135
Val Lys Lys Tyr Asn Asp Val Gln Leu Asp Gly Lys Pro Met Lys Ile		140
145	150	155
Glu Ile Val Gly Thr Asn Leu Gln Thr Ala Ala Pro Ser Gly Arg		160
	165	170
Pro Ala Asn Gly Asn Ser Asn Gly Ala Pro Trp Arg Gly Gly Gln Gly		175
	180	185
Arg Gly Gly Gln Arg Gly Gly Gly Arg Gly Gly Gly Arg Gly Gly		190
	195	200
Gly Gly Arg Gly Arg Arg Pro Gly Lys Gly Pro Ala Glu Lys Ile Ser		205
	210	215
Ala Glu Asp Leu Asp Ala Asp Leu Asp Lys Tyr His Ser Gly Asp Met		220
225	230	235
Glu Thr Asn		240

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..237
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498054

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Met Ser Leu Asp Asp Met Ile Ala Lys Asn Arg Lys Ser Arg Gly Gly	
1	15
Ala Gly Pro Ala Arg Gly Thr Gly Ser Gly Ser Gly Pro Gly Pro Thr	
	20
Arg Arg Asn Asn Pro Asn Arg Lys Ser Thr Arg Ser Ala Pro Tyr Gln	
	25
Ser Ala Lys Ala Pro Glu Ser Thr Trp Gly His Asp Met Phe Ser Asp	
50	40
Arg Ser Glu Asp His Arg Ser Gly Arg Ser Ser Ala Gly Ile Glu Thr	
65	55
Gly Thr Lys Leu Tyr Ile Ser Asn Leu Asp Tyr Gly Val Met Asn Glu	
	60
Asp Ile Lys Glu Leu Phe Ala Glu Val Gly Glu Leu Lys Arg Tyr Thr	
	65
Val His Phe Asp Arg Ser Gly Arg Ser Lys Gly Thr Ala Glu Val Val	
	70
Tyr Ser Arg Arg Gly Asp Ala Leu Ala Ala Val Lys Lys Tyr Asn Asp	
130	75
Val Gln Leu Asp Gly Lys Pro Met Lys Ile Glu Ile Val Gly Thr Asn	
145	80
Leu Gln Thr Ala Ala Pro Ser Gly Arg Pro Ala Asn Gly Asn Ser	
	85
	90
	95
	100
	105
	110
	115
	120
	125
	130
	135
	140
	145
	150
	155
	160
	165
	170
	175

Asn Gly Ala Pro Trp Arg Gly Gly Gln Gly Arg Gly Gly Gln Arg Gly
180 185 190
Gly Gly Arg Gly Gly Gly Arg Gly Gly Gly Arg Gly Arg Arg
195 200 205
Pro Gly Lys Gly Pro Ala Glu Lys Ile Ser Ala Glu Asp Leu Asp Ala
210 215 220
Asp Leu Asp Lys Tyr His Ser Gly Asp Met Glu Thr Asn
225 230 235

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 539 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..539
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498061

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

scagcggttc	cyggtcaagc	acctctttt	aacaacaagc	tttgcgacat	aagacacgtg	60
tcaagcaggg	acgagaacgt	taagagacgg	agccgtgggtg	catgcgaagg	agagagaaac	120
gtgaggtctt	tgagtcatga	gtcgtcactg	agtcacgagt	caccggtgtc	ttctgaggag	180
acgacgacgg	aggaaccaaa	gacttggatc	gggcttgagc	tgactttggg	gttgagacct	240
ttagcacgtg	gaaatcacgt	gggtgtaccg	atgaagaaaa	gaaagttaga	gaggtgtggc	300
acgtctgagg	atgaggacac	gtgtaagatt	gagcttgac	tggtgtgcag	tgagtgaatg	360
gttctttttt	tgtggtgggt	cttaattaca	agttttgggt	ttgagtttta	gggtgtacaaa	420
tagagattaa	cgaatctctc	ttttttctct	ttttgagttt	tatgttttgk	tttgktttct	480
tttgcattgt	cggtgttctt	cataaatatg	tatgatgaat	gataaagagg	tcttaactt	

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498062

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

Xaa	Ala	Val	Xaa	Gly	Gln	Ala	Pro	Pro	Phe	Asn	Asn	Lys	Leu	Cys	Asp
1		5						10					15		
Ile	Arg	His	Val	Ser	Ser	Arg	Asp	Glu	Asn	Val	Lys	Arg	Arg	Ser	Arg
		20						25					30		
Gly	Ala	Cys	Lys	Glu	Glu	Arg	Asn	Val	Arg	Ser	Leu	Ser	His	Glu	Ser
		35					40				45				
Ser	Leu	Ser	His	Glu	Ser	Pro	Val	Ser	Ser	Glu	Glu	Thr	Thr	Thr	Glu
		50					55				60				
Glu	Pro	Lys	Thr	Trp	Ile	Gly	Leu	Glu	Leu	Thr	Leu	Gly	Leu	Glu	Pro
							70				75			80	
Leu	Ala	Arg	Gly	Asn	His	Val	Val	Val	Pro	Met	Lys	Lys	Arg	Lys	Leu
							85			90				95	
Glu	Arg	Cys	Gly	Thr	Ser	Glu	Asp	Glu	Asp	Thr	Cys	Lys	Ile	Glu	Leu
								105					110		
Gly	Leu	Val	Cys	Ser	Glu										

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 676 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..676
(D) OTHER INFORMATION: / Ceres Seq. ID 1498063
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:
aaaaaaaaca aaaagatctg aaacaaaaat ggtgaatcaa agaaaagctac aagaagaaga 60
agagcgaaaaa ggagaattat cctctcatta caaccaaagt agttgagtat ttgcagccag 120
taattgtgtcg agagcttctc tgcaaatctc cagataaact tgccttttggg ttgcactact 180
cacagagctc tcttttgtct cctctcttgc ctcgaaatta cgccagtcct tcagatctag 240
actccgacac ttgcgtttgt cggaatctta agctaggggga gtttcaagta ggcaagaaga 300
agaagatgaa gatgatgtca atgaagaaga acaagaagaa gagtaaatga ctgaaactag 360
acataccttc aatgaagaat gatgattctt ctctaaaaat ttgctgtttt cctcttctca 420
ccaagggatg gaattggtgt ttaaaggcag cttcaaaaaca ttcaagaaga tcgaaaaaga 480
agagagattc attcgctgat gccaaagctc tcgacttcaa atactaagat tatagcaact 540
tcaattgctt ttcatttgtat tcaataatta ctagaccttt gatgaattgt gaagttagac 600
tgtttctatt ttggtcatca tgtaatcatt tggagtgttt gatcatagat atatccatga 660
ctgcttttga tttctg

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 134 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..134
(D) OTHER INFORMATION: / Ceres Seq. ID 1498064
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:
Met Cys Arg Glu Leu Cys Lys Phe Pro Asp Asn Ser Ala Phe Gly
1 5 10 15
Phe Asp Tyr Ser Gln Ser Ser Leu Trp Ser Pro Leu Leu Pro Arg Asn
20 25 30
Tyr Ala Ser Pro Ser Asp Leu Asp Ser Asp Ser Cys Val Cys Arg Asn
35 40 45
Leu Lys Leu Gly Glu Phe Gln Val Gly Lys Lys Lys Lys Met Lys Met
50 55 60
Met Ser Met Lys Lys Asn Lys Lys Lys Ser Lys Leu Leu Lys Leu Asp
65 70 75 80
Ile Pro Ser Met Lys Asn Asp Asp Ser Ser Pro Lys Ile Gly Cys Phe
85 90 95
Pro Leu Pro Thr Lys Gly Trp Asn Gly Val Leu Lys Ala Ala Ser Lys
100 105 110
His Phe Lys Lys Ser Lys Lys Arg Asp Ser Phe Ala Asp Ala Lys
115 120 125
Leu Leu Asp Phe Lys Tyr
130

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..73
(D) OTHER INFORMATION: / Ceres Seq. ID 1498065

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

Met Lys Met Met Ser Met Lys Lys Asn Lys Lys Lys Ser Lys Leu Leu
1 5 10 15
Lys Leu Asp Ile Pro Ser Met Lys Asn Asp Asp Ser Ser Pro Lys Ile
20 25 30
Gly Cys Phe Pro Leu Pro Thr Lys Gly Trp Asn Gly Val Leu Lys Ala
35 40 45
Ala Ser Lys His Phe Lys Lys Ser Lys Lys Lys Arg Asp Ser Phe Ala
50 55 60
Asp Ala Lys Leu Leu Asp Phe Lys Tyr
65 70

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..71
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498066

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Met Met Ser Met Lys Lys Asn Lys Lys Lys Ser Lys Leu Leu Lys Leu
1 5 10 15
Asp Ile Pro Ser Met Lys Asn Asp Asp Ser Ser Pro Lys Ile Gly Cys
20 25 30
Phe Pro Leu Pro Thr Lys Gly Trp Asn Gly Val Leu Lys Ala Ala Ser
35 40 45
Lys His Phe Lys Lys Ser Lys Lys Lys Arg Asp Ser Phe Ala Asp Ala
50 55 60
Lys Leu Leu Asp Phe Lys Tyr
65 70

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 869 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..869
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

aacattctca	gagaagccgt	cttcttcctc	cttcaatctc	tctcgttcgt	atcatctgct	60
ctcgatttc	aatggcggag	cgttgggtga	gacctgaggt	gtatcctttg	ttcgctgtcta	120
ccggagttgc	cgttggggatc	tgtgcggtttt	cottgatcag	aaacatcaccc	ggaacccctg	180
aagtcagatg	caccacaggag	aacaggggctg	ctggaaatttt	ggataaacccat	gcagagggag	240
agaagataaa	ggaaaatttc	ctgagggaaga	ggaatttaggt	ttatccgatc	tgattctcag	300
gttttcttgt	ttcttaactc	aaattgttaa	aggtacttcc	atacaagggt	gaagccatcc	360
aagcttgcat	ggaactgccat	gtacagaaag	caacacaaga	aggatgcagc	acaagagggct	420
gtgaagataa	ggagacgtgc	caccaagaag	ccataactcaa	ggtcatttgt	tggtgctacc	480
ttggaagtaa	ttcagaagaa	gagagctgag	aagcctgaag	tctggtatgc	agccaggggaa	540
gctgctctgc	gtgagatcaa	gaaagaatc	aaaaagacca	aagatgaaaa	gaaggctaaag	600
aaggtggaat	ttgcttctaa	gcaacagaag	gtcaaggcta	attcccccaa	agctgctgct	660
gcatacaagg	gtctaaaggt	gggaggtggg	ggtggcaaac	gctgaagagc	ttaaagccat	720
ctttctctac	tctcgctctt	ttctgctagt	agctactttt	agtagttgat	gttcatcttt	780
gaatatttgc	aaaacataaa	ccttggttatt	ttcgtttttg	tctctcactt	ttgctactct	840
tataatatca	gaattgagaa	ttttgctgc				

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 91 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..91
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498068
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:
His Ser Gln Arg Ser Arg Leu Leu Pro Pro Ser Ile Ser Leu Val Arg
1 5 10 15
Ile Ile Cys Ser Ala Ile Ser Met Ala Ser Arg Trp Leu Arg Pro Glu
 20 25 30
Val Tyr Pro Leu Phe Ala Ala Thr Gly Val Ala Val Gly Ile Cys Ala
 35 40 45
Phe Ser Leu Ile Arg Asn Ile Thr Gly Asn Pro Glu Val Arg Cys Thr
 50 55 60
Lys Glu Asn Arg Ala Ala Gly Ile Leu Asp Asn His Ala Glu Gly Glu
65 70 75 80
Lys Tyr Lys Glu Asn Phe Leu Arg Lys Arg Asn
 85 90
(2) INFORMATION FOR SEQ ID NO:163:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 108 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..108
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498069
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:
Met Tyr Arg Lys Gln His Lys Lys Asp Ala Ala Gln Glu Ala Val Lys
1 5 10 15
Arg Arg Arg Arg Ala Thr Lys Lys Pro Tyr Ser Arg Ser Ile Val Gly
 20 25 30
Ala Thr Leu Glu Val Ile Gln Lys Lys Arg Ala Glu Lys Pro Glu Val
 35 40 45
Arg Asp Ala Ala Arg Glu Ala Ala Leu Arg Glu Ile Lys Glu Arg Ile
 50 55 60
Lys Lys Thr Lys Asp Glu Lys Lys Ala Lys Lys Val Glu Phe Ala Ser
65 70 75 80
Lys Gln Gln Lys Val Lys Ala Asn Phe Pro Lys Ala Ala Ala Ala Ser
 85 90 95
Lys Gly Pro Lys Val Gly Gly Gly Gly Gly Lys Arg
 100 105
(2) INFORMATION FOR SEQ ID NO:164:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 80 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..80
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498070
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Met	Gln	Pro	Gly	Lys	Leu	Leu	Cys	Val	Arg	Ser	Arg	Lys	Glu	Ser	Lys
1			5					10					15		
Arg	Pro	Lys	Met	Lys	Arg	Arg	Leu	Arg	Arg	Trp	Asn	Leu	Leu	Leu	Ser
		20						25					30		
Asn	Arg	Arg	Ser	Arg	Leu	Ile	Ser	Pro	Lys	Leu	Leu	Leu	His	Pro	Arg
		35					40					45			
Val	Leu	Arg	Trp	Glu	Val	Val	Val	Ala	Asn	Ala	Glu	Glu	Leu	Lys	Ala
	50					55					60				
Ile	Phe	Ser	His	Ser	Ala	Ser	Phe	Leu	Leu	Val	Ala	Thr	Phe	Ser	Ser
65				70						75				80	

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1104

(D) OTHER INFORMATION: / Ceres Seq. ID 1498071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

accaccgaaa	cccactaaga	atacagcaaa	tcgtctcttc	gccattaaaa	cacctctcctt	60
tgcaaacaaaa	gcttcaaaact	ttctctttaa	acacccccaa	atcagcaaaag	atagggttaa	120
tcgaagaacc	tcaccgtaag	tcactgagg	attcaagtgc	ttgctttggg	ttagaagaa	180
agaacagcaa	aaacctcaag	gagaagaaga	agtcacaaat	gactcgaagt	caaacacaa	240
acggagctgg	agctggagct	gttacgacgg	tagaatctgt	tcctcctcag	ccctaacttc	300
agcctcagcc	tcagcccgag	cagcagagca	acgagatggg	tcgtcatcac	ggaagcttga	360
gttttagtag	tcataatgtc	agagaagacg	aagagatgac	tcgtctctgt	ctttcgcggt	420
ttagagctaa	agaagatgag	attgagaaga	ggaggatgga	agttcgtgaa	cggatccaa	480
ctcaattggg	tcgggtcgaa	caagaaacca	aacgtctctc	tactattcgt	gaggagcttg	540
agtcctatgg	agatcctatg	aggaaggaag	ttctgtgtgt	tcgtaagaag	attgatagt	600
ttaaacaaaga	actcaaacct	ctaggttcca	ctgttcaaaa	gaaggaaagg	gaatacaaa	660
aagcacttga	tgayattcaa	cgagaagaac	agggagaaag	tacagctgat	cacaaaactc	720
atggagatgg	aacagttggt	tggagaagac	gagaagttag	ggatgattaa	gctggaggag	780
ctgagcaaga	gcatagaaac	cgtgtgaaaa	aggttgttca	agaagaacta	attgggttct	840
tttgtgtgat	gtacctacct	agtttaaaat	tttcatcatg	taagatgtgt	gggtgtcttt	900
ttttttttat	gbatatgttt	ttttaaagtc	tttgggggtt	tgatttggtaa	aatttgggg	960
ttctctcttt	tttttgatta	accaaaattta	gggatatggg	aaaatgggag	attcttagga	1020
tactgaaact	catcacagtg	attattcttt	ctttctctgt	attatgtttt	gtatctgtct	1080
tttgaagaat	ttattatttt	tttt				

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..183

(D) OTHER INFORMATION: / Ceres Seq. ID 1498072

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Met	Thr	Gln	Ser	Gln	Thr	Asn	Asp	Gly	Ala	Gly	Ala	Val	Thr
1			5					10				15	
Thr	Val	Glu	Ser	Val	Pro	Pro	Gln	Ser	Gln	Pro	Gln	Pro	Gln
		20					25				30		
Pro	Gln	Gln	Gln	Ser	Asn	Glu	Met	Val	Leu	His	Thr	Gly	Ser
	35					40					45		

Phe Ser Ser His Met Ser Arg Glu Asp Glu Glu Met Thr Arg Ser Ala
50 55 60
Leu Ser Ala Phe Arg Ala Lys Glu Asp Glu Ile Glu Lys Arg Arg Met
65 70 75 80
Glu Val Arg Glu Arg Ile Gln Ala Gln Leu Gly Arg Val Glu Gln Glu
85 90 95
Thr Lys Arg Leu Ser Thr Ile Arg Glu Glu Leu Glu Ser Met Ala Asp
100 105 110
Pro Met Arg Lys Glu Val Ser Val Val Arg Lys Lys Ile Asp Ser Val
115 120 125
Asn Lys Glu Leu Lys Pro Leu Gly Ser Thr Val Gln Lys Lys Glu Arg
130 135 140
Glu Tyr Lys Glu Ala Leu Asp Xaa Ile Gln Arg Glu Glu Gln Gly Glu
145 150 155 160
Ser Thr Ala Asp His Lys Thr His Gly Asp Gly Thr Val Gly Trp Arg
165 170 175
Lys Arg Glu Val Glu Asp Asp
180

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

Met Val Leu His Thr Gly Ser Leu Ser Phe Ser Ser His Met Ser Arg
1 5 10 15
Glu Asp Glu Glu Met Thr Arg Ser Ala Leu Ser Ala Phe Arg Ala Lys
20 25 30
Glu Asp Glu Ile Glu Lys Arg Arg Met Glu Val Arg Glu Arg Ile Gln
35 40 45
Ala Gln Leu Gly Arg Val Glu Gln Glu Thr Lys Arg Leu Ser Thr Ile
50 55 60
Arg Glu Glu Leu Glu Ser Met Ala Asp Pro Met Arg Lys Glu Val Ser
65 70 75 80
Val Val Arg Lys Lys Ile Asp Ser Val Asn Lys Glu Leu Lys Pro Leu
85 90 95
Gly Ser Thr Val Gln Lys Lys Glu Arg Glu Tyr Lys Glu Ala Leu Asp
100 105 110
Xaa Ile Gln Arg Glu Glu Gln Gly Glu Ser Thr Ala Asp His Lys Thr
115 120 125
His Gly Asp Gly Thr Val Gly Trp Arg Lys Arg Glu Val Glu Asp Asp
130 135 140

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..131
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Met Ser Arg Glu Asp Glu Glu Met Thr Arg Ser Ala Leu Ser Ala Phe
1 5 10 15
Arg Ala Lys Glu Asp Glu Ile Glu Lys Arg Arg Met Glu Val Arg Glu
20 25 30
Arg Ile Gln Ala Gln Leu Gly Arg Val Glu Gln Glu Thr Lys Arg Leu
35 40 45
Ser Thr Ile Arg Glu Glu Leu Glu Ser Met Ala Asp Pro Met Arg Lys
50 55 60
Glu Val Ser Val Val Arg Lys Lys Ile Asp Ser Val Asn Lys Glu Leu
65 70 75 80
Lys Pro Leu Gly Ser Thr Val Gln Lys Lys Glu Arg Glu Tyr Lys Glu
85 90 95
Ala Leu Asp Xaa Ile Gln Arg Glu Glu Gln Gly Glu Ser Thr Ala Asp
100 105 110
His Lys Thr His Gly Asp Gly Thr Val Gly Trp Arg Lys Arg Glu Val
115 120 125
Glu Asp Asp
130

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 757 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..757
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498075

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

aacccaaaaca aaccataaaa aaacaagtgg aagcttttaa acgagagggga gagagcaaaa 60
atggcgacgt cggaacgta cgtgacggaa gtcccgctaa aaggatcggc cgagaaatac 120
tacaaagaggt ggaagaacga gaaccatgtc ttccctgagt ctatcgggca ccacatccaa 180
aatgtttaccg ttcacgaagg cgaacatgac tctcacgggt ctatcaggag ttggaactac 240
acatgggatg gaaaggagga ggtgttcaag gagagaagag agatagacga tgagaccaaa 300
acgttgacgt taagaggact tgagggtcac gtgatggagc agctcaaaag gtacgacgtc 360
gtctaccaat tcattcccaa atctgaggat acctgcatcg gcaaaatac ttaatatgg 420
gagaagcgca acgatgattc cccagaacca agcgggtaca tgaattctgt caagagcttg 480
gttgctgaca tgggaacca cgttagcaaa acttaatacat cattcccaca gtgctgctcg 540
tcgtcatcat catcatcatc atcatcatca tcatcatcat catcatcatc atcatrctca 600
tcactatctc gatttataag ttaagatggt ttcagtataa taaatggggt cttgtggatc 660
gttcatttct atgtgtaaac cgtttgtgtc tgtatgatgc ttcgatatat tgttatgttc 720
atgatcatat gtcgggttcg atataatgat tottaag

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Met Ala Thr Ser Gly Thr Tyr Val Thr Glu Val Pro Leu Lys Gly Ser
1 5 10 15
Ala Glu Lys Tyr Tyr Lys Arg Trp Lys Asn Glu Asn His Val Phe Pro
20 25 30
Asp Ala Ile Gly His His Ile Gln Asn Val Thr Val His Glu Gly Glu

(2) INFORMATION FOR SEQ ID NO:171:

(A) LENGTH: 1944 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: sing

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (g

(A) NAME

(B) LOCATION: 1

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:171:

(XI) SEQUENCE DESCRIPTION: SEQ ID NO:17:1
caaaaag gagaataaaca aacmaaaaaaa caagaaacaaa a

ttctccaaatg	gagagagag	cactagggat	atgtctgatg	ttagtagtag	catcaagtg	120
aaataaata	gcgaagaatt	cggtcttact	aaacggattac	ttgaagaaga	attttccaa	180
gactatgata	ggcgcaaggaa	cttcaagctaa	caacccgttag	ataacgttgg	tgaccgatct	240
gaatcggcaac	gagttttacg	cttcaagctaa	caacccgttag	ttacacagat	tcaagttctc	300
cgaagtgatg	atgcgcggcca	ctacagagtt	caagacatttc	ttacacagat	tgacgtacga	360
catgtgtttc	agtcgacaaa	ctacgcgcctc	aacaaaaaatt	gtgtgatcgc	agatgacaga	420
taaatgtgac	gggtttttca	agccgatctt	tgcatttgagt	gctagtaaa	gcgtcaaatc	480
agccgatgct	ggcgatgtga	agatgacctt	gtttgtcgat	ggaaagactt	tggttgagca	540
aaagaagaat	acaaaagtaa	tgacatttga	ggaaaagaaa	tacttggtca	tagatattgt	600
gaaatggact	aaaaatggct	ctacatttgg	tcggacgaca	ccgaagaagtc	gggaagatc	660
ttatcaaatat	gcactcttatg	gtcttgatgt	cgatgttaac	gatagttcta	tgttcgggtg	720
agctgcgaag	agtgaaatcat	cctccactaaa	ctctggatct	gtttccagta	cgggaagatgt	780
ttctaccaga	tcgaaagaat	cgagtagtag	atggaagttct	gccagtggaa	gtgtgtctac	840
caaatccaaa	acactcagcg	gtggaaatgc	tgttaccaaa	tccaagaagc	ctagccggtg	900
aaagtgtgct	acccaatacca	agaattctag	tggtcgaaat	gctactacag	ctaaaaattc	960
ggcgactcgc	agcggaagtc	ctaaggccag	cccaattgct	tcagttagtg	cgaaatcatc	1020
ttcgaagga	agccgcaagt	ctcaaggaa	cgaagtgtgt	caagtaagtg	gaagattgca	1080
gggaagcgca	agtgctagaa	gaagtgcaag	tgctcaaa	agagaaaatg	gggcataggc	1140
tatgtccaag	agcagcaaaa	caaaagcacc	gagccaaa	caatccaagt	catcgatgtg	1200
aagttctcat	cttagacaaa	acaccacaa	agtgaaacaa	gtcggagagt	agacttccaa	1260
agaagtaatg	tcattctaaa	tgcaactcga	gaagaagtat	gcagacaaag	cgggaataaa	1320
gtgtctcttc	gagttctctaa	agtccttcat	cgaaagcttc	gcgaagcggt	gttccaaaac	1380
cgggaagaag	tatgtttctg	octcaaaagc	agccactggt	aaactctccg	agacgatggc	1440
ttcagtgagt	ttcaaaaaatg	tcaaaatagc	aaagaatgat	agcaacttgc	acactgacaa	1500
agatgaatag	cttaggtgtg	tcaaacaaat	tcaagatata	aacgataaaa	tgtgtgattg	1560
caagaccgtg	tcatacaaac	aacagctcga	ctcgaatcgc	acaatcacc	agttgggaag	1620
ggtcaccacc	caatttgttg	agaccgtctg	ttcttcaagt	tcattgctat	cctctaccct	1680
atctccatct	tcattctctg	ctgtctctca	gcagcagggc	aatgcagcaa	gtgtcaagac	1740
taattgagtt	taaaagtgaa	gttaacttat	tgcgcagaaa	atcaccaaga	aagacacac	1800
cadgataatg	aaatattata	ataagtagtt	aactattaga	tcatttcttc	tgtaataaaa	1860
actaaagtgc	tatatgttaa	cgatttgatg	cttataaac	gatgatgca	agtaaaattc	1920
ctgtataaaa	acgaatcaga	tagattgtaa	ccgcttgtga	tgtaaacata	caaaagttag	
tgatgctata	aqaaqqattt	tttg				

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 446 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..446
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498078

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:
Met Ala Arg Ile Ser Leu Gly Ile Cys Leu Met Leu Val Val Ala Ser
1 5 10 15
Ser Val Ile Tyr Glu Ala Gln Gly Thr Phe Leu Leu Asn His Tyr Leu
 20 25 30
Lys Lys Asn Phe Pro Lys Lys Cys Asn Glu Phe Thr Pro Tyr Ala Asn
 35 40 45
Lys Gly Met Ile Thr Leu Val Thr Asp Leu Glu Gly Ser Ser Pro Ala
 50 55 60
Thr Thr Glu Phe Lys Thr Phe Phe Thr Gln Phe Lys Ser Tyr Met Ser
65 70 75 80
Phe Ile Glu Thr Thr Ser Ala Ser Thr Lys Asn Val Asp Ala Glu Met
 85 90 95
Thr Ala Lys Cys Asp Gly Leu Phe Lys Ala Met Ser Ala Leu Ser Ala
 100 105 110
Ser Lys Gly Val Lys Ser Ala Asp Ala Gly Ser Met Lys Met Thr Met
 115 120 125
Leu Ser Met Gly Lys Thr Leu Val Glu Gln Lys Lys Asn Thr Lys Ile
 130 135 140
Met Thr Leu Lys Glu Lys Lys Glu Leu Val Ile Asp Met Val Lys Trp
145 150 155 160
Thr Lys Met Val Ala Thr Phe Val Lys Ser Ala Ser Glu Gln Lys Gly
 165 170 175
Lys Ser Ile Asn Ile Ala Ser Tyr Gly Leu Asp Val Asp Val Asn Asp
 180 185 190
Ser Ser Ile Val Gly Gly Ala Ala Ser Ser Glu Ser Ser Ser Thr Lys
 195 200 205
Ser Gly Ser Val Ser Ser Ser Gly Ser Val Ser Thr Lys Ser Lys Glu
210 215 220
Ser Ser Ser Ser Gly Ser Ser Ala Ser Gly Ser Val Ala Thr Lys Ser
225 230 235 240
Lys Glu Ser Ser Gly Gly Ser Ala Ala Thr Lys Ser Lys Glu Ser Ser
 245 250 255
Gly Gly Ser Ala Ala Thr Lys Ser Lys Glu Ser Ser Gly Gly Ser Ala
 260 265 270
Thr Thr Gly Lys Thr Ser Gly Ser Pro Ser Gly Ser Pro Lys Ala Ser
275 280 285
Pro Ser Gly Ser Val Ser Gly Lys Ser Ser Ser Lys Gly Ser Ala Ser
290 295 300
Ala Gln Gly Ser Ala Ser Ala Gln Gly Ser Ala Ser Ala Gln Gly Ser
305 310 315
Ala Ser Ala Gln Gly Ser Ala Ser Ala Glu Arg Arg Glu Ser Gly Ala
 325 330 335
Met Ala Met Ser Lys Ser Arg Glu Thr Lys Thr Ser Ser Gln Arg Gln
 340 345 350
Ser Lys Ser Ser Ser Glu Ser Ser Ser Ser Thr Thr Thr Thr Thr
 355 360 365
Val Lys Gln Val Glu Ser Glu Thr Ser Lys Glu Val Met Ser Phe Ile
370 375 380
Met Gln Leu Glu Lys Lys Tyr Ala Ala Lys Ala Glu Leu Lys Val Phe
385 390 395 400

Phe Glu Ser Leu Lys Ser Ser Met Gln Ala Ser Ala Ser Val Gly Ser
405 410 415
Lys Thr Ala Lys Asp Tyr Val Ser Ala Ser Lys Ala Ala Thr Gly Lys
420 425 430
Leu Ser Glu Ala Met Ala Ser Val Ser Ser Lys Asn Val Lys
435 440 445

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..436
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498079

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

Met Leu Val Val Ala Ser Ser Val Ile Tyr Glu Ala Gln Gly Thr Phe
1 5 10 15
Leu Leu Asn His Tyr Leu Lys Lys Asn Phe Pro Lys Lys Cys Asn Glu
20 25 30
Phe Thr Pro Tyr Ala Asn Lys Gly Met Ile Thr Leu Val Thr Asp Leu
35 40 45
Glu Gly Ser Ser Pro Ala Thr Thr Glu Phe Lys Thr Phe Thr Gln
50 55 60
Phe Lys Ser Tyr Met Ser Phe Ile Glu Thr Thr Ser Ala Ser Thr Lys
65 70 75 80
Asn Val Asp Ala Glu Met Thr Ala Lys Cys Asp Gly Leu Phe Lys Ala
85 90 95
Met Ser Ala Leu Ser Ala Ser Lys Gly Val Lys Ser Ala Asp Ala Gly
100 105 110
Ser Met Lys Met Thr Met Leu Ser Met Gly Lys Thr Leu Val Glu Gln
115 120 125
Lys Lys Asn Thr Lys Ile Met Thr Leu Lys Glu Lys Lys Glu Leu Val
130 135 140
Ile Asp Met Val Lys Trp Thr Lys Met Val Ala Thr Phe Val Lys Ser
145 150 155 160
Ala Ser Glu Gln Lys Gly Lys Ser Ile Asn Ile Ala Ser Tyr Gly Leu
165 170 175
Asp Val Asp Val Asn Asp Ser Ser Ile Val Gly Gly Ala Ala Ser Ser
180 185 190
Glu Ser Ser Ser Thr Lys Ser Gly Ser Val Ser Ser Ser Gly Ser Val
195 200 205
Ser Thr Lys Ser Lys Glu Ser Ser Ser Gly Ser Ser Ala Ser Gly
210 215 220
Ser Val Ala Thr Lys Ser Lys Glu Ser Ser Gly Gly Ser Ala Ala Thr
225 230 235 240
Lys Ser Lys Glu Ser Ser Gly Gly Ser Ala Ala Thr Lys Ser Lys Glu
245 250 255
Ser Ser Gly Gly Ser Ala Thr Thr Gly Lys Thr Ser Gly Ser Pro Ser
260 265 270
Gly Ser Pro Lys Ala Ser Pro Ser Gly Ser Val Ser Gly Lys Ser Ser
275 280 285
Ser Lys Gly Ser Ala Ser Ala Gln Gly Ser Ala Ser Ala Gln Gly Ser
290 295 300
Ala Ser Ala Gln Gly Ser Ala Ser Ala Gln Gly Ser Ala Ser Ala Gln
305 310 315 320
Arg Arg Glu Ser Gly Ala Met Ala Met Ser Lys Ser Arg Glu Thr Lys
325 330 335
Thr Ser Ser Gln Arg Gln Ser Lys Ser Ser Ser Glu Ser Ser Ser Ser

[illegible]

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..396
(D) OTHER INFORMATION

(D) OTHER INFORMATION: / Ceres Seq. ID 1498080

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Met	Ile	Thr	Leu	Val	Thr	Asp	Leu	Glu	Gly	Ser	Ser	Pro	Ala	Thr	Thr
1			5					10						15	
Glu	Phe	Lys	Thr	Phe	Phe	Thr	Gln	Phe	Lys	Ser	Tyr	Met	Ser	Phe	Ile
			20					25					30		
Glu	Thr	Thr	Ser	Ala	Ser	Thr	Lys	Val	Asp	Ala	Glu	Met	Thr	Ala	
		35					40				45				
Lys	Cys	Asp	Gly	Leu	Phe	Lys	Ala	Met	Ser	Ala	Leu	Ser	Ala	Ser	Lys
		50				55					60				
Gly	Val	Lys	Ser	Ala	Asp	Ala	Gly	Ser	Met	Lys	Met	Thr	Met	Leu	Ser
65					70					75				80	
Met	Gly	Lys	Thr	Leu	Val	Glu	Gln	Lys	Lys	Asn	Thr	Lys	Ile	Met	Thr
			85					90					95		
Leu	Lys	Glu	Lys	Lys	Glu	Leu	Val	Ile	Asp	Met	Val	Lys	Trp	Thr	Lys
			100					105					110		
Met	Val	Ala	Thr	Phe	Val	Lys	Ser	Ala	Ser	Glu	Gln	Lys	Gly	Lys	Ser
		115					120					125			
Ile	Asn	Ile	Ala	Ser	Tyr	Gly	Leu	Asp	Val	Asp	Val	Asn	Asp	Ser	Ser
		130				135					140				
Ile	Val	Gly	Gly	Ala	Ala	Ser	Ser	Glu	Ser	Ser	Ser	Thr	Lys	Ser	Gly
145					150						155			160	
Ser	Val	Ser	Ser	Ser	Gly	Ser	Val	Ser	Thr	Lys	Ser	Lys	Glu	Ser	Ser
			165						170				175		
Ser	Ser	Gly	Ser	Ser	Ala	Ser	Gly	Ser	Val	Ala	Thr	Lys	Ser	Lys	Glu
		180						185					190		
Ser	Ser	Gly	Gly	Ser	Ala	Ala	Thr	Lys	Ser	Lys	Glu	Ser	Ser	Gly	Gly
		195					200					205			
Ser	Ala	Ala	Thr	Lys	Ser	Lys	Glu	Ser	Ser	Gly	Gly	Ser	Ala	Thr	Thr
		210				215					220				
Gly	Lys	Thr	Ser	Gly	Ser	Pro	Ser	Gly	Ser	Pro	Lys	Ala	Ser	Pro	Ser
225					230						235			240	
Gly	Ser	Val	Ser	Gly	Lys	Ser	Ser	Ser	Lys	Gly	Ser	Ala	Ser	Ala	Gln
			245						250				255		
Gly	Ser	Ala	Ser	Ala	Gln	Gly	Ser	Ala	Ser	Ala	Gln	Gly	Ser	Ala	Ser
		260						265				270			
Ala	Gln	Gly	Ser	Ala	Ser	Ala	Gln	Arg	Arg	Glu	Ser	Gly	Ala	Met	Ala
		275				280						285			

Met Ser Lys Ser Arg Glu Thr Lys Thr Ser Ser Gln Arg Gln Ser Lys
290 295 300
Ser Ser Ser Glu Ser Ser Ser Ser Thr Thr Thr Thr Val Lys
305 310 315 320
Gln Val Glu Ser Glu Thr Ser Lys Glu Val Met Ser Phe Ile Met Gln
325 330 335
Leu Glu Lys Lys Tyr Ala Ala Lys Ala Glu Leu Lys Val Phe Phe Glu
340 345 350
Ser Leu Lys Ser Ser Met Gln Ala Ser Ala Ser Val Gly Ser Lys Thr
355 360 365
Ala Lys Asp Tyr Val Ser Ala Ser Lys Ala Ala Thr Gly Lys Leu Ser
370 375 380
Glu Ala Met Ala Ser Val Ser Ser Lys Asn Val Lys
385 390 395

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 760 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..760

(D) OTHER INFORMATION: / Ceres Seq. ID 1498083

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

attaacaaat	tgtttctgat	ctattttatt	ttatttttgg	tatcaggaag	agaagaaaac	60
agaagcagca	gaggaaaaga	aaatggaaga	gaagaaaacca	gaagagaaaa	aagaaggaga	120
agacaagaaa	gtggatgctg	agaaaaaagg	agaagattct	gacaagaagc	ctcaagaagg	180
agaaactaac	aaagattcca	aaagaagattc	tgctccggcg	gcgcctgagg	ctccagcacc	240
gcctcctccg	ccgcaagagg	ttgttcttaa	ggtttacatg	cactgtgaag	gatgtgctag	300
aaaagtccgc	cggtgtctca	aaggcttcga	aggagtggaa	gatgtgatga	ctgattgtaa	360
aacggggaaa	gtggtgggtg	aaggtgagaa	agctgatcca	ttgaaagat	tagctagagt	420
tcagaggaag	accacccgtc	aagttcaggc	tagtgtttgt	ggactttgaa	gatggacgta	480
agaggtatct	gaagaaatca	gctaagtgg	ttaggagatt	gttgaaagga	gcrcatcggtg	540
ggacgaatga	gcaggtgggt	gttatttta	aaaccacgag	tcattgggtc	atttagtcta	600
ctgtttcttt	tgctctatgt	acagaaaaga	aataaacttt	ccaaaataag	agggtggctt	660
gtttggactt	tggtatgtac	tatatata	ggtaattctt	ggcgtttgtt	agtttccaaa	720
ccaaacatta	ataaataaat	aaataaaga	gtttgaggtt			

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1498084

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Met	Glu	Glu	Lys	Lys	Pro	Glu	Glu	Lys	Lys	Glu	Gly	Glu	Asp	Lys	Lys
1			5					10						15	
Val	Asp	Ala	Glu	Lys	Lys	Gly	Glu	Asp	Ser	Asp	Lys	Lys	Pro	Gln	Glu
		20						25					30		
Gly	Glu	Thr	Asn	Lys	Asp	Ser	Lys	Glu	Asp	Ser	Ala	Pro	Ala	Ala	Pro
		35						40				45			
Glu	Ala	Pro	Ala	Pro	Pro	Pro	Pro	Gln	Glu	Val	Val	Leu	Lys	Val	
		50					55				60				
Tyr	Met	His	Cys	Glu	Gly	Cys	Ala	Arg	Lys	Val	Arg	Arg	Cys	Leu	Lys
65				70				75						80	

Gly	Phe	Glu	Gly	Val	Glu	Asp	Val	Met	Thr	Asp	Cys	Lys	Thr	Gly	Lys	
				85					90						95	
Val	Val	Val	Lys	Gly	Glu	Lys	Ala	Asp	Pro	Leu	Lys	Val	Leu	Ala	Arg	
			100					105						110		
Val	Gln	Arg	Lys	Thr	His	Arg	Gln	Val	Gln	Ala	Ser	Val	Cys	Gly	Leu	
			115				120						125			

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..70
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498085

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

Met	Leu	Arg	Lys	Lys	Glu	Lys	Ile	Leu	Thr	Arg	Ser	Leu	Lys	Lys	Glu	
1				5					10					15		
Lys	Leu	Thr	Lys	Ile	Pro	Lys	Lys	Ile	Leu	Leu	Arg	Arg	Arg	Leu	Arg	
			20				25						30			
Leu	Gln	His	Arg	Leu	Leu	Arg	Arg	Lys	Arg	Leu	Phe	Leu	Arg	Phe	Thr	
		35					40					45				
Cys	Thr	Val	Lys	Asp	Val	Leu	Glu	Lys	Ser	Ala	Val	Val	Ser	Lys	Ala	
		50				55						60				
Ser	Lys	Glu	Trp	Lys	Met											
65					70											

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..67
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498086

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Met	Val	Gly	Arg	Met	Ser	Arg	Trp	Leu	Leu	Phe	Asn	Lys	Pro	Arg	Val	
1				5					10					15		
Ile	Gly	Gln	Phe	Ser	Leu	Leu	Phe	Leu	Leu	Tyr	Val	Gln	Lys	Glu		
			20				25						30			
Asn	Lys	Leu	Ser	Lys	Ile	Arg	Gly	Gly	Phe	Val	Trp	Thr	Leu	Asp	Val	
		35					40					45				
Thr	Ile	Tyr	Ile	Gly	Asn	Ser	Trp	Arg	Leu	Leu	Val	Ser	Lys	Pro	Asn	
		50				55						60				
Ile	Asn	Lys														
65																

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..748

(D) OTHER INFORMATION: / Ceres Seq. ID 1498090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

aaatcactta	cttaacatac	taagagagtt	attagaacct	gcaaaaaaatg	gcttccaagg	60
ctttgattct	gttaggtctc	ttctcagttc	ttctcgctgt	ctcgcgaagt	gtcgccgcaa	120
ggaatcgggc	atgggtgaagc	cagagagtga	ggaacctgtg	caacctgaag	gttatrgcgg	180
tggccacgga	ggacatgggt	gtcacggagg	gggaggaggc	cacggacatg	gaggacacaa	240
cggaggaggg	ggccacggac	ttgacggata	cggaggaggt	ggaggacact	atggaggarg	300
tggaggacac	tacggaggag	gtggaggaca	ctacggagga	ggtggaggac	actacggagg	360
aggtgggtgga	gaggattaaa	gctactgttt	cttgtgatgt	tggaggagga	gcgtagtttt	420
ttttcagaag	aagtaagaat	aagagaaaaa	gaaggattaa	gagcggttat	ggttttccat	480
tttgtgtttt	ttgaaatcca	aaggaagtca	agaacgcacc	ttttgcgttt	aatttcacot	540
caagctgatg	aaaaaagtta	aagtgtgttc	ggtattgact	tctgtcggaa	accacggttt	600
taaattgtct	attttgcgtt	tcgttgacac	ttttttgaac	accttttggg	tttccctttt	660
ttgcgttctc	cgaccocaag	tgtcarwttc	tttgtgtttt	tgtattgtaa	gcocctttgt	720
tgcacttgac	agatatggag	ttaaaatc				

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1498091

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

Asn	His	Leu	Leu	Asn	Ile	Leu	Arg	Glu	Leu	Leu	Glu	Leu	Ala	Lys	Asn	
1			5					10						15		
Gly	Phe	Gln	Gly	Phe	Asp	Ser	Val	Arg	Ser	Leu	Leu	Ser	Ser	Ser	Arg	
			20					25					30			
Arg	Leu	Arg	Ser	Val	Cys	Arg	Lys	Glu	Ser	Gly	Met	Val	Lys	Pro	Glu	
			35				40				45					
Ser	Glu	Glu	Thr	Val	Gln	Pro	Glu	Gly	Tyr	Xaa	Gly	Gly	His	Gly	Gly	
			50				55				60					
His	Gly	Gly	His	Gly	Gly	Gly	Gly	Gly	His	Gly	His	Gly	Gly	His	Asn	
			65				70				75				80	
Gly	Gly	Gly	Gly	His	Gly	Leu	Asp	Gly	Tyr	Gly	Gly	Gly	Gly	Gly	His	
				85				90						95		
Tyr	Gly	Gly	Xaa	Gly	Gly	His	Tyr	Gly	Gly	Gly	Gly	Gly	His	Tyr	Gly	
			100				105						110			
Gly	Gly	Gly	Gly	His	Tyr	Gly	Gly	Gly	Gly	Glu	Asp					
			115			120				125						

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..82

(D) OTHER INFORMATION: / Ceres Seq. ID 1498092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

Met	Val	Lys	Pro	Glu	Ser	Glu	Glu	Thr	Val	Gln	Pro	Glu	Gly	Tyr	Xaa	
1				5					10					15		
Gly	Gly	His	Gly	Gly	His	Gly	Gly	His	Gly	Gly	Gly	Gly	Gly	His	Gly	
				20			25						30			
His	Gly	Gly	His	Asn	Gly	Gly	Gly	Gly	His	Gly	Leu	Asp	Gly	Tyr	Gly	

35 40 45
Gly Gly Gly Gly His Tyr Gly Gly Xaa Gly Gly His Tyr Gly Gly Gly
50 55 60
Gly Gly His Tyr Gly Gly Gly Gly Gly His Tyr Gly Gly Gly Gly Gly
65 70 75 80
Glu Asp

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..73
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Met Val Val Thr Glu Gly Glu Glu Ala Thr Asp Met Glu Asp Thr Thr
1 5 10 15
Glu Glu Gly Ala Thr Asp Leu Thr Asp Thr Glu Glu Val Glu Asp Thr
20 25 30
Met Glu Xaa Val Glu Asp Thr Thr Glu Glu Val Glu Asp Thr Thr Glu
35 40 45
Glu Val Glu Asp Thr Thr Glu Glu Val Val Glu Arg Ile Lys Ala Thr
50 55 60
Val Ser Cys Asp Val Gly Gly Ala
65 70

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1526
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498097

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

aaaaataaaa agtgttcttg ttgctgtaga acacaaacag aacaaacaaa aaatcaattg 60
aagagctctc cagtcgttag gggaagcaaa tagagaaatg gctagcttta ctgcctccgc 120
ttccaccgct ccgcgcgctc gtccggctct ccttctcaag cctaccgtcg ccattctcgc 180
tctctgttct gggttgcttc caatgggttaa gaagaaggga ggagtgagat gttcaatgga 240
gacaaagcag gaacgctctc agtcatgggg gctggagttt cagctgcacg aacagctcgt 300
ttgacggcgg tgatgagcaa tccgcgcatg gctttggttg atgagaggat gtcaacagaa 360
ggacacagga taccttttgg tctaagcaac aaacctcttg gttggattct gtttgagtc 420
tttggtttga wctggaacttt ctctctctgc tacacttcat ctctcgagga ggatgaagaa 480
tctggtcttt cactctgaag gaagaatcaa tcttttgtt tctcatttcc atttccatg 540
gagaacatga atcaaaaagt ttccaccttc tagtttcttg taattgttaa gtaaaagact 600
aaaactagaa ggggtgaacac tattcattca ttctcatcat gtcacatgaa tctgaaatcc 660
cgccggtgtc gtcatcaaac gccgcagcgg aggaatcttg agagaagacc agcaagaagag 720
cggtcaagaa ggaagctgcc aagctagaga agttaagacg tcgtcaagaa caagaggaag 780
caacgcgctg aacagctctg atctctctgg aagagaatga cgagttttcc aataactacg 840
gcgacgtgac tcttaccgag ttgcaatcgt cggcgcatcc gaaagccggg aagtggaatg 900
aggctgttga gggaaaggag tggaccgatg tgagcgattt ggtggaagag atgttggatg 960
cagaggttct gatcagaggg cgatgacaca cgaatcgctc aactgtctaac aaattggggt 1020
ttgtgttctt gagggagagc ggaatcaactg ttccagtgcg ggttagccaa tcagagaaga 1080
ccaaactagg tgccaacatg gttaaatatt tcaagcagct gagtcgcgaa tcttttgtcg 1140
atgttatcgg tgtcgtcact cctcccaagg agccgctgac gggaaactac cagcaggttg 1200

aaattcaagt gagaaaagt tactgcatca acaaatccctt ggccaaatta ccacttagtg 1260
tggaggatgc tgctcggagt gaagcagata tcgaagcatc tcttcagact ccactctcag 1320
ctgctcgtgt caatcaggat acacgtttga actatagggt gctcgacctc agaacaccgg 1380
ctaatacagc caatctccag ctccagtagc aagtcgaata tgccctcaga gaaaataac 1440
gatttaagaa ttttgttgga atccacacac caaaactgat ggctggtagt agtgaaggag 1500
gtctcgtgt atttaggttg gaatac

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..296
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498098

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Met	Ser	Ser	Glu	Ser	Glu	Ile	Pro	Pro	Leu	Ser	Ser	Ser	Thr	Ala	Ala
1			5						10					15	
Ala	Glu	Glu	Ser	Gly	Glu	Lys	Thr	Ser	Lys	Lys	Ala	Ala	Lys	Lys	Glu
			20					25					30		
Ala	Ala	Lys	Leu	Glu	Lys	Leu	Arg	Arg	Arg	Gln	Glu	Gln	Glu	Glu	Ala
			35				40						45		
Thr	Arg	Arg	Thr	Ala	Ser	Ile	Ser	Leu	Glu	Glu	Asn	Asp	Glu	Phe	Ser
			50				55					60			
Asn	Asn	Tyr	Gly	Asp	Val	Thr	Leu	Thr	Glu	Leu	Gln	Ser	Ser	Ala	Asp
			65				70							80	
Pro	Lys	Ala	Gly	Lys	Trp	Ile	Glu	Ala	Val	Glu	Gly	Lys	Glu	Trp	Thr
			85					90						95	
Asp	Val	Ser	Asp	Leu	Val	Glu	Glu	Met	Leu	Glu	Ser	Glu	Val	Leu	Ile
			100					105					110		
Arg	Gly	Arg	Val	His	Thr	Asn	Arg	Pro	Thr	Ser	Asn	Lys	Leu	Gly	Phe
			115				120						125		
Val	Val	Leu	Arg	Glu	Ser	Gly	Ser	Thr	Val	Gln	Cys	Val	Val	Ser	Gln
			130				135						140		
Ser	Glu	Lys	Thr	Lys	Leu	Gly	Ala	Asn	Met	Val	Lys	Tyr	Leu	Lys	Gln
			145				150						155		160
Leu	Ser	Arg	Glu	Ser	Phe	Val	Asp	Val	Ile	Gly	Val	Val	Thr	Leu	Pro
			165					170					175		
Lys	Glu	Pro	Leu	Thr	Gly	Thr	Thr	Gln	Gln	Val	Glu	Ile	Gln	Val	Arg
			180					185					190		
Lys	Val	Tyr	Cys	Ile	Asn	Lys	Ser	Leu	Ala	Lys	Leu	Pro	Leu	Ser	Val
			195				200						205		
Glu	Asp	Ala	Ala	Arg	Ser	Glu	Ala	Asp	Ile	Glu	Ala	Ser	Leu	Gln	Thr
			210				215						220		
Pro	Ser	Pro	Ala	Ala	Arg	Val	Asn	Gln	Asp	Thr	Arg	Leu	Asn	Tyr	Arg
			225				230						235		240
Val	Leu	Asp	Leu	Arg	Thr	Pro	Ala	Asn	Gln	Ala	Ile	Phe	Gln	Leu	Gln
			245					250						255	
Tyr	Glu	Val	Glu	Tyr	Ala	Phe	Arg	Glu	Lys	Leu	Arg	Phe	Lys	Asn	Phe
			260					265					270		
Val	Gly	Ile	His	Thr	Pro	Lys	Leu	Met	Ala	Gly	Ser	Ser	Glu	Gly	Gly
			275				280						285		
Ser	Ala	Val	Phe	Arg	Leu	Glu	Tyr								
			290				295								

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..192
(D) OTHER INFORMATION: / Ceres Seq. ID 1498099
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:
Met Leu Glu Ser Glu Val Leu Ile Arg Gly Arg Val His Thr Asn Arg
1 5 10 15
Pro Thr Ser Asn Lys Leu Gly Phe Val Val Leu Arg Glu Ser Gly Ser
 20 25 30
Thr Val Gln Cys Val Val Ser Gln Ser Glu Lys Thr Lys Leu Gly Ala
 35 40 45
Asn Met Val Lys Tyr Leu Lys Gln Leu Ser Arg Glu Ser Phe Val Asp
 50 55 60
Val Ile Gly Val Val Thr Leu Pro Lys Glu Pro Leu Thr Gly Thr Thr
65 70 75 80
Gln Gln Val Glu Ile Gln Val Arg Lys Val Tyr Cys Ile Asn Lys Ser
 85 90 95
Leu Ala Lys Leu Pro Leu Ser Val Glu Asp Ala Ala Arg Ser Glu Ala
 100 105 110
Asp Ile Glu Ala Ser Leu Gln Thr Pro Ser Pro Ala Ala Arg Val Asn
 115 120 125
Gln Asp Thr Arg Leu Asn Tyr Arg Val Leu Asp Leu Arg Thr Pro Ala
 130 135 140
Asn Gln Ala Ile Phe Gln Leu Gln Tyr Glu Val Glu Tyr Ala Phe Arg
145 150 155 160
Glu Lys Leu Arg Phe Lys Asn Phe Val Gly Ile His Thr Pro Lys Leu
 165 170 175
Met Ala Gly Ser Ser Glu Gly Gly Ser Ala Val Phe Arg Leu Glu Tyr
 180 185 190

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 697 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..697
(D) OTHER INFORMATION: / Ceres Seq. ID 1498100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

aacaccttct	ttaatccaga	acaacaaaaa	aaccaaacag	aagaagaaaa	aagaaaaaaa	60
actacaaaaa	aaaaaaatct	ctgcccgcct	ctccgttctc	ggggttgcg	cgaaattgga	120
ccaaattgat	caaaacctac	ccagaaatca	tttttggtca	caggggatag	gcgggcagat	180
ttaaaaaatt	tcttcttttt	ttcttctggt	tgaatttgta	ttgattcggt	aaatgtgtgt	240
tgtttgtagg	gttttttggt	ggatacccaa	aaggaaaggag	gtggacattc	atgggggttac	300
gttagaagtt	tggttagaag	gaacaaagtc	gactctgtcta	atggccaatc	tcattggtcac	360
gaacttgcta	gagccctcac	tgttctccat	ctcggttgcaa	ttgggtgttg	agcaacaata	420
ggagctggag	tttatattct	tgtaggaaca	gttcgcgagag	agcattcagg	acctctctct	480
gctttgtctt	ttcttattgc	tggaattgct	gctgggtcttt	ctcgcttttg	ttatgctgaa	540
ctctctagtc	gttgtcnttc	agctggggagt	gcgtatcac	attcttaccat	ttgtgttggt	600
gaagggtgtg	cgtggataat	cagttgggcg	ttgattctca	agtgaagat	tgtacttgta	660
aacaaaaat	gtattatata	aaagtgttat	ttgtttcc			

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..144
(D) OTHER INFORMATION: / Ceres Seq. ID 1498101
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:
Met Gly Phe Leu Val Asp Thr Gln Lys Glu Gly Gly His Ser Trp
1 5 10 15
Gly Tyr Val Arg Ser Leu Val Arg Arg Lys Gln Val Asp Ser Ala Asn
20 25 30
Gly Gln Ser Ser His Gly His Gln Leu Ala Arg Ala Leu Thr Val Pro His
35 40 45
Leu Val Ala Ile Gly Val Gly Ala Thr Ile Gly Ala Gly Val Tyr Ile
50 55 60
Leu Val Gly Thr Val Ala Arg Glu His Ser Gly Pro Ser Leu Ala Leu
65 70 75 80
Ser Phe Leu Ile Ala Gly Ile Ala Ala Gly Leu Ser Ala Phe Cys Tyr
85 90 95
Ala Glu Leu Ser Ser Arg Cys Xaa Ser Ala Gly Ser Ala Tyr His Tyr
100 105 110
Ser Tyr Ile Cys Val Gly Glu Gly Val Ala Trp Ile Ile Gly Trp Ala
115 120 125
Leu Ile Leu Lys Cys Lys Ile Val Leu Val Asn Lys Lys Cys Ile Ile
130 135 140

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 771 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..771

(D) OTHER INFORMATION: / Ceres Seq. ID 1498102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

acaattccaat caaaacacac agagagaaga aaaactcaga agaaaagcca aagagtgaaa 60
caaaaatggc gtcgacgact ctctcaatcg caacaacaat ccgttctcta ccttatccta 120
ctctcgtctc catcaatcac ttcccttccc gaaccamcac catogaatto cctctcgtct 180
tcggtggtgg ttcatcatcc acattgaccc accgtgcaac ccattctcgt ccaatcgccg 240
ccgtcgaaagc tccggagaaa atcgagaaga tcggatccga aatctcatcc ctaacctcgc 300
aagaagctcg tatctctgtc gactatctcc aagacaaatt ccgtgtctcc ccaactctct 360
tagcccccgc agcagcggcg gttgctgtc cagccgacgg tggcgcgccg cgtgtagtgg 420
aagagcaaac agagtctgat gtggttatca atgaagtcc cagcagttcc cgtattgcag 480
tgattaaagc tgttagggct ttaactagct tggcggtgaa ggaagctaag gagctaatcg 540
aagattacc aaagaagttt aaagaaggta tcaactaaaga tgaagctgaa gaagctaaga 600
agactcttga agaagctggg gctaaagtct ccattgctta aggtttttat taataaaaaa 660
aaagaagttg ttactctttc tggaaattga ttggtctttt gtgttgttta gatatgttg 720
cgtctggaat tgttgagaaa ttgttgtaat ttggaatcaca ttgtgtttcc c

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..212
(D) OTHER INFORMATION: / Ceres Seq. ID 1498103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

Asn	Pro	Ile	Lys	Thr	His	Arg	Glu	Lys	Lys	Asn	Ser	Glu	Glu	Lys	Pro
1			5				10							15	
Lys	Ser	Glu	Thr	Lys	Met	Ala	Ser	Thr	Leu	Ser	Ile	Ala	Thr	Thr	
			20				25						30		
Ile	Arg	Ser	Ser	Ser	Tyr	Pro	Thr	Leu	Ala	Ser	Ile	Asn	His	Phe	Pro
			35				40					45			
Ser	Arg	Thr	Xaa	Thr	Ile	Glu	Phe	Pro	Ser	Arg	Phe	Gly	Gly	Gly	Ser
			50				55					60			
Ser	Ser	Thr	Leu	Thr	His	Arg	Ala	Thr	His	Leu	Arg	Pro	Ile	Ala	Ala
65					70					75				80	
Val	Glu	Ala	Pro	Glu	Lys	Ile	Glu	Lys	Ile	Gly	Ser	Glu	Ile	Ser	Ser
					85					90				95	
Leu	Thr	Leu	Glu	Glu	Ala	Arg	Ile	Leu	Val	Asp	Tyr	Leu	Gln	Asp	Lys
					100				105				110		
Phe	Gly	Val	Ser	Pro	Leu	Ser	Leu	Ala	Pro	Ala	Ala	Ala	Val	Ala	
					115				120				125		
Ala	Pro	Ala	Asp	Gly	Gly	Ala	Ala	Ala	Val	Val	Glu	Glu	Gln	Thr	Glu
					130				135				140		
Phe	Asp	Val	Val	Ile	Asn	Glu	Val	Pro	Ser	Ser	Ser	Arg	Ile	Ala	Val
145					150					155				160	
Ile	Lys	Ala	Val	Arg	Ala	Leu	Thr	Ser	Leu	Ala	Leu	Lys	Glu	Ala	Lys
					165					170				175	
Glu	Leu	Ile	Glu	Gly	Leu	Pro	Lys	Lys	Phe	Lys	Glu	Gly	Ile	Thr	Lys
					180					185				190	
Asp	Glu	Ala	Glu	Glu	Ala	Lys	Lys	Thr	Leu	Glu	Glu	Ala	Gly	Ala	Lys
					195			200				205			
Val	Ser	Ile	Ala												
					210										

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..191
(D) OTHER INFORMATION: / Ceres Seq. ID 1498104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Met	Ala	Ser	Thr	Thr	Leu	Ser	Ile	Ala	Thr	Thr	Ile	Arg	Ser	Ser	Ser
1				5						10				15	
Tyr	Pro	Thr	Leu	Ala	Ser	Ile	Asn	His	Phe	Pro	Ser	Arg	Thr	Xaa	Thr
				20					25				30		
Ile	Glu	Phe	Pro	Ser	Arg	Phe	Gly	Gly	Gly	Ser	Ser	Ser	Thr	Leu	Thr
				35					40				45		
His	Arg	Ala	Thr	His	Leu	Arg	Pro	Ile	Ala	Ala	Val	Glu	Ala	Pro	Glu
				50					55			60			
Lys	Ile	Glu	Lys	Ile	Gly	Ser	Glu	Ile	Ser	Ser	Leu	Thr	Leu	Glu	Glu
65					70					75				80	
Ala	Arg	Ile	Leu	Val	Asp	Tyr	Leu	Gln	Asp	Lys	Phe	Gly	Val	Ser	Pro
					85					90				95	
Leu	Ser	Leu	Ala	Pro	Ala	Ala	Ala	Ala	Val	Ala	Ala	Pro	Ala	Asp	Gly
					100				105				110		
Gly	Ala	Ala	Ala	Val	Val	Glu	Glu	Gln	Thr	Glu	Phe	Asp	Val	Val	Ile
					115				120				125		
Asn	Glu	Val	Pro	Ser	Ser	Ser	Arg	Ile	Ala	Val	Ile	Lys	Ala	Val	Arg

130	135	140
Ala Leu Thr Ser Leu Ala Leu Lys Glu Ala Lys Glu Leu Ile Glu Gly		
145	150	155
Leu Pro Lys Lys Phe Lys Glu Gly Ile Thr Lys Asp Glu Ala Glu Glu		160
	165	170
Ala Lys Lys Thr Leu Glu Glu Ala Gly Ala Lys Val Ser Ile Ala		175
	180	185

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..2443

(D) OTHER INFORMATION: / Ceres Seq. ID 1498109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

aattgtctctc	tcaattttctc	tctctctccc	cttctgtcttc	tctcccttaa	caagaacctat	60
gagctctctcc	gatggcggct	ctcttagggt	tctgattcct	taccatctcc	gctaaaacct	120
tcagaaaaatc	agagagtata	cgggaaagca	gcactcggat	gaggatattct	ttgcgcgtcta	180
taaggatcttc	tccaatgata	ctcatgagac	cgcctagaag	ctcctctctt	tagatacatt	240
tcatgaggtg	agaagtaaaa	gggagaaaaa	gaaggagcct	atagtgccag	ttacacaaac	300
aagtggcaga	gggtgtcgga	ggaactttgc	ttcaagtaac	tcttatcaa	gtagtgggaag	360
aaatgtctct	tttaaaagg	aaaatggagc	taatcatgta	acaagaggtt	ctagaactgc	420
tcagcctgcc	actaacaagg	camgcaacat	cacagtacct	aatgaaacaa	aggtttctgc	480
tcctgtcgtt	attctcgagt	aggtcagcaa	tcataaagct	caagatgata	cttcttttgt	540
ttctgcttca	cgttgtagta	gccagtcaga	tcaagccatt	gaaattgaga	ctcgcgtccaa	600
acaaggcaca	aatcaatcgc	ttcttaagcc	agatgtttag	gaacagtcac	atcgtaacct	660
ccctttccac	cttcaggttg	ccaaaggact	gcaaaatggt	ctgacgtttg	gcagttttga	720
ttccaatttt	gtgaaaagg	tatctttctg	caatggtgct	agtggcggat	atgactcaaa	780
ttttgagctc	tctcaccgga	caggggatga	tgagagggaa	tcttctccca	ctaccaattg	840
tattactggg	gttgcttcgc	ctagagaaga	aacatcaaca	gtttctgaag	ataaggatta	900
tgggatatca	aattctgcga	ctggagctga	gcctgtgtgt	cactcggatc	acattgtccc	960
acctgtgaga	gaagtaccga	aggaggaagc	tttatcaaac	acagaaaatc	atcaaatgtc	1020
ttatggtcaa	gaagctccac	tcagttgtgt	tggtcttgtc	ccctcgttgt	cagcaaatag	1080
ccaacccggt	aacacagaag	cagcggagac	tcagcccaga	aattccaact	ctccagctat	1140
ttcattagta	tcatatcttc	cagatcagag	ctccatagca	gcagccactc	acaagacaaa	1200
ttttcttagg	cagcaataacc	ctcccaattt	cttccctaac	ggctatttct	caaccgtatta	1260
tatgccaccg	ccgtacattc	accagttctt	gagcccaaac	ggatctcttc	agcagtttta	1320
ttttccacaa	ggagctgcct	taacagcacc	ttctcatgca	aaaccagttg	acaacactga	1380
aaacctctcc	accacaacac	cttacctaca	caactctccc	atggttgcta	gcagcactcc	1440
atctacaacc	accttaaaat	ctatccatag	tgaagaaaaa	gcattctacc	tgactgaaag	1500
tgacactgca	tgagattggc	agggatttgg	caacctgcag	gtgaatccaa	tgtataacct	1560
agcataccaa	ggtcagccac	ttggttttcc	agtcgtgcag	gctgtgcatg	gtggcctcac	1620
gggaatgcac	caaccaacac	agcccatggc	agctgcttta	actacatatc	agaccttaac	1680
accacgcgca	cacacacaaa	cggctatggc	tccgagcgtg	gtggtgggata	cggttctcaa	1740
cgtagtggtg	gtgtgttacg	agggtctcaa	cgttccagtt	atggtctcgg	gtcagggtcc	1800
ggttggtgct	caggttcaag	aaacccgtct	tacgtgggca	acctttgttg	gggtgttgat	1860
gacatggcac	ttgagaactt	gtttaaacag	caaggaaaag	tagttgragc	tagggtttwc	1920
gcctacagac	agggacagcg	gtagatccaa	gggttttgga	tttgtgacac	ttagtctctc	1980
ccaagaggtt	cagaaggcga	tcaattcctt	gaatggagca	gatttggatg	gaagacaaat	2040
aaagctctca	gaggtcgagg	ctaggccacc	aaagagccaa	ttttgagcgg	tcacacctct	2100
ttcatattct	caaaaatcgc	aaaattctgga	gggttctttg	aagcatatag	ggtttagtga	2160
aaatggcggg	ttcagacagt	actaaaaact	cactgtgtgt	gcacgctagg	ctttctccgc	2220
cttttagtca	tgaaggtcgt	taaggaaatg	tctttttttg	agaaaagata	caattagatt	2280
aaagcagaga	accatgtggt	cttgctctgt	cgaactcctg	gagattgggt	gtagttgaag	2340
ttgcattttc	ttctgtgtct	ttttgttgtt	attttgacac	aatttggcct	tttggcataa	2400
gagagtgaat	gtagcagctc	gtttttattg	atgttcttga	tcc		

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 633 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..633
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498110
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

Ile	Ala	Leu	Ser	Ile	Ser	Leu	Ser	Ser	Arg	Phe	Cys	Phe	Ser	Pro	Leu
1			5						10					15	
Thr	Arg	Thr	Met	Ser	Ser	Ser	Asp	Gly	Gly	Ser	Ser	Arg	Val	Ser	Ile
			20					25					30		
Pro	Tyr	His	Leu	Arg	Lys	Thr	Leu	Gln	Lys	Ile	Arg	Glu	Tyr	Thr	Gly
			35				40					45			
Lys	Gln	His	Ser	Asp	Glu	Asp	Ile	Phe	Ala	Val	Tyr	Lys	Asp	Ser	Phe
			50				55				60				
Asn	Asp	Pro	His	Glu	Thr	Ala	Gln	Lys	Leu	Leu	Phe	Leu	Asp	Thr	Phe
65				70					75					80	
His	Glu	Val	Arg	Ser	Lys	Arg	Glu	Lys	Lys	Lys	Glu	Pro	Ile	Val	Pro
			85					90					95		
Val	Thr	Gln	Pro	Ser	Gly	Arg	Gly	Gly	Arg	Arg	Asn	Phe	Ala	Ser	Ser
			100					105					110		
Asn	Ser	Tyr	Gln	Gly	Ser	Gly	Arg	Asn	Ala	Ser	Phe	Lys	Arg	Glu	Asn
			115				120					125			
Gly	Ala	Asn	His	Val	Thr	Arg	Gly	Ser	Arg	Thr	Ala	Gln	Pro	Ala	Thr
			130				135				140				
Asn	Lys	Ala	Xaa	Asn	Ile	Thr	Val	Pro	Asn	Glu	Thr	Lys	Val	Ser	Gly
145				150					155				160		
Pro	Ala	Ser	Ile	Leu	Ser	Glu	Val	Ser	Asn	His	Lys	Ala	Gln	Asp	Asp
			165					170					175		
Pro	Ser	Leu	Ile	Ser	Ala	Ser	Arg	Cys	Ser	Ser	Gln	Ser	Asp	Gln	Ala
			180					185					190		
Ile	Glu	Ile	Glu	Thr	Ala	Ser	Lys	Gln	Gly	Lys	Asn	Gln	Ser	Leu	Pro
			195				200					205			
Lys	Pro	Asp	Val	Ser	Glu	Gln	Ser	His	Val	Thr	Phe	Pro	Phe	His	Leu
			210				215				220				
Gln	Val	Ala	Lys	Gly	Leu	Gln	Asn	Gly	Leu	Thr	Phe	Gly	Ser	Phe	Asp
225				230					235					240	
Ser	Asn	Phe	Val	Lys	Glu	Val	Ser	Ser	Ser	Asn	Gly	Ala	Ser	Gly	Gly
			245						250				255		
Tyr	Asp	Ser	Asn	Phe	Glu	Ser	Ser	His	Gly	Thr	Gly	Asp	Asp	Glu	Arg
			260					265					270		
Glu	Ser	Ser	Pro	Thr	Thr	Asn	Gly	Ile	Thr	Gly	Val	Ala	Ser	Ala	Arg
			275				280					285			
Glu	Glu	Thr	Ser	Thr	Val	Ser	Glu	Asp	Lys	Asp	Tyr	Gly	Ile	Ser	Asn
			290				295				300				
Ser	Ala	Thr	Gly	Ala	Glu	Pro	Val	Val	His	Ser	Asp	His	Ile	Val	Pro
305				310					315					320	
Pro	Val	Glu	Glu	Val	Pro	Lys	Glu	Glu	Ala	Leu	Ser	Asn	Thr	Glu	Thr
			325						330				335		
His	Gln	Ile	Ala	Tyr	Gly	Gln	Glu	Ala	Pro	Leu	Ser	Val	Phe	Gly	Leu
			340					345					350		
Val	Pro	Ser	Leu	Ser	Ala	Ile	Gly	Gln	Pro	Val	Asn	Thr	Glu	Ala	Ala
			355				360					365			
Glu	Thr	Gln	Pro	Gly	Asn	Ser	Asn	Ser	Pro	Ala	Ile	Ser	Leu	Val	Ser
			370				375					380			
Tyr	Pro	Pro	Asp	Gln	Ser	Ser	Ile	Ala	Ala	Ala	Thr	Gln	Gln	Thr	Asn
385				390							395				400

Phe Leu Arg Gln Gln Tyr Pro Pro Asn Phe Phe Pro Tyr Gly Tyr Xaa
405 410 415
Ser Pro Tyr Tyr Met Pro Pro Pro Tyr Ile His Gln Phe Leu Ser Pro
420 425 430
Asn Gly Ile Pro Gln Gln Ser Tyr Phe Pro Gln Gly Ala Ala Leu Thr
435 440 445
Ala Pro Ser His Ala Lys Pro Val Asp Asn Thr Glu Asn Pro Pro Thr
450 455 460
Thr Asn Pro Tyr Leu His Thr Ser Pro Met Val Ala Ser Ser Ile Pro
465 470 475 480
Ser Thr Thr Thr Leu Asn Ser Ile His Ser Glu Glu Lys Ala Ser His
485 490 495
Leu Thr Glu Ser Ala Ala Ala Trp Ile Gly Gln Gly Phe Gly Asn Leu
500 505 510
Gln Val Asn Pro Met Tyr Asn Leu Ala Tyr Gln Gly Gln Pro Leu Gly
515 520 525
Phe Pro Val Val Gln Ala Gly His Gly Gly Leu Met Gly Met His Gln
530 535 540
Pro Thr Gln Pro Met Ala Ala Ala Leu Thr Thr Tyr Gln Thr Leu Pro
545 550 555 560
Pro Pro Pro His Thr Thr Thr Ala Met Val Pro Ser Val Val Val Asp
565 570 575
Thr Val Leu Asn Val Val Val Val Thr Glu Gly Leu Asn Val Pro
580 585 590
Val Met Val Arg Gly Gln Gly Pro Val Arg Ala Gln Val Gln Glu Thr
595 600 605
Val Ser Thr Trp Ala Thr Phe Leu Gly Val Leu Met Thr Trp His Leu
610 615 620
Arg Thr Cys Leu Thr Ser Lys Glu Arg
625 630

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 614 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..614

(D) OTHER INFORMATION: / Ceres Seq. ID 1498111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

Met Ser Ser Ser Asp Gly Gly Ser Ser Arg Val Ser Ile Pro Tyr His
1 5 10 15
Leu Arg Lys Thr Leu Gln Lys Ile Arg Glu Tyr Thr Gly Lys Gln His
20 25 30
Ser Asp Glu Asp Ile Phe Ala Val Tyr Lys Asp Ser Phe Asn Asp Pro
35 40 45
His Glu Thr Ala Gln Lys Leu Leu Phe Leu Asp Thr Phe His Glu Val
50 55 60
Arg Ser Lys Arg Glu Lys Lys Lys Glu Pro Ile Val Pro Val Thr Gln
65 70 75 80
Pro Ser Gly Arg Gly Gly Arg Arg Asn Phe Ala Ser Ser Asn Ser Tyr
85 90 95
Gln Gly Ser Gly Arg Asn Ala Ser Phe Lys Arg Glu Asn Gly Ala Asn
100 105 110
His Val Thr Arg Gly Ser Arg Thr Ala Gln Pro Ala Thr Asn Lys Ala
115 120 125
Xaa Asn Ile Thr Val Pro Asn Glu Thr Lys Val Ser Gly Pro Ala Ser
130 135 140
Ile Leu Ser Glu Val Ser Asn His Lys Ala Gln Asp Asp Pro Ser Leu

145	150	155	160
Ile Ser Ala Ser Arg Cys Ser Ser Gln Ser Asp Gln Ala Ile Glu Ile			
	165	170	175
Glu Thr Ala Ser Lys Gln Gly Lys Asn Gln Ser Leu Pro Lys Pro Asp			
	180	185	190
Val Ser Glu Gln Ser His Val Thr Phe Pro Phe His Leu Gln Val Ala			
	195	200	205
Lys Gly Leu Gln Asn Gly Leu Thr Phe Gly Ser Phe Asp Ser Asn Phe			
	210	215	220
Val Lys Glu Val Ser Ser Ser Asn Gly Ala Ser Gly Tyr Asp Ser			
	225	230	235
Asn Phe Glu Ser Ser His Gly Thr Gly Asp Asp Glu Arg Glu Ser Ser			
	245	250	255
Pro Thr Thr Asn Gly Ile Thr Gly Val Ala Ser Ala Arg Glu Glu Thr			
	260	265	270
Ser Thr Val Ser Glu Asp Lys Asp Tyr Gly Ile Ser Asn Ser Ala Thr			
	275	280	285
Gly Ala Glu Pro Val Val His Ser Asp His Ile Val Pro Pro Val Glu			
	290	295	300
Glu Val Pro Lys Glu Glu Ala Leu Ser Asn Thr Glu Thr His Gln Ile			
	305	310	315
Ala Tyr Gly Gln Glu Ala Pro Leu Ser Val Phe Gly Leu Val Pro Ser			
	325	330	335
Leu Ser Ala Ile Gly Gln Pro Val Asn Thr Glu Ala Ala Glu Thr Gln			
	340	345	350
Pro Gly Asn Ser Asn Ser Pro Ala Ile Ser Leu Val Ser Tyr Pro Pro			
	355	360	365
Asp Gln Ser Ser Ile Ala Ala Ala Thr Gln Gln Thr Asn Phe Leu Arg			
	370	375	380
Gln Gln Tyr Pro Pro Asn Phe Phe Pro Tyr Gly Tyr Xaa Ser Pro Tyr			
	385	390	395
Tyr Met Pro Pro Pro Tyr Ile His Gln Phe Leu Ser Pro Asn Gly Ile			
	405	410	415
Pro Gln Gln Ser Tyr Phe Pro Gln Gly Ala Ala Leu Thr Ala Pro Ser			
	420	425	430
His Ala Lys Pro Val Asp Asn Thr Glu Asn Pro Pro Thr Asn Pro			
	435	440	445
Tyr Leu His Thr Ser Pro Met Val Ala Ser Ser Ile Pro Ser Thr Thr			
	450	455	460
Thr Leu Asn Ser Ile His Ser Glu Glu Lys Ala Ser His Leu Thr Glu			
	465	470	475
Ser Ala Ala Ala Trp Ile Gly Gln Gly Phe Gly Asn Leu Gln Val Asn			
	485	490	495
Pro Met Tyr Asn Leu Ala Tyr Gln Gly Gln Pro Leu Gly Phe Pro Val			
	500	505	510
Val Gln Ala Gly His Gly Gly Leu Met Gly Met His Gln Pro Thr Gln			
	515	520	525
Pro Met Ala Ala Ala Leu Thr Thr Tyr Gln Thr Leu Pro Pro Pro Pro			
	530	535	540
His Thr Thr Thr Ala Met Val Pro Ser Val Val Val Asp Thr Val Leu			
	545	550	555
Asn Val Val Val Val Val Thr Glu Gly Leu Asn Val Pro Val Met Val			
	565	570	575
Arg Gly Gln Gly Pro Val Arg Ala Gln Val Gln Glu Thr Val Ser Thr			
	580	585	590
Trp Ala Thr Phe Leu Gly Val Leu Met Thr Trp His Leu Arg Thr Cys			
	595	600	605
Leu Thr Ser Lys Glu Arg			
610			

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 657 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..657
(D) OTHER INFORMATION: / Ceres Seq. ID 1498112
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

actcaactta	aactctttta	gtaacaatgg	ttctcttctc	tttaaccaag	cttgtgttct	60
ttgggtgtct	cctcctgtct	acattcacgg	acaaccttgg	ggctggaaaa	ctgggcaaa	120
tgaagctcaa	tctttactac	gaatcaacttt	gtcccggttg	tcaggaaattc	atcgctgaat	180
acctaggtaa	aatctttgac	tacgatctct	acacaatcac	tgatctcaag	ctgtttccat	240
ttggtaatgg	cgaaactctcc	gataatctga	ctgtcaacttg	ccagcatgggt	gaagaggaa	300
gcaaaactaaa	cgcccttgaa	gcttgagatc	agtgtattgtg	tagagatcgt	agtcaaagat	360
tttacagaag	tcattctcca	gtcccaagag	gaagaccttg	atcaatgcag	aaaacagaag	420
cttcgaagaa	tgagtttttc	gaaaggggtaa	atttatctat	gttgtgtttt	gagttagaag	480
atgtgttttg	atgttttgaa	atccttggtta	actttgggat	cttagacttt	tatcttaaaa	540
tcagtagaaa	cttcataatg	gcgctttgtc	acgatctgtt	acttggttca	tatactcttt	600
tcattcgtca	taaattattc	taartcccat	ataaattaac	aatgacacaa	gtttgcc	

(2) INFORMATION FOR SEQ ID NO:195:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..59
(D) OTHER INFORMATION: / Ceres Seq. ID 1498113
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

Leu	Asn	Leu	Asn	Ser	Phe	Ser	Asn	Asn	Gly	Phe	Phe	Phe	Asn	Gln
1			5					10					15	
Ala	Cys	Val	Leu	Trp	Leu	Ser	Pro	Pro	Ala	His	Ile	His	Gly	Gln
			20					25					30	Pro
Cys	Gly	Trp	Lys	Ile	Trp	Gln	Ser	Glu	Ala	Gln	Ser	Leu	Leu	Arg
			35					40					45	Ile
Thr	Leu	Ser	Arg	Leu	Ser	Gly	Ile	His	Arg	Arg				
			50				55							

(2) INFORMATION FOR SEQ ID NO:196:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 99 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..99
(D) OTHER INFORMATION: / Ceres Seq. ID 1498114
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Met	Val	Ser	Ser	Ser	Leu	Thr	Lys	Leu	Val	Phe	Phe	Gly	Cys	Leu	Leu
1				5				10					15		
Leu	Leu	Thr	Phe	Thr	Asp	Asn	Leu	Val	Ala	Gly	Lys	Ser	Gly	Lys	Val
				20				25					30		
Lys	Leu	Asn	Leu	Tyr	Tyr	Glu	Ser	Leu	Cys	Pro	Gly	Cys	Gln	Glu	Phe
				35				40					45		
Ile	Val	Asp	Asp	Leu	Gly	Lys	Ile	Phe	Asp	Tyr	Asp	Leu	Tyr	Thr	Ile
				50			55						60		

Thr Asp Leu Lys Leu Phe Pro Phe Gly Asn Ala Glu Leu Ser Asp Asn
65 70 75 80
Leu Thr Val Thr Cys Gln His Gly Glu Glu Cys Lys Leu Asn Ala
85 90 95
Leu Glu Ala

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 772 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..772
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

tcctttctttt	gagtcgcttc	acttctcttg	catccttcaa	actcatccac	agcaaggaat	60
ggctacagca	gcagcaccag	cagtgatttc	atggacaaga	tcaggcattg	tgctccaaatc	120
cggacaacaac	cagaagaaat	ctgagatgaa	agtttcttac	ataactggac	ttaaactcata	180
tggttggtctc	aaggcacaga	acaacaaggt	tgcttcaatg	ggatcaccac	ctgtcacaga	240
acagtggtttt	gctaacgcttg	tgatgtctct	caaaggaaga	agaggtaatg	gaggagcctt	300
atccaccacg	tgtaacgctg	tcggagagat	tttcaagatt	gcagcaaaac	actgttctgt	360
gaagagtggg	ataagtatct	agcaatgttc	tggaactctg	tacctccgag	tgaagaagac	420
acacctgagg	ctaaactaga	ccacatcctg	aaaacaacca	caggagatga	agaacaggtt	480
tcgaagcacat	tagcagagaa	gtaaaacctt	cacatttgat	cgtgggttcc	tctttgtaca	540
gtcacaagtgc	tggtggagga	gataagtaag	tctctcagtt	gctgagaaca	taacaattata	600
caaattccacc	acttgatttt	gatgtggttt	taattcgctc	tggactcgca	tatcttttgg	660
tttaactctgt	ccagtcacg	ttagtaataa	aacgaaatcc	agcatgcttg	tctttgtgat	720
ggaaacatca	ttagtcttcc	gattcccgat	tattaagaaa	gggttttcga	tt	

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..126
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Pro	Phe	Phe	Glu	Ser	Leu	His	Phe	Ser	Cys	Ile	Leu	Gln	Thr	His	Pro
1			5					10					15		
Gln	Gln	Gly	Met	Ala	Thr	Ala	Ala	Ala	Pro	Ala	Val	Ile	Ser	Trp	Thr
			20					25					30		
Arg	Ser	Gly	Ile	Val	Ser	Lys	Ser	Gly	Gln	Thr	Gln	Lys	Lys	Ser	Glu
			35					40				45			
Met	Lys	Val	Ser	Tyr	Ile	Thr	Gly	Leu	Asn	Ser	Tyr	Gly	Gly	Leu	Lys
			50					55				60			
Ala	Gln	Asn	Asn	Lys	Val	Val	Ser	Met	Gly	Ser	Pro	Leu	Cys	Thr	Glu
65				70						75				80	
Gln	Cys	Phe	Ala	Asn	Val	Val	Met	Ser	Leu	Lys	Gly	Arg	Arg	Gly	Asn
			85						90					95	
Gly	Gly	Ala	Leu	Ser	Thr	Thr	Cys	Asn	Ala	Val	Gly	Glu	Ile	Phe	Lys
			100					105						110	
Ile	Ala	Ala	Lys	His	Cys	Ser	Val	Lys	Ser	Gly	Ile	Ser	Ile		
			115				120					125			

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..107
(D) OTHER INFORMATION: / Ceres Seq. ID 1498121
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:
Met Ala Thr Ala Ala Pro Ala Val Ile Ser Trp Thr Arg Ser Gly
1 5 10 15
Ile Val Ser Lys Ser Gly Gln Thr Gln Lys Lys Ser Glu Met Lys Val
20 25 30
Ser Tyr Ile Thr Gly Leu Asn Ser Tyr Gly Gly Leu Lys Ala Gln Asn
35 40 45
Asn Lys Val Val Ser Met Gly Ser Pro Leu Cys Thr Glu Gln Cys Phe
50 55 60
Ala Asn Val Val Met Ser Leu Lys Gly Arg Arg Gly Asn Gly Gly Ala
65 70 75 80
Leu Ser Thr Thr Cys Asn Ala Val Gly Glu Ile Phe Lys Ile Ala Ala
85 90 95
Lys His Cys Ser Val Lys Ser Gly Ile Ser Ile
100 105
(2) INFORMATION FOR SEQ ID NO:200:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..78
(D) OTHER INFORMATION: / Ceres Seq. ID 1498122
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:
Met Lys Val Ser Tyr Ile Thr Gly Leu Asn Ser Tyr Gly Gly Leu Lys
1 5 10 15
Ala Gln Asn Asn Lys Val Val Ser Met Gly Ser Pro Leu Cys Thr Glu
20 25 30
Gln Cys Phe Ala Asn Val Val Met Ser Leu Lys Gly Arg Arg Gly Asn
35 40 45
Gly Gly Ala Leu Ser Thr Thr Cys Asn Ala Val Gly Glu Ile Phe Lys
50 55 60
Ile Ala Ala Lys His Cys Ser Val Lys Ser Gly Ile Ser Ile
65 70 75
(2) INFORMATION FOR SEQ ID NO:201:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 671 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..671
(D) OTHER INFORMATION: / Ceres Seq. ID 1498123
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:
cacctakaac atcctaatacg aaacccggcg ccaccattaa aatctctcga tctctatctg 60
cgaaaattcca cggtagggtat tgaataatggc gacagttcca ggacaattga tctggggagat 120
cgtgaagaac aacaactggtt tcttggtgaa gcagttcggg agaggaaact ctaaggttca 180

attcagcaag	gagactaaca	acctcaccaa	cgttcactct	tacaagcact	ctggtcttgc	240
aaacaaaaag	actgtgacca	tccaggccgc	tgacaaggac	caagctgttg	tgctcgccac	300
caccaagacc	aagaagcaga	acaagcctaa	gctctctgtc	aacaagtcta	tcctcaagaa	360
ggaattcccc	aggatgtcaa	aggctgttgc	taaccagggt	gtggacaact	actacaggcc	420
ggacttgaag	aaagctgcac	ttgctagact	cagcgccatc	agcaaaggtc	tcagggttgc	480
caagtccggt	gccaaagcaa	gaaacagaca	agcttaagct	tctctcttca	caatctgttt	540
tttttgaagt	aaaagatttt	gtytgaacag	gttttattta	agttgttgtc	ttgaagtttg	600
aaccataatg	ctattctcct	tttctattat	ccttattata	aaggagttag	aagtttatct	660
tgttatgctt	g					

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..143
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Met	Ala	Thr	Val	Pro	Gly	Gln	Leu	Ile	Trp	Glu	Ile	Val	Lys	Asn	Asn	
1			5						10					15		
Asn	Cys	Phe	Leu	Val	Lys	Gln	Phe	Gly	Arg	Gly	Asn	Ser	Lys	Val	Gln	
			20				25						30			
Phe	Ser	Lys	Glu	Thr	Asn	Asn	Leu	Thr	Asn	Val	His	Ser	Tyr	Lys	His	
			35				40					45				
Ser	Gly	Leu	Ala	Asn	Lys	Lys	Thr	Val	Thr	Ile	Gln	Ala	Ala	Asp	Lys	
			50				55				60					
Asp	Gln	Ala	Val	Val	Leu	Ala	Thr	Thr	Lys	Thr	Lys	Lys	Gln	Asn	Lys	
			65			70				75				80		
Pro	Lys	Leu	Ser	Val	Asn	Lys	Ser	Ile	Leu	Lys	Lys	Glu	Phe	Pro	Arg	
			85					90					95			
Met	Ser	Lys	Ala	Val	Ala	Asn	Gln	Val	Val	Asp	Asn	Tyr	Tyr	Arg	Pro	
			100				105						110			
Asp	Leu	Lys	Lys	Ala	Ala	Leu	Ala	Arg	Leu	Ser	Ala	Ile	Ser	Lys	Gly	
			115				120						125			
Leu	Arg	Val	Ala	Lys	Ser	Gly	Ala	Lys	Gln	Arg	Asn	Arg	Gln	Ala		
			130			135					140					

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1065 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1065
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

taatttcgac	ttttgtagat	ctttttctgc	tctctctctc	tctctctctc	60
tctctctctc	ttgtattatt	tctatctccc	cgcgcgtcga	aagagaagac	120
aacctttgaa	atgtcgactg	gattagatat	gtctctcgac	gacatgatcg	180
taagtctcgt	ggttgagccg	gccccgctcg	tggaaccgga	tccggatccg	240
gactcgccgc	aacaacccta	atcgggaatc	aaccgatctc	gctccatacc	300
ggcgccggag	tccacctggg	gtcacgacat	gttctccgat	agatctgaag	360
gggacgttcc	tccgcccggaa	tcgaaactgg	aaccaagctc	tacatttcca	420
cgggtccatg	aacgaagaca	tcaaggaact	gtttggctga	aggttgagg	480
tacacagttc	attttgatag	aagtggaaga	tcaaggagaa	ctgctgaagt	540
cggcgtggcg	atgcactcgc	agctgtgaag	aagtataatg	atgttcacst	600
				ggatggaaaa	

ccccatgaaga tagagattgt gggcactaat cttcaaaactg ctgcagcccc gtctggtaga	660
cctgcgaatg gaaactccaa tgggtgctcca tggagaggag gacaaggagg aggaaggtcaa	720
caacgagggt gtggacgagg aggcggtggc cgaggtggtg gtggtcgtgg taggcgtctc	780
ggtaagggcc ctgcagagaa gatttctgcg gaagatcttg atcgcgatct tgataagtac	840
cattctggag atatggagac aaactaagga acgtgactga tcttctcaa ccggtagggg	900
tttttaggagg aagagaatcg agaaaaatgt tgcacagagg tttaccactt agcgcccttt	960
tggctgtgtt gtctatttgt ttcattagaa tgactttaca gaattgagaa tatgtgttat	1020
ttaaagtgtt tgtctatctt aataccotca agtgaaaggg agagg	

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..152

(D) OTHER INFORMATION: / Ceres Seq. ID 1498130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Asn	Phe	Asp	Phe	Cys	Arg	Ser	Phe	Ser	Ala	Leu	Ser	Leu	Ser		
1				5					10			15			
Leu	Ser	Leu	Ser	Leu	Ser	Leu	Leu	Tyr	Tyr	Phe	Tyr	Leu	Pro	Arg	Arg
				20				25				30			
Arg	Lys	Arg	Asn	Val	Asp	Arg	Arg	Thr	Phe	Glu	Met	Ser	Thr	Gly	Leu
				35				40				45			
Asp	Met	Ser	Leu	Asp	Asp	Met	Ile	Ala	Lys	Asn	Arg	Lys	Ser	Arg	Gly
				50				55				60			
Gly	Ala	Gly	Pro	Ala	Arg	Gly	Thr	Gly	Ser	Gly	Ser	Gly	Pro	Gly	Pro
				65				70				75			80
Thr	Arg	Arg	Asn	Asn	Pro	Asn	Arg	Lys	Ser	Thr	Arg	Ser	Ala	Pro	Tyr
				85				90				95			
Gln	Ser	Ala	Lys	Ala	Pro	Glu	Ser	Thr	Trp	Gly	His	Asp	Met	Phe	Ser
				100				105				110			
Asp	Arg	Ser	Glu	Asp	His	Arg	Ser	Gly	Arg	Ser	Ser	Ala	Gly	Ile	Glu
				115				120				125			
Thr	Gly	Thr	Lys	Leu	Tyr	Ile	Ser	Asn	Leu	Asp	Tyr	Gly	Val	Met	Asn
				130				135				140			
Glu	Asp	Ile	Lys	Glu	Leu	Phe	Gly								
				145				150							

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..109

(D) OTHER INFORMATION: / Ceres Seq. ID 1498131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

Met	Ser	Thr	Gly	Leu	Asp	Met	Ser	Leu	Asp	Asp	Met	Ile	Ala	Lys	Asn
1				5				10				15			
Arg	Lys	Ser	Arg	Gly	Gly	Ala	Gly	Pro	Ala	Arg	Gly	Thr	Gly	Ser	Gly
				20				25				30			
Ser	Gly	Pro	Gly	Pro	Thr	Arg	Arg	Asn	Asn	Pro	Asn	Arg	Lys	Ser	Thr
				35				40				45			
Arg	Ser	Ala	Pro	Tyr	Gln	Ser	Ala	Lys	Ala	Pro	Glu	Ser	Thr	Trp	Gly
				50				55				60			
His	Asp	Met	Phe	Ser	Asp	Arg	Ser	Glu	Asp	His	Arg	Ser	Gly	Arg	Ser

65 70 75 80
Ser Ala Gly Ile Glu Thr Gly Thr Lys Leu Tyr Ile Ser Asn Leu Asp
85 90 95
Tyr Gly Val Met Asn Glu Asp Ile Lys Glu Leu Phe Gly
100 105

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..103
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

Met Ser Leu Asp Asp Met Ile Ala Lys Asn Arg Lys Ser Arg Gly Gly
1 5 10 15
Ala Gly Pro Ala Arg Gly Thr Gly Ser Gly Ser Gly Pro Gly Pro Thr
20 25 30
Arg Arg Asn Asn Pro Asn Arg Lys Ser Thr Arg Ser Ala Pro Tyr Gln
35 40 45
Ser Ala Lys Ala Pro Glu Ser Thr Trp Gly His Asp Met Phe Ser Asp
50 55 60
Arg Ser Glu Asp His Arg Ser Gly Arg Ser Ser Ala Gly Ile Glu Thr
65 70 75 80
Gly Thr Lys Leu Tyr Ile Ser Asn Leu Asp Tyr Gly Val Met Asn Glu
85 90 95
Asp Ile Lys Glu Leu Phe Gly
100

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1247
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

ctcttgccttc	tcttcaactca	caatctcaca	gcaaacgcctc	tcggttgctag	aggaatcaaaa	60
caatggtgtgt	tgtgaagtcc	accaagtcca	atgcttacct	caagagggtac	caagtgaagt	120
tcaggagaga	aagagatgga	aagactgact	acaggggcaag	gatccgtctt	atcaaccaag	180
acaagaaacaa	gtacaataca	cctaagtatc	gtttgttgtt	coggtttaac	aacaaagaca	240
tagtggcaca	gattgtatct	gcaagcattg	ctgggtgacat	tgtttaaagct	tctgcttacg	300
cacatgaact	gcctcagtat	ggtctcactg	ttgggtcttac	aaactatgct	gcagcttact	360
gtactggcct	tcttttggct	cgccgtgttt	taaaagatgtt	ggaaatggat	gacgagtatg	420
agggaaacgt	tgaggccact	ggagaggact	tttccgttga	gccaaactgat	tcaggagagac	480
ctttccgtgc	tcttcttgat	gttggaactta	tcaggagacc	aacaggaaaac	cgtgtgttccg	540
gtgctcttaa	gggtgctttg	gatggtgtgc	ttgatatccc	tcacagtgac	aagagatttg	600
ctgggtttcca	caaggagaac	aagcaacttg	atgctgaaat	ccacagggaac	tacatctatg	660
gtggccatgt	ctcaaaactac	atgaagctgt	tgggagaaga	tgagccagag	aagtacaaa	720
ctcaacttcag	tgctttacatc	aagaaaggag	ttgaagctga	gagcattgag	gagttgtaca	780
agaaggttca	cgcagctatt	ctgtctgrcc	ccaacccaag	gaaaaccgtg	aaacctgtct	840
ccaagcaaca	caagaggtta	aacttgaaga	aacttactta	cgaggagagag	aagaacaagt	900
tgatcgagag	agtcaggcat	tgaatggagc	agggtgtgat	gatgatgatg	aggacgatga	960
asagtaaact	agtcaagcct	tctttatctc	atgcctcttg	tattttttta	tcttttgagc	1020
ttaatgcctc	aaattttctg	ttttcagact	aaaaactaca	gcttttttgt	tcacatttta	1080

attgtgttcg aggattttga tattgaggat acattttctt tgaagtatca ttattcttatt 1140
attacctcca tcataatttt caagaatttg tatgacaata gtttgatgac ttgattttat 1200
ctgtagtgttg ctattgttaa atgtaagaac tgttgactt catctat

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 286 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..286

(D) OTHER INFORMATION: / Ceres Seq. ID 1498134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Met	Val	Phe	Val	Lys	Ser	Thr	Lys	Ser	Asn	Ala	Tyr	Phe	Lys	Arg	Tyr
1			5						10					15	
Gln	Val	Lys	Phe	Arg	Arg	Arg	Arg	Asp	Gly	Lys	Thr	Asp	Tyr	Arg	Ala
			20					25					30		
Arg	Ile	Arg	Leu	Ile	Asn	Gln	Asp	Lys	Asn	Lys	Tyr	Asn	Thr	Pro	Lys
			35				40					45			
Tyr	Arg	Phe	Val	Val	Arg	Phe	Thr	Asn	Lys	Asp	Ile	Val	Ala	Gln	Ile
			50				55				60				
Val	Ser	Ala	Ser	Ile	Ala	Gly	Asp	Ile	Val	Lys	Ala	Ser	Ala	Tyr	Ala
65					70				75					80	
His	Glu	Leu	Pro	Glu	Tyr	Gly	Leu	Thr	Val	Gly	Leu	Thr	Asn	Tyr	Ala
					85				90				95		
Ala	Ala	Tyr	Cys	Thr	Gly	Leu	Leu	Leu	Ala	Arg	Arg	Val	Leu	Lys	Met
			100					105					110		
Leu	Glu	Met	Asp	Asp	Glu	Tyr	Glu	Gly	Asn	Val	Glu	Ala	Thr	Gly	Glu
			115				120					125			
Asp	Phe	Ser	Val	Glu	Pro	Thr	Asp	Ser	Arg	Arg	Pro	Phe	Arg	Ala	Leu
			130			135					140				
Leu	Asp	Val	Gly	Leu	Ile	Arg	Thr	Thr	Thr	Gly	Asn	Arg	Val	Phe	Gly
145					150					155				160	
Ala	Leu	Lys	Gly	Ala	Leu	Asp	Gly	Gly	Leu	Asp	Ile	Pro	His	Ser	Asp
			165						170					175	
Lys	Arg	Phe	Ala	Gly	Phe	His	Lys	Glu	Asn	Lys	Gln	Leu	Asp	Ala	Glu
			180				185						190		
Ile	His	Arg	Asn	Tyr	Ile	Tyr	Gly	Gly	His	Val	Ser	Asn	Tyr	Met	Lys
		195				200						205			
Leu	Leu	Gly	Glu	Asp	Glu	Pro	Glu	Lys	Leu	Gln	Thr	His	Phe	Ser	Ala
			210			215					220				
Tyr	Ile	Lys	Lys	Gly	Val	Glu	Ala	Glu	Ser	Ile	Glu	Glu	Leu	Tyr	Lys
225					230					235				240	
Lys	Val	His	Ala	Ala	Ile	Arg	Ala	Xaa	Pro	Asn	Xaa	Arg	Lys	Thr	Val
			245						250				255		
Lys	Pro	Ala	Pro	Lys	Gln	His	Lys	Arg	Tyr	Asn	Leu	Lys	Lys	Leu	Thr
			260					265					270		
Tyr	Glu	Glu	Arg	Lys	Asn	Lys	Leu	Ile	Glu	Arg	Val	Arg	His		
			275			280						285			

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1498135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

Met Leu Glu Met Asp Asp Glu Tyr Glu Gly Asn Val Glu Ala Thr Gly
1 5 10 15
Glu Asp Phe Ser Val Glu Pro Thr Asp Ser Arg Arg Pro Phe Arg Ala
20 25 30
Leu Leu Asp Val Gly Leu Ile Arg Thr Thr Thr Gly Asn Arg Val Phe
35 40 45
Gly Ala Leu Lys Gly Ala Leu Asp Gly Gly Leu Asp Ile Pro His Ser
50 55 60
Asp Lys Arg Phe Ala Gly Phe His Lys Glu Asn Lys Gln Leu Asp Ala
65 70 75 80
Glu Ile His Arg Asn Tyr Ile Tyr Gly Gly His Val Ser Asn Tyr Met
85 90 95
Lys Leu Leu Gly Glu Asp Glu Pro Glu Lys Leu Gln Thr His Phe Ser
100 105 110
Ala Tyr Ile Lys Lys Gly Val Glu Ala Glu Ser Ile Glu Glu Leu Tyr
115 120 125
Lys Lys Val His Ala Ala Ile Arg Ala Xaa Pro Asn Xaa Arg Lys Thr
130 135 140
Val Lys Pro Ala Pro Lys Gln His Lys Arg Tyr Asn Leu Lys Lys Leu
145 150 155 160
Thr Tyr Glu Glu Arg Lys Asn Lys Leu Ile Glu Arg Val Arg His
165 170 175

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 172 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..172

(D) OTHER INFORMATION: / Ceres Seq. ID 1498136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

Met Asp Asp Glu Tyr Glu Gly Asn Val Glu Ala Thr Gly Glu Asp Phe
1 5 10 15
Ser Val Glu Pro Thr Asp Ser Arg Arg Pro Phe Arg Ala Leu Leu Asp
20 25 30
Val Gly Leu Ile Arg Thr Thr Thr Gly Asn Arg Val Phe Gly Ala Leu
35 40 45
Lys Gly Ala Leu Asp Gly Gly Leu Asp Ile Pro His Ser Asp Lys Arg
50 55 60
Phe Ala Gly Phe His Lys Glu Asn Lys Gln Leu Asp Ala Glu Ile His
65 70 75 80
Arg Asn Tyr Ile Tyr Gly Gly His Val Ser Asn Tyr Met Lys Leu Leu
85 90 95
Gly Glu Asp Glu Pro Glu Lys Leu Thr His Phe Ser Ala Tyr Ile
100 105 110
Lys Lys Gly Val Glu Ala Glu Ser Ile Glu Glu Leu Tyr Lys Lys Val
115 120 125
His Ala Ala Ile Arg Ala Xaa Pro Asn Xaa Arg Lys Thr Val Lys Pro
130 135 140
Ala Pro Lys Gln His Lys Arg Tyr Asn Leu Lys Lys Leu Thr Tyr Glu
145 150 155 160
Glu Arg Lys Asn Lys Leu Ile Glu Arg Val Arg His
165 170

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1186 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1186
(D) OTHER INFORMATION: / Ceres Seq. ID 1498137
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

aaaaaattcg	ctattcaatt	cccttagtaa	gcttcacttt	tcacacttct	ctcactttct	60
ggtcagaaac	tttgtggatc	tagaagaaca	cacaaatcac	aagagtgtgaa	aaagatgaac	120
gacttgatga	cgaaatcggt	tatgagttac	gttgacttga	aaaaagcagc	gatgaaggat	180
atgggaagcag	gacctgactt	tgatctttgag	atggcttcga	cgaagcagag	caagatggat	240
gagaatctgt	catctttctt	acaagaagca	gagtatgtga	aagcagagat	gggttttatt	300
agtagacact	ggctcggatt	gaavcragta	ccatgaagag	agtaaagggtg	ttcaacaaggc	360
agagtctgtg	aagtctcttc	gtaacaagat	ctctaakgag	attgtgtctg	gtttgaggaa	420
ggcgaatacg	attaagtcga	agctggaaga	gatggataaa	gcaaaccaagg	agattaaaaag	480
gctctctggg	actocggttt	acaggagcag	aacgcgtgtg	actaacgggc	tgagggaagaa	540
acttaaggrra	gtgmtgatgg	agtttcaggg	gctgaggcaa	aaagatgatga	gtgagtacaa	600
ggagactggt	gagagaaggt	acttcaactgt	cactggagaa	catgctaagt	atgagatgat	660
tgagaagact	attactgata	acgctggagg	tgaagagttt	ctcacgcgag	caattcaagga	720
acatggtaaa	ggaaagggtct	tgaaactgtg	ggttgagatt	caagataggt	acgatgcagc	780
aaaggagatt	gagaagagtc	tggttgagct	tcaccaagtg	ttcttgata	tggtctgtgat	840
ggttgagatt	caaggtgaac	agatggacga	gatcgagcat	catgttgatta	atgcgagcca	900
ttacgtggct	gatggagcta	atgagctgaa	gactgcgaaag	agtcacacga	gaacacagag	960
aaaatggtat	tgcatctgta	tcatttgtct	gcttttgatc	attctcattg	ttgttatccc	1020
catcatacc	agtttcagct	cttcttgaga	tactgctgat	gttcaactct	ttgtttttgt	1080
ttgcctcttc	tttgtaccaa	tggaatgtct	aatccttttg	tgttctcttaa	ggatgtctta	1140
atccctctgt	gtcttgtatc	caatttcaat	gaaatggtag	atgttt		

(2) INFORMATION FOR SEQ ID NO:212:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 198 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..198
(D) OTHER INFORMATION: / Ceres Seq. ID 1498138
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

Met	Asp	Lys	Ala	Asn	Lys	Glu	Ile	Lys	Arg	Leu	Ser	Gly	Thr	Pro	Val
1			5					10					15		
Tyr	Arg	Ser	Arg	Thr	Ala	Val	Thr	Asn	Gly	Leu	Arg	Lys	Lys	Leu	Lys
			20				25					30			
Xaa	Val	Xaa	Met	Glu	Phe	Gln	Gly	Leu	Arg	Gln	Lys	Met	Met	Ser	Glu
			35			40					45				
Tyr	Lys	Glu	Thr	Val	Glu	Arg	Arg	Tyr	Phe	Thr	Val	Thr	Gly	Glu	His
			50			55					60				
Ala	Asn	Asp	Glu	Met	Ile	Glu	Lys	Ile	Ile	Thr	Asp	Asn	Ala	Gly	Gly
			65			70				75				80	
Glu	Glu	Phe	Leu	Thr	Arg	Ala	Ile	Gln	Glu	His	Gly	Lys	Gly	Lys	Val
			85						90				95		
Leu	Glu	Thr	Val	Val	Glu	Ile	Gln	Asp	Arg	Tyr	Asp	Ala	Ala	Lys	Glu
			100			105						110			
Ile	Glu	Lys	Ser	Leu	Leu	Glu	Leu	His	Gln	Val	Phe	Leu	Asp	Met	Ala
			115			120					125				
Val	Met	Val	Glu	Ser	Gln	Gly	Glu	Gln	Met	Asp	Glu	Ile	Glu	His	His
			130			135					140				
Val	Ile	Asn	Ala	Ser	His	Tyr	Val	Ala	Asp	Gly	Ala	Asn	Glu	Leu	Lys
			145			150				155				160	

Thr Ala Lys Ser His Gln Arg Asn Ser Arg Lys Trp Met Cys Ile Gly
 165 170 175
Ile Ile Val Leu Leu Leu Ile Ile Leu Ile Val Val Ile Pro Ile Ile
 180 185 190
Thr Ser Phe Ser Ser Ser
 195

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..163

(D) OTHER INFORMATION: / Ceres Seq. ID 1498139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

Met Glu Phe Gln Gly Leu Arg Gln Lys Met Met Ser Glu Tyr Lys Glu
1 5 10 15
Thr Val Glu Arg Arg Tyr Phe Thr Val Thr Gly Glu His Ala Asn Asp
 20 25 30
Glu Met Ile Glu Lys Ile Ile Thr Asp Asn Ala Gly Gly Glu Glu Phe
 35 40 45
Leu Thr Arg Ala Ile Gln Glu His Gly Lys Gly Lys Val Leu Glu Thr
 50 55 60
Val Val Glu Ile Gln Asp Arg Tyr Asp Ala Ala Lys Glu Ile Glu Lys
65 70 75 80
Ser Leu Leu Glu Leu His Gln Val Phe Leu Asp Met Ala Val Met Val
 85 90 95
Glu Ser Gln Gly Glu Gln Met Asp Glu Ile Glu His His Val Ile Asn
 100 105 110
Ala Ser His Tyr Val Ala Asp Gly Ala Asn Glu Leu Lys Thr Ala Lys
 115 120 125
Ser His Gln Arg Asn Ser Arg Lys Trp Met Cys Ile Gly Ile Ile Val
130 135 140
Leu Leu Leu Ile Ile Leu Ile Val Val Ile Pro Ile Ile Thr Ser Phe
145 150 155 160
Ser Ser Ser

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1498140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Met Met Ser Glu Tyr Lys Glu Thr Val Glu Arg Arg Tyr Phe Thr Val
1 5 10 15
Thr Gly Glu His Ala Asn Asp Glu Met Ile Glu Lys Ile Ile Thr Asp
 20 25 30
Asn Ala Gly Gly Glu Glu Phe Leu Thr Arg Ala Ile Gln Glu His Gly
 35 40 45
Lys Gly Lys Val Leu Glu Thr Val Val Glu Ile Gln Asp Arg Tyr Asp
50 55 60
Ala Ala Lys Glu Ile Glu Lys Ser Leu Leu Glu Leu His Gln Val Phe

65				70					75					80
Leu	Asp	Met	Ala	Val	Met	Val	Glu	Ser	Gln	Gly	Glu	Gln	Met	Asp
				85					90					95
Ile	Glu	His	His	Val	Ile	Asn	Ala	Ser	His	Tyr	Val	Ala	Asp	Gly
				100					105					110
Asn	Glu	Leu	Lys	Thr	Ala	Lys	Ser	His	Gln	Arg	Asn	Ser	Arg	Lys
				115					120					125
Met	Cys	Ile	Gly	Ile	Ile	Val	Leu	Leu	Leu	Ile	Ile	Leu	Ile	Val
				130					135					140
Ile	Pro	Ile	Ile	Thr	Ser	Phe	Ser	Ser	Ser					
				145					150					

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 768 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..768
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

acc	aaa	aat	ctc	ttc	ttc	ttc	taa	gga	acca	aacc	gaga	aat	ctc	ta	60
tg	tta	ctag	a	aact	actag	t	acc	acga	agaa	tgg	agac	caa	at	acga	120
tt	atg	gcg	gga	gaag	atg	gtt	gaag	agt	tgt	atc	aga	g	gtt	atc	180
tg	ctt	gcg	gga	tcc	agag	aga	cat	ctc	atca	cag	ctg	agtc	tct	aa	240
tac	ttg	gga	at	tga	aggt	atg	acga	agaa	atg	ctc	aa	g	aat	ggt	300
tcg	atg	ggag	a	tgg	kgct	cct	aac	caaac	ccg	aatt	ctg	cgt	tct	cat	360
ctg	agat	gat	gga	agac	gc	g	raac	ttg	gk	tgg	aat	gg	gtg	gtc	420
aag	aaaa	acct	at	att	ctat	ca	gag	atct	tga	gct	taac	aaa	gg	acg	480
gtt	ccac	aaa	cag	ag	gaag	t	ata	atg	ca	c	gtt	ctt	cc	aa	540
att	tc	atg	gg	ac	ctt	ctt	ca	ga	gat	ctc	t	ttc	ctt	ctt	600
gata	aaat	ga	t	tc	atata	ag	gtt	ga	at	tt	gtg	at	ttt	gt	660
tg	caat	ggag	tata	at	gaat	gtata	at	tcg	t	ctt	ttt	ttt	t	taa	720
tg	ctata	at	aatt	gc	ct	gatt	att	att	a	at	ca	at	tt	t	

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..200
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

Gln	Asn	Leu	Phe	Ser	Leu	Phe	His	Cys	Leu	Pro	Leu	Met	Glu	Pro	Thr
1				5				10					15		
Glu	Lys	Ser	Met	Leu	Leu	Glu	Thr	Ser	Thr	Thr	Lys	Met	Glu	Thr	
				20				25					30		
Lys	Tyr	Glu	Asp	Met	Leu	Pro	Val	Met	Ala	Glu	Lys	Met	Asp	Val	Glu
				35				40					45		
Glu	Phe	Val	Ser	Glu	Leu	Cys	Lys	Gly	Phe	Ser	Leu	Leu	Ala	Asp	Pro
				50				55					60		
Glu	Arg	His	Leu	Ile	Thr	Ala	Glu	Ser	Leu	Arg	Arg	Asn	Ser	Gly	Ile
				65				70					75		80
Leu	Gly	Ile	Glu	Gly	Met	Ser	Lys	Glu	Asp	Ala	Gln	Gly	Met	Val	Arg
				85				90					95		
Glu	Gly	Asp	Xaa	Asp	Gly	Asp	Xaa	Ala	Leu	Asn	Gln	Thr	Glu	Phe	Cys

100 105 110
Val Leu Met Val Arg Leu Ser Pro Glu Met Met Glu Asp Ala Xaa Thr
115 120 125
Trp Xaa Glu Trp Gly Trp Val Met Gly Ser Phe Gln Glu Asn Leu Tyr
130 135 140
Ser Ser Glu Ile Leu Ser Leu Thr Lys Asp Glu Ala Lys Ser Ile Gly
145 150 155 160
Ser Gln Asn Arg Gly Ser Ile Met His Val Phe Phe Lys Leu Arg Ser
165 170 175
Gln Ile Arg Asn Phe Met Gly Pro Ser Ser Glu Asp Ser Leu Pro Leu
180 185 190
Ser Cys Lys Tyr Lys Arg Gln Arg
195 200

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 188 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..188

(D) OTHER INFORMATION: / Ceres Seq. ID 1498143

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

Met Glu Pro Thr Glu Lys Ser Met Leu Leu Glu Thr Thr Ser Thr Thr
1 5 10 15
Lys Met Glu Thr Lys Tyr Glu Asp Met Leu Pro Val Met Ala Glu Lys
20 25 30
Met Asp Val Glu Glu Phe Val Ser Glu Leu Cys Lys Gly Phe Ser Leu
35 40 45
Leu Ala Asp Pro Glu Arg His Leu Ile Thr Ala Glu Ser Leu Arg Arg
50 55 60
Asn Ser Gly Ile Leu Gly Ile Glu Gly Met Ser Lys Glu Asp Ala Gln
65 70 75 80
Gly Met Val Arg Glu Gly Asp Xaa Asp Gly Asp Xaa Ala Leu Asn Gln
85 90 95
Thr Glu Phe Cys Val Leu Met Val Arg Leu Ser Pro Glu Met Met Glu
100 105 110
Asp Ala Xaa Thr Trp Xaa Glu Trp Gly Trp Val Met Gly Ser Phe Gln
115 120 125
Glu Asn Leu Tyr Ser Ser Glu Ile Leu Ser Leu Thr Lys Asp Glu Ala
130 135 140
Lys Ser Ile Gly Ser Gln Asn Arg Gly Ser Ile Met His Val Phe Phe
145 150 155 160
Lys Leu Arg Ser Gln Ile Arg Asn Phe Met Gly Pro Ser Ser Glu Asp
165 170 175
Ser Leu Pro Leu Ser Cys Lys Tyr Lys Arg Gln Arg
180 185

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 181 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..181

(D) OTHER INFORMATION: / Ceres Seq. ID 1498144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

```

Met Leu Leu Glu Thr Thr Ser Thr Thr Lys Met Glu Thr Lys Tyr Glu
1      5      10      15
Asp Met Leu Pro Val Met Ala Glu Lys Met Asp Val Glu Glu Phe Val
20      25      30
Ser Glu Leu Cys Lys Gly Phe Ser Leu Ala Asp Pro Glu Arg His
35      40      45
Leu Ile Thr Ala Glu Ser Leu Arg Arg Asn Ser Gly Ile Leu Gly Ile
50      55      60
Glu Gly Met Ser Lys Glu Asp Ala Gln Gly Met Val Arg Glu Gly Asp
65      70      75      80
Xaa Asp Gly Asp Xaa Ala Leu Asn Gln Thr Glu Phe Cys Val Leu Met
85      90      95
Val Arg Leu Ser Pro Glu Met Met Glu Asp Ala Xaa Thr Trp Xaa Glu
100      105      110
Trp Gly Trp Val Met Gly Ser Phe Gln Glu Asn Leu Tyr Ser Ser Glu
115      120      125
Ile Leu Ser Leu Thr Lys Asp Glu Ala Lys Ser Ile Gly Ser Gln Asn
130      135      140
Arg Gly Ser Ile Met His Val Phe Phe Lys Leu Arg Ser Gln Ile Arg
145      150      155      160
Asn Phe Met Gly Pro Ser Ser Glu Asp Ser Leu Pro Leu Ser Cys Lys
165      170      175
Tyr Lys Arg Gln Arg
180

```

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1440
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

```

atttcgagat cctctcggtt tggctgttct tctgtgaacga tcccatctat tgtttctcgc 60
tggtctcaga ttcgactaac ttggatatct ccgatactga agaagcctcc ttctctcttt 120
tccgcctcttc cccgatgccga tccgataagat ctccaaagat gatgctagtg aagagaaggg 180
agaacgtgctc aggatggcat catttgttgg tgcgaatggct atcagtgatc tggtaagtc 240
tacttttaggg ccacaaggcca tggataaaat cttaaatctc actggtagag gtcactgcgtt 300
cactgttaact aacgatgggt ctactattct caagtcaact cacatagaca accctgcagc 360
taaaagtctct gttagacatct cgaagtttca agatgatgag gttggtgatg gaactacctc 420
tgtttgtgtc ttggccggcg agctctctgag ggaagcagaa aagcttctgg ctctcaagat 480
tcaccctatg accatcatag caggtttacag aatggcttcg gaatgtgctc gtaagtcttt 540
actgaaaaga gtcattgata acaaggacaa tgcagagaag tttaggtcag acttgttgaa 600
gattgcgatg actactttat gttccaaaat tctctcacag gacaaggaaac attttgcaga 660
aatggccgtg gatgctgttt tcaggctaaa ggggaagcaca aacttggaa gctattcagat 720
catcaaaaaa cctggagggtt cctctgaagga ttctgttttg gatgaagggt ttattcttga 780
caagaaaaaa ggaattgggc agcctaagcg catagagaat gcaaatatct tagtagctaa 840
tactgctatg gataccgata aagtgaagat ttacgttgca cgtgtccgtg tggattccat 900
gaccaaagggt cctgagattg aaggtcaaca gtttgacctc aacgcctcta agcttgcagt 960
cgagcgtgtc ttcaaaaggca ttgttcggcat gaccactgac cctgcgcgtg tccaagagct 1020
cgaagtttaa cctcagaaga tcttggatgt ctacagaggt aggcctgccaa atcttgagtt 1080
cttgctgtgt gattccttca ctcttctgta tcttcaaccac ctcccagcca tcattacttt 1140
gttggtgact gactccaagg tctcctttga ctctgcacct aaggttgacg aactgaattaa 1200
gaagatctct gccaggcctg ctctgggctaa gggtattgac ctccagaagc agtagtgacc 1260
ctctctcttt ctctactctt ttctctttcc ttgtgcccac ataaacgagt ccagtgattt 1320
tcttttctgt gcttaagtac ttgtgttttc agtattattt atgtcatcat catctctctc 1380
ttttgtgtta ttgttggtt cattcacatt tgtgcaatta aaaaccagag ttttaacgcc 1440

```

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..353

(D) OTHER INFORMATION: / Ceres Seq. ID 1498146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

Met	Pro	Ile	Asp	Lys	Ile	Phe	Lys	Asp	Asp	Ala	Ser	Glu	Glu	Lys	Gly	
1			5					10					15			
Glu	Arg	Ala	Arg	Met	Ala	Ser	Phe	Val	Gly	Ala	Met	Ala	Ile	Ser	Asp	
			20					25					30			
Leu	Val	Lys	Ser	Thr	Leu	Gly	Pro	Lys	Gly	Met	Asp	Lys	Ile	Leu	Gln	
			35				40					45				
Ser	Thr	Gly	Arg	Gly	His	Ala	Val	Thr	Val	Thr	Asn	Asp	Gly	Ala	Thr	
			50			55					60					
Ile	Leu	Lys	Ser	Leu	His	Ile	Asp	Asn	Pro	Ala	Ala	Lys	Val	Leu	Val	
						70				75				80		
Asp	Ile	Ser	Lys	Val	Gln	Asp	Asp	Glu	Val	Gly	Asp	Gly	Thr	Thr	Ser	
				85					90					95		
Val	Val	Val	Leu	Ala	Gly	Glu	Leu	Leu	Arg	Glu	Ala	Glu	Lys	Leu	Val	
			100					105					110			
Ala	Ser	Lys	Ile	His	Pro	Met	Thr	Ile	Ile	Ala	Gly	Tyr	Arg	Met	Ala	
			115				120					125				
Ser	Glu	Cys	Ala	Arg	Asn	Ala	Leu	Leu	Lys	Arg	Val	Ile	Asp	Asn	Lys	
			130			135					140					
Asp	Asn	Ala	Glu	Lys	Phe	Arg	Ser	Asp	Leu	Leu	Lys	Ile	Ala	Met	Thr	
			145			150					155				160	
Thr	Leu	Cys	Ser	Lys	Ile	Leu	Ser	Gln	Asp	Lys	Glu	His	Phe	Ala	Glu	
				165					170					175		
Met	Ala	Val	Asp	Ala	Val	Phe	Arg	Leu	Lys	Gly	Ser	Thr	Asn	Leu	Glu	
			180					185						190		
Ala	Ile	Gln	Ile	Ile	Lys	Lys	Pro	Gly	Gly	Ser	Leu	Lys	Asp	Ser	Phe	
			195				200					205				
Leu	Asp	Glu	Gly	Phe	Ile	Leu	Asp	Lys	Lys	Ile	Gly	Ile	Gly	Gln	Pro	
			210				215					220				
Lys	Arg	Ile	Glu	Asn	Ala	Asn	Ile	Leu	Val	Ala	Asn	Thr	Ala	Met	Asp	
			225			230					235				240	
Thr	Asp	Lys	Val	Lys	Ile	Tyr	Gly	Ala	Arg	Val	Arg	Val	Asp	Ser	Met	
				245					250					255		
Thr	Lys	Val	Ala	Glu	Ile	Glu	Gly	Gln	Gln	Phe	Asp	Pro	Asn	Ala	Ser	
			260				265							270		
Lys	Leu	Ala	Phe	Glu	Arg	Val	Phe	Lys	Gly	Met	Phe	Gly	Met	Thr	Thr	
			275				280					285				
Asp	Pro	Ala	Ala	Val	Gln	Glu	Leu	Glu	Gly	Lys	Leu	Gln	Lys	Val	Leu	
			290			295					300					
Asp	Val	Tyr	Glu	Ala	Arg	Leu	Ala	Lys	Ser	Glu	Phe	Leu	Ala	Gly	Asp	
			305			310				315					320	
Ser	Phe	Thr	Leu	Ala	Asp	Leu	His	His	Leu	Pro	Ala	Ile	His	Tyr	Leu	
				325					330					335		
Leu	Gly	Thr	Asp	Ser	Lys	Val	Leu	Phe	Asp	Ser	Arg	Pro	Lys	Val	Ser	
			340					345						350		

Glu

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..333
(D) OTHER INFORMATION: / Ceres Seq. ID 1498147

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

Met	Ala	Ser	Phe	Val	Gly	Ala	Met	Ala	Ile	Ser	Asp	Leu	Val	Lys	Ser
1				5					10					15	
Thr	Leu	Gly	Pro	Lys	Gly	Met	Asp	Lys	Ile	Leu	Gln	Ser	Thr	Gly	Arg
			20					25				30			
Gly	His	Ala	Val	Thr	Val	Thr	Asn	Asp	Gly	Ala	Thr	Ile	Leu	Lys	Ser
		35					40					45			
Leu	His	Ile	Asp	Asn	Pro	Ala	Ala	Lys	Val	Leu	Val	Asp	Ile	Ser	Lys
	50					55					60				
Val	Gln	Asp	Asp	Glu	Val	Gly	Asp	Gly	Thr	Thr	Ser	Val	Val	Val	Leu
	65				70				75					80	
Ala	Gly	Glu	Leu	Leu	Arg	Glu	Ala	Glu	Lys	Leu	Val	Ala	Ser	Lys	Ile
			85						90					95	
His	Pro	Met	Thr	Ile	Ile	Ala	Gly	Tyr	Arg	Met	Ala	Ser	Glu	Cys	Ala
			100					105					110		
Arg	Asn	Ala	Leu	Leu	Lys	Arg	Val	Ile	Asp	Asn	Lys	Asp	Asn	Ala	Glu
		115					120					125			
Lys	Phe	Arg	Ser	Asp	Leu	Leu	Lys	Ile	Ala	Met	Thr	Thr	Leu	Cys	Ser
		130				135						140			
Lys	Ile	Leu	Ser	Gln	Asp	Lys	Glu	His	Phe	Ala	Glu	Met	Ala	Val	Asp
		145			150					155				160	
Ala	Val	Phe	Arg	Leu	Lys	Gly	Ser	Thr	Asn	Leu	Glu	Ala	Ile	Gln	Ile
			165						170				175		
Ile	Lys	Lys	Pro	Gly	Gly	Ser	Leu	Lys	Asp	Ser	Phe	Leu	Asp	Glu	Gly
			180					185					190		
Phe	Ile	Leu	Asp	Lys	Lys	Ile	Gly	Ile	Gly	Gln	Pro	Lys	Arg	Ile	Glu
		195					200					205			
Asn	Ala	Asn	Ile	Leu	Val	Ala	Asn	Thr	Ala	Met	Asp	Thr	Asp	Lys	Val
		210				215					220				
Lys	Ile	Tyr	Gly	Ala	Arg	Val	Arg	Val	Asp	Ser	Met	Thr	Lys	Val	Ala
	225				230					235				240	
Glu	Ile	Glu	Gly	Gln	Gln	Phe	Asp	Pro	Asn	Ala	Ser	Lys	Leu	Ala	Phe
			245						250					255	
Glu	Arg	Val	Phe	Lys	Gly	Met	Phe	Gly	Met	Thr	Thr	Asp	Pro	Ala	Ala
		260						265					270		
Val	Gln	Glu	Leu	Glu	Gly	Lys	Leu	Gln	Lys	Val	Leu	Asp	Val	Tyr	Glu
		275					280					285			
Ala	Arg	Leu	Ala	Lys	Ser	Glu	Phe	Leu	Ala	Gly	Asp	Ser	Phe	Thr	Leu
		290					295					300			
Ala	Asp	Leu	His	His	Leu	Pro	Ala	Ile	His	Tyr	Leu	Leu	Gly	Thr	Asp
		305			310					315				320	
Ser	Lys	Val	Leu	Phe	Asp	Ser	Arg	Pro	Lys	Val	Ser	Glu			
			325						330						

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..326

(D) OTHER INFORMATION: / Ceres Seq. ID 1498148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Met	Ala	Ile	Ser	Asp	Leu	Val	Lys	Ser	Thr	Leu	Gly	Pro	Lys	Gly	Met
1					5					10				15	
Asp	Lys	Ile	Leu	Gln	Ser	Thr	Gly	Arg	Gly	His	Ala	Val	Thr	Val	Thr
			20				25						30		
Asn	Asp	Gly	Ala	Thr	Ile	Leu	Lys	Ser	Leu	His	Ile	Asp	Asn	Pro	Ala
			35				40					45			
Ala	Lys	Val	Leu	Val	Asp	Ile	Ser	Lys	Val	Gln	Asp	Asp	Glu	Val	Gly
			50				55				60				
Asp	Gly	Thr	Thr	Ser	Val	Val	Val	Leu	Ala	Gly	Glu	Leu	Leu	Arg	Glu
65					70					75					80
Ala	Glu	Lys	Leu	Val	Ala	Ser	Lys	Ile	His	Pro	Met	Thr	Ile	Ile	Ala
			85						90				95		
Gly	Tyr	Arg	Met	Ala	Ser	Glu	Cys	Ala	Arg	Asn	Ala	Leu	Leu	Lys	Arg
			100						105				110		
Val	Ile	Asp	Asn	Lys	Asp	Asn	Ala	Glu	Lys	Phe	Arg	Ser	Asp	Leu	Leu
			115				120					125			
Lys	Ile	Ala	Met	Thr	Thr	Leu	Cys	Ser	Lys	Ile	Leu	Ser	Gln	Asp	Lys
			130				135				140				
Glu	His	Phe	Ala	Glu	Met	Ala	Val	Asp	Ala	Val	Phe	Arg	Leu	Lys	Gly
145					150					155					160
Ser	Thr	Asn	Leu	Glu	Ala	Ile	Gln	Ile	Ile	Lys	Lys	Pro	Gly	Gly	Ser
			165						170				175		
Leu	Lys	Asp	Ser	Phe	Leu	Asp	Glu	Gly	Phe	Ile	Leu	Asp	Lys	Lys	Ile
			180					185					190		
Gly	Ile	Gly	Gln	Pro	Lys	Arg	Ile	Glu	Asn	Ala	Asn	Ile	Leu	Val	Ala
			195				200					205			
Asn	Thr	Ala	Met	Asp	Thr	Asp	Lys	Val	Lys	Ile	Tyr	Gly	Ala	Arg	Val
			210				215				220				
Arg	Val	Asp	Ser	Met	Thr	Lys	Val	Ala	Glu	Ile	Glu	Gly	Gln	Gln	Phe
225					230					235					240
Asp	Pro	Asn	Ala	Ser	Lys	Leu	Ala	Phe	Glu	Arg	Val	Phe	Lys	Gly	Met
			245						250				255		
Phe	Gly	Met	Thr	Thr	Asp	Pro	Ala	Ala	Val	Gln	Glu	Leu	Glu	Gly	Lys
			260					265					270		
Leu	Gln	Lys	Val	Leu	Asp	Val	Tyr	Glu	Ala	Arg	Leu	Ala	Lys	Ser	Glu
			275				280					285			
Phe	Leu	Ala	Gly	Asp	Ser	Phe	Thr	Leu	Ala	Asp	Leu	His	His	Leu	Pro
			290				295				300				
Ala	Ile	His	Tyr	Leu	Leu	Gly	Thr	Asp	Ser	Lys	Val	Leu	Phe	Asp	Ser
					310					315					320
Arg	Pro	Lys	Val	Ser	Glu										
					325										

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 964 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..964
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

aatccattcc	tttccaatcc	acgtccaata	aaacaaaccca	aaaaaaaaa	aaaaaaaaa	60
acaaaaaaaa	atgaacactc	caataaaact	cgcctttctc	attctctgca	ttgccttaac	120
cgcacccgca	tttatagtcc	cagcaaaaacg	tgacgcgctt	tcaccacacc	acaaaaaagc	180
cgctcgatgga	attctgcagcg	ttgtgcaaga	caaacgtcta	tgacgacatta	ccttaagaaa	240
cgtcccaagc	gatgatcccg	ccgttttggg	tcgttactta	gccacggcag	cagaagcgctc	300

cggtataaaag	gggtttgaagt	tcctctccgg	aatcaaacca	aaatacaaaag	gaaacgcctt	360
gcgccacaaca	tgcatcaccg	gctgckwgaa	acagctacac	aacgccttgg	acgactttgc	420
agatttttgg	aaagccgcag	gaaaaaatct	aacgagcatg	gctgagatt	mettccatg	480
taagaagaag	atgacttcca	tcttcaacta	ccattccact	tgtctcgatg	acatttacga	540
caagacgttg	cacaaagtgg	tcgaaggagg	gattggcctt	gggaaaagaa	tgagtgggtga	600
gtctgtggat	gtgttcctgt	gaatggggcaa	agtotttaac	actttcaaca	taaagaccaca	660
acttaaacag	aaagataccg	acacgttgct	cccaccactt	ttgtcctttt	actactattg	720
attttattta	tcaatatata	tatatataca	taaaacacaa	caaaatgtac	tgcttcggtc	780
gatgggtgat	aataattttc	atcgatttgg	ttttcagata	ttttggggat	cttgaaccaca	840
aaggttcctt	ttgatgtatg	tttgtattta	atatgttatg	gattataatc	acgtatggac	900
ctcgtgattg	gaaaggata	ggaataatgt	gattatctaa	taataaaaac	gtaattaata	960

tcgc

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..239
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

Ile	His	Ser	Phe	Pro	Ile	His	Val	Gln	Lys	Thr	Lys	Pro	Lys	Lys	Lys
1					5				10					15	
Lys	Lys	Lys	Arg	Gln	Lys	Lys	Met	Asn	Thr	Pro	Ile	Lys	Leu	Ala	Phe
			20					25					30		
Leu	Ile	Leu	Cys	Ile	Ala	Leu	Thr	Ala	Thr	Ala	Phe	Ile	Val	Pro	Ala
		35				40					45				
Lys	Arg	Asp	Ala	Val	Ser	Pro	His	His	Gln	Lys	Ala	Val	Asp	Gly	Ile
		50				55					60				
Cys	Ser	Val	Val	Gln	Asp	Lys	Arg	Leu	Cys	Ser	Ile	Thr	Leu	Arg	Asn
65				70					75					80	
Val	Pro	Ser	Asp	Asp	Pro	Ala	Val	Leu	Val	Arg	Tyr	Leu	Ala	Thr	Ala
			85						90				95		
Ala	Glu	Ala	Ser	Val	Lys	Lys	Gly	Leu	Lys	Phe	Leu	Ser	Gly	Ile	Lys
			100					105					110		
Pro	Lys	Tyr	Lys	Gly	Asn	Ala	Phe	Ala	Thr	Thr	Cys	Ile	Thr	Gly	Cys
			115			120						125			
Xaa	Lys	Gln	Leu	His	Asn	Ala	Leu	Asp	Asp	Phe	Ala	Asp	Phe	Trp	Lys
			130			135					140				
Ala	Ala	Gly	Lys	Asn	Leu	Thr	Ser	Met	Ala	Glu	Asn	Xaa	Phe	Thr	Cys
145				150					155					160	
Lys	Lys	Lys	Met	Thr	Ser	Ile	Phe	Thr	Tyr	His	Ser	Thr	Cys	Leu	Asp
			165					170					175		
Asp	Ile	Tyr	Asp	Lys	Thr	Leu	His	Lys	Val	Val	Glu	Gly	Gly	Ile	Gly
			180					185					190		
Leu	Gly	Lys	Arg	Met	Ser	Gly	Glu	Ser	Val	Asp	Val	Phe	Ala	Gly	Met
			195					200					205		
Gly	Lys	Val	Phe	Asn	Thr	Phe	Asn	Ile	Lys	Thr	Lys	Leu	Asn	Gln	Lys
			210				215					220			
Asp	Thr	Asp	Thr	Leu	Leu	Pro	Pro	Pro	Leu	Ser	Phe	Tyr	Tyr	Tyr	
225				230						235					

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..216

(D) OTHER INFORMATION: / Ceres Seq. ID 1498151

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

```
Met Asn Thr Pro Ile Lys Leu Ala Phe Leu Ile Leu Cys Ile Ala Leu
1      5      10      15
Thr Ala Thr Ala Phe Ile Val Pro Ala Lys Arg Asp Ala Val Ser Pro
20      25      30
His His Gln Lys Ala Val Asp Gly Ile Cys Ser Val Val Gln Asp Lys
35      40      45
Arg Leu Cys Ser Ile Thr Leu Arg Asn Val Pro Ser Asp Asp Pro Ala
50      55      60
Val Leu Val Arg Tyr Leu Ala Thr Ala Ala Glu Ala Ser Val Lys Lys
65      70      75      80
Gly Leu Lys Phe Leu Ser Gly Ile Lys Pro Lys Tyr Lys Gly Asn Ala
85      90      95
Phe Ala Thr Thr Cys Ile Thr Gly Cys Xaa Lys Gln Leu His Asn Ala
100     105     110
Leu Asp Asp Phe Ala Asp Phe Trp Lys Ala Ala Gly Lys Asn Leu Thr
115     120     125
Ser Met Ala Glu Asn Xaa Phe Thr Cys Lys Lys Lys Met Thr Ser Ile
130     135     140
Phe Thr Tyr His Ser Thr Cys Leu Asp Asp Ile Tyr Asp Lys Thr Leu
145     150     155     160
His Lys Val Val Glu Gly Gly Ile Gly Leu Gly Lys Arg Met Ser Gly
165     170     175
Glu Ser Val Asp Val Phe Ala Gly Met Gly Lys Val Phe Asn Thr Phe
180     185     190
Asn Ile Lys Thr Lys Leu Asn Gln Lys Asp Thr Asp Thr Leu Pro
195     200     205
Pro Pro Leu Ser Phe Tyr Tyr Tyr
210     215
```

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 426 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..426

(D) OTHER INFORMATION: / Ceres Seq. ID 1498152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

```
aaaacacatta ctatttcaca aaaccatctt aaagcaacta cacaaatctt gaaattttct 60
catattttct atttactata taaactttta atcaaatcaa gattaactat ggctgaggag 120
tacaagaaca acgttcocga gcacgagaca ccaacggtcg caacagagga atcaccagcg 180
acgacaacag aggttacgga tcgtggattg ttgtatttct tgggggaaga ggaagaggaa 240
gtgaaacctc aagagacaac gacgctcgag tctgagttcg atcataaggc tcagattctc 300
gaaccggagt tagctcgga sacgaggaag tgaaggagaa caagattact ctgctcaaac 360
agtctctagt ggctctctcg aatacwtgca tcccatgaat cttagcacca tcctcaccgt 420
tgrttc
```

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..110
(D) OTHER INFORMATION: / Ceres Seq. ID 1498153
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:
Lys Asn Ile Thr His Ser Gln Asn His Leu Lys Ala Thr Thr Gln Ile
1 5 10 15
Leu Lys Phe Ser His Ile Phe Tyr Leu Tyr Lys Leu Ile Lys
20 25 30
Ser Arg Leu Thr Met Ala Glu Glu Tyr Lys Asn Asn Val Pro Glu His
35 40 45
Glu Thr Pro Thr Val Ala Thr Glu Glu Ser Pro Ala Thr Thr Thr Glu
50 55 60
Val Thr Asp Arg Gly Leu Phe Asp Phe Leu Gly Lys Lys Glu Glu Glu
65 70 75 80
Val Lys Pro Gln Glu Thr Thr Thr Leu Glu Ser Glu Phe Asp His Lys
85 90 95
Ala Gln Ile Ser Glu Pro Glu Leu Ala Ala Xaa Thr Arg Lys
100 105 110

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

Met Ala Glu Glu Tyr Lys Asn Asn Val Pro Glu His Glu Thr Pro Thr
1 5 10 15
Val Ala Thr Glu Glu Ser Pro Ala Thr Thr Thr Glu Val Thr Asp Arg
20 25 30
Gly Leu Phe Asp Phe Leu Gly Lys Lys Glu Glu Glu Val Lys Pro Gln
35 40 45
Glu Thr Thr Thr Leu Glu Ser Glu Phe Asp His Lys Ala Gln Ile Ser
50 55 60
Glu Pro Glu Leu Ala Ala Xaa Thr Arg Lys
65 70

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1011 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1011
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

tcttcata	ttattatatt	cgattttgca	tctgtctctg	aagacgatat	tagcaatcat	60
ggagcgtcta	acatctctc	ctogtttgat	gattgtctct	gatcttgatc	atactatggt	120
tgatcatcat	gattcctgaga	atctatctct	gctgagattc	aattcgttgt	gggaacacgc	180
ttatcgccat	gactctcttc	ttgtgttttc	tacgggaaga	tcaccgacat	tgtataaaga	240
actgagaaag	gagaaaacctt	tggtgacccc	tgatattacc	attatgtctg	taggaactga	300
gattacttat	ggtaactcta	tggttcctga	tcattggttg	gttgaggctc	tgaacaataa	360
atgggatttg	ggatttgtcta	acaagaagc	tagcaacttc	cctgagttaa	agcttcaggc	420
agaaactgag	cagaggccac	acaagggttag	cttttatgtt	gaaaagagta	aggctcagga	480
agttactaag	gagctatcac	agaggttcct	gaaacgtggg	ctggatgtca	aaataattta	540

cagtgagggt atggatttgg atattttacc acaaggtgcc ggaaaggggac aagcgcttgc 600
atatctgctg aagaaactga agactgaggg gaaactccct gtcaatactc ttgcttgggtg 660
cgactctggg aatgatgctg agctgttttag tattcccgat gtttatgggtg ttatgggtaag 720
caatgctcaa gaagagctgt tgaagtgcca tgctgaaaaa gcaaaagaca accctaaggt 780
aatccatgca aaggagaggt gtgcaggtgg gattatacaa gccattgggtc acctcaagct 840
tggtccaac ctttctccaa gagatgtctc tgacttctta gagatcaagg cagagaatgt 900
gaaccctggt cagcaggttg tgaagttttt ttgtttctac gagaatgga gacggggcga 960
ggttgagaac tctgaggtat acacagcaag ccccgctctc atttctcgta g

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..336

(D) OTHER INFORMATION: / Ceres Seq. ID 1498156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

Leu	His	Ile	Leu	Leu	Tyr	Ser	Ile	Leu	His	Pro	Ala	Leu	Lys	Thr	Ile
1				5					10					15	
Leu	Ala	Ile	Met	Glu	Arg	Leu	Thr	Ser	Pro	Pro	Arg	Leu	Met	Ile	Val
			20					25					30		
Ser	Asp	Leu	Asp	His	Thr	Met	Val	Asp	His	His	Asp	Pro	Glu	Asn	Leu
		35					40					45			
Ser	Leu	Leu	Arg	Phe	Asn	Ser	Leu	Trp	Glu	His	Ala	Tyr	Arg	His	Asp
	50					55				60					
Ser	Leu	Leu	Val	Phe	Ser	Thr	Gly	Arg	Ser	Pro	Thr	Leu	Tyr	Lys	Glu
	65				70				75					80	
Leu	Arg	Lys	Glu	Lys	Pro	Leu	Leu	Thr	Pro	Asp	Ile	Thr	Ile	Met	Ser
			85					90					95		
Val	Gly	Thr	Glu	Ile	Thr	Tyr	Gly	Asn	Ser	Met	Val	Pro	Asp	His	Gly
			100					105					110		
Trp	Val	Glu	Ala	Leu	Asn	Asn	Lys	Trp	Asp	Leu	Gly	Ile	Val	Lys	Gln
		115					120								
Glu	Ala	Ser	Asn	Phe	Pro	Glu	Leu	Lys	Leu	Gln	Ala	Glu	Thr	Glu	Gln
	130				135						140				
Arg	Pro	His	Lys	Val	Ser	Phe	Tyr	Val	Glu	Lys	Ser	Lys	Ala	Gln	Glu
	145				150					155				160	
Val	Thr	Lys	Glu	Leu	Ser	Gln	Arg	Phe	Leu	Lys	Arg	Gly	Leu	Asp	Val
			165					170					175		
Lys	Ile	Ile	Tyr	Ser	Gly	Gly	Met	Asp	Leu	Asp	Ile	Leu	Pro	Gln	Gly
		180					185						190		
Ala	Gly	Lys	Gly	Gln	Ala	Leu	Ala	Tyr	Leu	Leu	Lys	Lys	Leu	Lys	Thr
		195					200					205			
Glu	Gly	Lys	Leu	Pro	Val	Asn	Thr	Leu	Ala	Cys	Gly	Asp	Ser	Gly	Asn
	210				215						220				
Asp	Ala	Glu	Leu	Phe	Ser	Ile	Pro	Asp	Val	Tyr	Gly	Val	Met	Val	Ser
	225				230					235				240	
Asn	Ala	Gln	Glu	Glu	Leu	Leu	Lys	Trp	His	Ala	Glu	Asn	Ala	Lys	Asp
			245					250						255	
Asn	Pro	Lys	Val	Ile	His	Ala	Lys	Glu	Arg	Cys	Ala	Gly	Gly	Ile	Ile
		260					265						270		
Gln	Ala	Ile	Gly	His	Phe	Lys	Glu	Gly	Pro	Asn	Leu	Ser	Pro	Arg	Asp
	275						280					285			
Val	Ser	Asp	Phe	Leu	Glu	Ile	Lys	Ala	Glu	Asn	Val	Asn	Pro	Gly	His
	290					295					300				
Glu	Val	Val	Lys	Phe	Phe	Leu	Phe	Tyr	Glu	Lys	Trp	Arg	Arg	Gly	Glu
	305				310					315					
Val	Glu	Asn	Ser	Glu	Ala	Tyr	Thr	Ala	Ser	Pro	Val	Ser	Ile	Ser	Arg

325

330

335

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..317
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

Met	Glu	Arg	Leu	Thr	Ser	Pro	Pro	Arg	Leu	Met	Ile	Val	Ser	Asp	Leu	
1			5						10						15	
Asp	His	Thr	Met	Val	Asp	His	His	Asp	Pro	Glu	Asn	Leu	Ser	Leu	Leu	
			20					25					30			
Arg	Phe	Asn	Ser	Leu	Trp	Glu	His	Ala	Tyr	Arg	His	Asp	Ser	Leu	Leu	
		35					40					45				
Val	Phe	Ser	Thr	Gly	Arg	Ser	Pro	Thr	Leu	Tyr	Lys	Glu	Leu	Arg	Lys	
		50				55					60					
Glu	Lys	Pro	Leu	Leu	Thr	Pro	Asp	Ile	Thr	Ile	Met	Ser	Val	Gly	Thr	
65					70					75					80	
Glu	Ile	Thr	Tyr	Gly	Asn	Ser	Met	Val	Pro	Asp	His	Gly	Trp	Val	Glu	
				85					90					95		
Ala	Leu	Asn	Asn	Lys	Trp	Asp	Leu	Gly	Ile	Val	Lys	Gln	Glu	Ala	Ser	
			100					105					110			
Asn	Phe	Pro	Glu	Leu	Lys	Leu	Gln	Ala	Glu	Thr	Glu	Gln	Arg	Pro	His	
		115				120					125					
Lys	Val	Ser	Phe	Tyr	Val	Glu	Lys	Ser	Lys	Ala	Gln	Glu	Val	Thr	Lys	
		130				135					140					
Glu	Leu	Ser	Gln	Arg	Phe	Leu	Lys	Arg	Gly	Leu	Asp	Val	Lys	Ile	Ile	
145				150						155				160		
Tyr	Ser	Gly	Gly	Met	Asp	Leu	Asp	Ile	Leu	Pro	Gln	Gly	Ala	Gly	Lys	
			165						170					175		
Gly	Gln	Ala	Leu	Ala	Tyr	Leu	Leu	Lys	Lys	Leu	Lys	Thr	Glu	Gly	Lys	
			180					185					190			
Leu	Pro	Val	Asn	Thr	Leu	Ala	Cys	Gly	Asp	Ser	Gly	Asn	Asp	Ala	Glu	
		195					200					205				
Leu	Phe	Ser	Ile	Pro	Asp	Val	Tyr	Gly	Val	Met	Val	Ser	Asn	Ala	Gln	
		210				215					220					
Glu	Glu	Leu	Leu	Lys	Trp	His	Ala	Glu	Asn	Ala	Lys	Asp	Asn	Pro	Lys	
225				230						235				240		
Val	Ile	His	Ala	Lys	Glu	Arg	Cys	Ala	Gly	Gly	Ile	Ile	Gln	Ala	Ile	
			245						250					255		
Gly	His	Phe	Lys	Leu	Gly	Pro	Asn	Leu	Ser	Pro	Arg	Asp	Val	Ser	Asp	
			260					265					270			
Phe	Leu	Glu	Ile	Lys	Ala	Glu	Asn	Val	Asn	Pro	Gly	His	Glu	Val	Val	
		275					280					285				
Lys	Phe	Phe	Leu	Phe	Tyr	Glu	Lys	Trp	Arg	Arg	Gly	Glu	Val	Glu	Asn	
		290				295					300					
Ser	Glu	Ala	Tyr	Thr	Ala	Ser	Pro	Val	Ser	Ile	Ser	Arg				
305				310						315						

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..307

(D) OTHER INFORMATION: / Ceres Seq. ID 1498158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

Met	Ile	Val	Ser	Asp	Leu	Asp	His	Thr	Met	Val	Asp	His	His	Asp	Pro
1			5					10						15	
Glu	Asn	Leu	Ser	Leu	Leu	Arg	Phe	Asn	Ser	Leu	Trp	Glu	His	Ala	Tyr
			20					25					30		
Arg	His	Asp	Ser	Leu	Leu	Val	Phe	Ser	Thr	Gly	Arg	Ser	Pro	Thr	Leu
		35					40					45			
Tyr	Lys	Glu	Leu	Arg	Lys	Glu	Lys	Pro	Leu	Leu	Thr	Pro	Asp	Ile	Thr
	50					55					60				
Ile	Met	Ser	Val	Gly	Thr	Glu	Ile	Thr	Tyr	Gly	Asn	Ser	Met	Val	Pro
	65				70					75				80	
Asp	His	Gly	Trp	Val	Glu	Ala	Leu	Asn	Asn	Lys	Trp	Asp	Leu	Gly	Ile
			85						90					95	
Val	Lys	Gln	Glu	Ala	Ser	Asn	Phe	Pro	Glu	Leu	Lys	Leu	Gln	Ala	Glu
			100					105					110		
Thr	Glu	Gln	Arg	Pro	His	Lys	Val	Ser	Phe	Tyr	Val	Glu	Lys	Ser	Lys
		115					120					125			
Ala	Gln	Glu	Val	Thr	Lys	Glu	Leu	Ser	Gln	Arg	Phe	Leu	Lys	Arg	Gly
	130					135					140				
Leu	Asp	Val	Lys	Ile	Ile	Tyr	Ser	Gly	Gly	Met	Asp	Leu	Asp	Ile	Leu
	145				150					155				160	
Pro	Gln	Gly	Ala	Gly	Lys	Gly	Gln	Ala	Leu	Ala	Tyr	Leu	Leu	Lys	Lys
			165					170						175	
Leu	Lys	Thr	Glu	Gly	Lys	Leu	Pro	Val	Asn	Thr	Leu	Ala	Cys	Gly	Asp
		180						185					190		
Ser	Gly	Asn	Asp	Ala	Glu	Leu	Phe	Ser	Ile	Pro	Asp	Val	Tyr	Gly	Val
		195						200				205			
Met	Val	Ser	Asn	Ala	Gln	Glu	Glu	Leu	Leu	Lys	Trp	His	Ala	Glu	Asn
	210					215					220				
Ala	Lys	Asp	Asn	Pro	Lys	Val	Ile	His	Ala	Lys	Glu	Arg	Cys	Ala	Gly
	225				230					235				240	
Gly	Ile	Ile	Gln	Ala	Ile	Gly	His	Phe	Lys	Leu	Gly	Pro	Asn	Leu	Ser
			245						250					255	
Pro	Arg	Asp	Val	Ser	Asp	Phe	Leu	Glu	Ile	Lys	Ala	Glu	Asn	Val	Asn
		260					265						270		
Pro	Gly	His	Glu	Val	Val	Lys	Phe	Phe	Leu	Phe	Tyr	Glu	Lys	Trp	Arg
		275					280					285			
Arg	Gly	Glu	Val	Glu	Asn	Ser	Glu	Ala	Tyr	Thr	Ala	Ser	Pro	Val	Ser
	290					295					300				

Ile Ser Arg

305

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1220 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1220

(D) OTHER INFORMATION: / Ceres Seq. ID 1498159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

gtaattctc	tttcgttcaa	tggtattctt	ttagatctcg	aacaaaacaa	aatctccaga	60
agaaaaaac	aaattccatg	gcgtctaaat	cgaagcagca	tcttcgttat	cagccgcgaa	120
aatctgtctg	acgatcaaca	caagctttca	cggtgcttat	actctctctc	ttagtgattc	180

tgattcttct	gggtctcggg	attttgtcac	tacctaatagc	taatagaaac	tcttccaaga	240
cgaatgattt	gaccaacatt	gtacgaaa	gtgagacgag	ttctggagat	gaagaaggga	300
atggtagaac	ttgggttgaa	gttatttctt	gggagcctcg	tgtctgtgtt	tatcacaatt	360
tcttgactaa	tgaagaatgt	gagcacttga	tcagccttgc	taaaccgagt	atggttaagt	420
caaccgttgt	agatgagaaa	accggtggga	gcaaagatag	cagagtggag	actagctcag	480
gaacttttct	tagaagagga	catgacgaag	ttgtcgaggt	gattgagaaa	aggatttcag	540
atttcacott	cattctctgt	gaaaatgggt	aaggtcttca	agttcttcac	taccaagtgt	600
ggcagaagta	tgagcctcac	tatgactatt	tcttagatga	gttcaacacc	aagaatggag	660
gacaaagaa	agctactgtg	cttatgtacc	tctctgatgt	cgatgatgtg	ggcgagactg	720
tgttccctgc	agcaagagga	aacatttagt	ctgtcccatt	gtggaaocag	cttccaaaat	780
tggtgtaaga	aggactatct	gtttacccaa	agragcgaga	tgctttactt	tcttggaaca	840
tgagccctga	tgcattctcta	gacccttcga	gcttgacagg	tggagtgtcca	ttggtgaaag	900
gaaacaaatg	gtcatccacg	aaatgggtcc	atgtccacga	gttcaaggtt	taagagmaa	960
caaacaaaaa	aagctaaaaa	atgagggagt	tttctatgga	agcttcgaat	gtgtgtggat	1020
acagttaaac	aggtataaat	tgtatttccc	ttttgaagtg	agagatccct	aggaattttg	1080
aggctgttct	tcatgtgggg	atatttgaac	ttttgttact	ttttcttcta	aattattttg	1140
aatgatttgt	acttttagac	atattcgaat	ctgagtcttg	taacttttaa	caactcaata	1200
cgaaccatga	attttccgtt					

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..316
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

Asn	Phe	Ser	Phe	Val	Gln	Cys	Tyr	Ser	Phe	Arg	Ser	Arg	Thr	Lys	Gln	
1				5				10					15			
Asn	Leu	Gln	Lys	Lys	Lys	Pro	Asn	Ser	Met	Ala	Ser	Lys	Ser	Lys	Gln	
			20				25					30				
His	Leu	Arg	Tyr	Gln	Pro	Arg	Lys	Ser	Val	Ser	Arg	Ser	Thr	Gln	Ala	
		35				40					45					
Phe	Thr	Val	Leu	Ile	Leu	Leu	Leu	Val	Val	Ile	Leu	Ile	Leu	Leu	Gly	
	50				55						60					
Leu	Gly	Ile	Leu	Ser	Leu	Pro	Asn	Ala	Asn	Arg	Asn	Ser	Ser	Lys	Thr	
	65			70					75					80		
Asn	Asp	Leu	Thr	Asn	Ile	Val	Arg	Lys	Ser	Glu	Thr	Ser	Ser	Gly	Asp	
		85							90					95		
Glu	Glu	Gly	Asn	Gly	Glu	Arg	Trp	Val	Glu	Val	Ile	Ser	Trp	Glu	Pro	
		100					105						110			
Arg	Ala	Val	Val	Tyr	His	Asn	Phe	Leu	Thr	Asn	Glu	Glu	Cys	Glu	His	
	115					120					125					
Leu	Ile	Ser	Leu	Ala	Lys	Pro	Ser	Met	Val	Lys	Ser	Thr	Val	Val	Asp	
	130				135						140					
Glu	Lys	Thr	Gly	Gly	Ser	Lys	Asp	Ser	Arg	Val	Arg	Thr	Ser	Ser	Gly	
	145				150					155					160	
Thr	Phe	Leu	Arg	Arg	Gly	His	Asp	Glu	Val	Val	Glu	Val	Ile	Glu	Lys	
		165						170						175		
Arg	Ile	Ser	Asp	Phe	Thr	Phe	Ile	Pro	Val	Glu	Asn	Gly	Glu	Gly	Leu	
	180						185						190			
Gln	Val	Leu	His	Tyr	Gln	Val	Gly	Gln	Lys	Tyr	Glu	Pro	His	Tyr	Asp	
	195					200						205				
Tyr	Phe	Leu	Asp	Glu	Phe	Asn	Thr	Lys	Asn	Gly	Gly	Gln	Arg	Ile	Ala	
	210				215						220					
Thr	Val	Leu	Met	Tyr	Leu	Ser	Asp	Val	Asp	Asp	Gly	Gly	Glu	Thr	Val	
	225				230					235					240	
Phe	Pro	Ala	Ala	Arg	Gly	Asn	Ile	Ser	Ala	Val	Pro	Trp	Trp	Asn	Glu	

245 250 255
Leu Ser Lys Cys Gly Lys Glu Gly Leu Ser Val Leu Pro Lys Xaa Arg
260 265 270
Asp Ala Leu Leu Phe Trp Asn Met Arg Pro Asp Ala Ser Leu Asp Pro
275 280 285
Ser Ser Leu His Gly Gly Cys Pro Val Val Lys Gly Asn Lys Trp Ser
290 295 300
Ser Thr Lys Trp Phe His Val His Glu Phe Lys Val
305 310 315

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 291 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..291

(D) OTHER INFORMATION: / Ceres Seq. ID 1498161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

Met Ala Ser Lys Ser Lys Gln His Leu Arg Tyr Gln Pro Arg Lys Ser
1 5 10 15
Val Ser Arg Ser Thr Gln Ala Phe Thr Val Leu Ile Leu Leu Val
20 25 30
Val Ile Leu Ile Leu Leu Gly Leu Gly Ile Leu Ser Leu Pro Asn Ala
35 40 45
Asn Arg Asn Ser Ser Lys Thr Asn Asp Leu Thr Asn Ile Val Arg Lys
50 55 60
Ser Glu Thr Ser Ser Gly Asp Glu Glu Gly Asn Gly Glu Arg Trp Val
65 70 75 80
Glu Val Ile Ser Trp Glu Pro Arg Ala Val Val Tyr His Asn Phe Leu
85 90 95
Thr Asn Glu Glu Cys Glu His Leu Ile Ser Leu Ala Lys Pro Ser Met
100 105 110
Val Lys Ser Thr Val Val Asp Glu Lys Thr Gly Gly Ser Lys Asp Ser
115 120 125
Arg Val Arg Thr Ser Ser Gly Thr Phe Leu Arg Arg Gly His Asp Glu
130 135 140
Val Val Glu Val Ile Glu Lys Arg Ile Ser Asp Phe Thr Phe Ile Pro
145 150 155 160
Val Glu Asn Gly Glu Gly Leu Gln Val Leu His Tyr Gln Val Gly Gln
165 170 175
Lys Tyr Glu Pro His Tyr Asp Tyr Phe Leu Asp Glu Phe Asn Thr Lys
180 185 190
Asn Gly Gly Gln Arg Ile Ala Thr Val Leu Met Tyr Leu Ser Asp Val
195 200 205
Asp Asp Gly Gly Glu Thr Val Phe Pro Ala Ala Arg Gly Asn Ile Ser
210 215 220
Ala Val Pro Trp Trp Asn Glu Leu Ser Lys Cys Gly Lys Glu Gly Leu
225 230 235 240
Ser Val Leu Pro Lys Xaa Arg Asp Ala Leu Leu Phe Trp Asn Met Arg
245 250 255
Pro Asp Ala Ser Leu Asp Pro Ser Ser Leu His Gly Gly Cys Pro Val
260 265 270
Val Lys Gly Asn Lys Trp Ser Ser Thr Lys Trp Phe His Val His Glu
275 280 285
Phe Lys Val
290

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..180
(D) OTHER INFORMATION: / Ceres Seq. ID 1498162
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

Met	Val	Lys	Ser	Thr	Val	Val	Asp	Glu	Lys	Thr	Gly	Gly	Ser	Lys	Asp
1			5					10					15		
Ser	Arg	Val	Arg	Thr	Ser	Ser	Gly	Thr	Phe	Leu	Arg	Arg	Gly	His	Asp
			20					25					30		
Glu	Val	Val	Glu	Val	Ile	Glu	Lys	Arg	Ile	Ser	Asp	Phe	Thr	Phe	Ile
			35					40					45		
Pro	Val	Glu	Asn	Gly	Glu	Gly	Leu	Gln	Val	Leu	His	Tyr	Gln	Val	Gly
			50					55				60			
Gln	Lys	Tyr	Glu	Pro	His	Tyr	Asp	Tyr	Phe	Leu	Asp	Glu	Phe	Asn	Thr
					70				75					80	
Lys	Asn	Gly	Gly	Gln	Arg	Ile	Ala	Thr	Val	Leu	Met	Tyr	Leu	Ser	Asp
			85						90					95	
Val	Asp	Asp	Gly	Gly	Glu	Thr	Val	Phe	Pro	Ala	Ala	Arg	Gly	Asn	Ile
			100					105					110		
Ser	Ala	Val	Pro	Trp	Trp	Asn	Glu	Leu	Ser	Lys	Cys	Gly	Lys	Glu	Gly
			115					120					125		
Leu	Ser	Val	Leu	Pro	Lys	Xaa	Arg	Asp	Ala	Leu	Leu	Phe	Trp	Asn	Met
			130					135					140		
Arg	Pro	Asp	Ala	Ser	Leu	Asp	Pro	Ser	Ser	Leu	His	Gly	Gly	Cys	Pro
					150					155				160	
Val	Val	Lys	Gly	Asn	Lys	Trp	Ser	Ser	Thr	Lys	Trp	Phe	His	Val	His
					165					170				175	
Glu	Phe	Lys	Val												
			180												

(2) INFORMATION FOR SEQ ID NO:237:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 496 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..496
(D) OTHER INFORMATION: / Ceres Seq. ID 1498163
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

aagagagaaaa	aaaggttgaa	tcgaaacaga	tcggaaaatc	gtcgcagagag	agagagagag	60
aagtcgaacg	acaggcagct	aatgctaagg	agtttgctga	ggaaaatggtt	cttgaagaca	120
ttcttatgca	gagagggatt	tcgataaacg	ctgctcgtaa	cttccttggt	gggtggtctg	180
agaaggattc	agacattatt	ttctgagggtg	tgggctctct	ctctctctct	ctctctctct	240
ctctctctct	ctctctctct	ctctctctct	ctctctctct	ctctctctct	ctttgtgcct	300
ctctgttttg	ctcggtttct	attttgcct	tcgcgctggt	attactctct	tcatacagact	360
tatgtttctt	caataaaaa	ggattgatg	tagatgaat	actgtatcat	cttgagattgt	420
gccttgatat	aaatttttc	gagagatttg	tgattattac	tgttttgagt	aattataatt	480
cccttgtttc	aaagat					

(2) INFORMATION FOR SEQ ID NO:238:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..48
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498164
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:
Lys Arg Glu Lys Arg Leu Asn Arg Asn Arg Ser Glu Asn Arg Arg Glu
1 5 10 15
Arg Glu Arg Glu Lys Ser Asn Asp Arg Gln Leu Met Leu Arg Ser Leu
 20 25 30
Leu Arg Lys Trp Phe Leu Lys Thr Ser Leu Cys Arg Glu Gly Phe Arg
 35 40 45

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 67 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..67
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498165
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:
Glu Arg Lys Lys Val Glu Ser Lys Gln Ile Gly Lys Ser Ser Arg Glu
1 5 10 15
Arg Glu Arg Glu Val Glu Arg Gln Ala Ala Asn Ala Lys Glu Phe Ala
 20 25 30
Glu Glu Met Val Leu Glu Asp Ile Ser Met Gln Arg Gly Ile Ser Ile
 35 40 45
Asn Ala Ala Arg Asn Phe Leu Val Gly Gly Ala Glu Lys Asp Ser Asp
 50 55 60
Ile Ile Phe
65

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..33
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498166
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:
Met Val Leu Glu Asp Ile Ser Met Gln Arg Gly Ile Ser Ile Asn Ala
1 5 10 15
Ala Arg Asn Phe Leu Val Gly Gly Ala Glu Lys Asp Ser Asp Ile Ile
 20 25 30
Phe

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1121 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1121

(D) OTHER INFORMATION: / Ceres Seq. ID 1498167

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

aaaccccaac	tttcgagttt	rccgatgagt	ctagcctcca	tgatctccgg	ctaaagatca	60
atgaatcgac	gccttccctt	gttcgtttgt	cgattgatta	caacgaaggt	gatatcctcg	120
cggtctgttac	tcctctcgatt	cgtctgattt	tagtgcgttt	gatcagaat	cggaasgaa	180
tcacaggag	attgttcgta	gattccgggtg	gcagcatgaa	tcctccnng	tgtaaaagg	240
ttaaaggcag	ctctcttgtt	gaaaaatata	ttgatggagg	aactctggta	cacttggtaa	300
ttgacgattg	tgatcatgat	tgttcatgct	gttatgttag	aactctggatt	tttgttgtt	360
ttgatcctga	tcactctatg	cgttttagct	ctcgaagaa	gaatttggtta	tcgttaact	420
ataccttaac	ttctgtgaaa	ggaatagtcg	gtttgaattt	tgagaaggag	gcgatgttgt	480
agtttatgga	tcctcttagtg	ttggtagttt	tgttcgtgtg	gtgtctattg	ataaacgtag	540
ctatgtgcac	attgttgatt	tacttatgga	aactttgaaa	tcgtgatga	aagaagatac	600
tttgagcatt	gactgtaaag	tactcgtgtg	gtggagaatg	ataaaagatg	gtattgttac	660
gcctctgttg	gttgatcttt	gtacaaaaac	tggttagaa	ctccaccctt	gctttatcac	720
tcacctcga	gagctaaaa	acaagatact	agagtcgctt	ccoggtgttg	atattgggac	780
attggcttgt	gtttctcttg	aactgcgaga	catggcttcg	tagaatgacc	tggtgaagca	840
gaagtgtctg	gaagagtgcc	aagatcttgt	gacagaaggc	aatcatgatg	tggttaactg	900
gaaggagagg	ttgtctactt	attggaggca	aaagggaag	ttctccttca	taagcagggc	960
atttcagggt	ttttcaggga	gcattggttc	gtcataaatc	ctggaagaag	actaaaaaga	1020
gaccatattg	aatccggtgg	agtgaattgt	gtttgttatt	caaatcttgc	aaataggcaa	1080
ttataggttt	aagatgggtg	aaagagcatt	ggaaccttag	t		

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1498168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

Thr	Pro	Thr	Phe	Glu	Phe	Xaa	Asp	Glu	Ser	Ser	Leu	His	Asp	Leu	Arg
1				5					10					15	
Leu	Lys	Ile	Asn	Glu	Ser	Thr	Pro	Ser	Ser	Val	Arg	Leu	Ser	Ile	Asp
			20					25				30			
Tyr	Asn	Asp	Gly	Asp	Ile	Leu	Ala	Ala	Val	Thr	Leu	Ser	Ile	Arg	Leu
			35				40				45				
Ile	Leu	Val	Arg	Leu	Ile	Arg	Asn	Arg	Lys	Xaa	Ile	Ile	Arg	Arg	Leu
			50				55				60				
Phe	Val	Asp	Ser	Gly	Gly	Ser	Met	Asn	Leu	Ser	Xaa	Cys	Lys	Lys	Val
			65			70			75					80	
Lys	Arg	Ala	Ser	Leu	Val	Glu	Lys	Tyr	Ile	Asp	Gly	Gly	Ile	Trp	
			85					90					95		

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 85 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..85

(D) OTHER INFORMATION: / Ceres Seq. ID 1498169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

Met Glu Thr Leu Lys Ser Asp Glu Glu Asp Thr Leu Ser Ile Asp

1 5 10 15
Cys Lys Val Leu Val Trp Trp Arg Met Ile Lys Asp Gly Ile Val Thr
20 25 30
Pro Leu Leu Val Asp Leu Cys Tyr Lys Thr Gly Leu Glu Leu Pro Pro
35 40 45
Cys Phe Ile Ser Leu Pro Arg Glu Leu Lys His Lys Ile Leu Glu Ser
50 55 60
Leu Pro Gly Val Asp Ile Gly Thr Leu Ala Cys Val Ser Ser Glu Leu
65 70 75 80
Arg Asp Met Ala Ser
85

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..61
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

Met Ile Lys Asp Gly Ile Val Thr Pro Leu Leu Val Asp Leu Cys Tyr
1 5 10 15
Lys Thr Gly Leu Glu Leu Pro Pro Cys Phe Ile Ser Leu Pro Arg Glu
20 25 30
Leu Lys His Lys Ile Leu Glu Ser Leu Pro Gly Val Asp Ile Gly Thr
35 40 45
Leu Ala Cys Val Ser Ser Glu Leu Arg Asp Met Ala Ser
50 55 60

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..775
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

actctctata cctcctcaag aaaatcaaa cagcagttat ggccgacgta gcaacaaagc 60
accccatgga agatgagggt aagaagacgg aggcgtctag tttggtgggg aagcttagaga 120
cagacgtgga gatcaaggct tcggctgata agttcacca catgttcgt gggaaaccac 180
accatgtctc caaagcaagt ccaggcaaca ttcagggatg tgatctgcac gaaggcgact 240
ggggcacagt cggctctatc gtctcttgga attacgtwca tgatrgggag gcaaaagttg 300
ctaagagagag gattgaggcr gtggagccrg ataagaactt gatcacgttt agggttatag 360
acggtgatct gatgaagag tacaagagct tcttgctcac catccagggt acccckaagc 420
ytggagcccc tggaaagtatt gtgcactggc accttgagta tgagaaaatw agcgaggagg 480
tagctcatcc ggaactctc ctccavttct gtgtcgaggt ctccaaagag atcgacgaac 540
atctttttgg cgaggaatag aggagtacta ctactcttcg tgtttgaatt taaatgcaat 600
aaataaggac taagagccat gtctttgtga gatatatgaa tgtgagtggt catcatgaat 660
gtgtgatgta agctagtata aatatataat aagtatgtta tatatgtttg ctaat 720

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..185

(D) OTHER INFORMATION: / Ceres Seq. ID 1498174

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

```
Ser Leu Tyr Leu Leu Lys Lys Ile Lys Ala Ala Val Met Ala Asp Val
1      5      10      15
Ala Thr Lys His Pro Met Glu Asp Glu Val Lys Lys Thr Glu Ala Ser
20      25      30
Ser Leu Val Gly Lys Leu Glu Thr Asp Val Glu Ile Lys Ala Ser Ala
35      40      45
Asp Lys Phe His His Met Phe Ala Gly Lys Pro His His Val Ser Lys
50      55      60
Ala Ser Pro Gly Asn Ile Gln Gly Cys Asp Leu His Glu Gly Asp Trp
65      70      75      80
Gly Thr Val Gly Ser Ile Val Phe Trp Asn Tyr Xaa His Asp Xaa Glu
85      90      95
Ala Lys Val Ala Lys Glu Arg Ile Glu Xaa Val Glu Xaa Asp Lys Asn
100      105      110
Leu Ile Thr Phe Arg Val Ile Asp Gly Asp Leu Met Lys Glu Tyr Lys
115      120      125
Ser Phe Leu Leu Thr Ile Gln Val Thr Xaa Lys Xaa Gly Gly Pro Gly
130      135      140
Ser Ile Val His Trp His Leu Glu Tyr Glu Lys Xaa Ser Glu Glu Val
145      150      155      160
Ala His Pro Glu Thr Leu Leu Xaa Phe Cys Val Glu Val Ser Lys Glu
165      170      175
Ile Asp Glu His Leu Leu Ala Glu Glu
180      185
```

- (2) INFORMATION FOR SEQ ID NO:247:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..173

(D) OTHER INFORMATION: / Ceres Seq. ID 1498175

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

```
Met Ala Asp Val Ala Thr Lys His Pro Met Glu Asp Glu Val Lys Lys
1      5      10      15
Thr Glu Ala Ser Ser Leu Val Gly Lys Leu Glu Thr Asp Val Glu Ile
20      25      30
Lys Ala Ser Ala Asp Lys Phe His His Met Phe Ala Gly Lys Pro His
35      40      45
His Val Ser Lys Ala Ser Pro Gly Asn Ile Gln Gly Cys Asp Leu His
50      55      60
Glu Gly Asp Trp Gly Thr Val Gly Ser Ile Val Phe Trp Asn Tyr Xaa
65      70      75      80
His Asp Xaa Glu Ala Lys Val Ala Lys Glu Arg Ile Glu Xaa Val Glu
85      90      95
Xaa Asp Lys Asn Leu Ile Thr Phe Arg Val Ile Asp Gly Leu Met
100      105      110
Lys Glu Tyr Lys Ser Phe Leu Leu Thr Ile Gln Val Thr Xaa Lys Xaa
115      120      125
Gly Gly Pro Gly Ser Ile Val His Trp His Leu Glu Tyr Glu Lys Xaa
130      135      140
```

Ser Glu Glu Val Ala His Pro Glu Thr Leu Leu Xaa Phe Cys Val Glu
145 150 155 160
Val Ser Lys Glu Ile Asp Glu His Leu Leu Ala Glu Glu
165 170

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 1498176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

Met Glu Asp Glu Val Lys Lys Thr Glu Ala Ser Ser Leu Val Gly Lys
1 5 10 15
Leu Glu Thr Asp Val Glu Ile Lys Ala Ser Ala Asp Lys Phe His His
20 25 30
Met Phe Ala Gly Lys Pro His His Val Ser Lys Ala Ser Pro Gly Asn
35 40 45
Ile Gln Gly Cys Asp Leu His Glu Gly Asp Trp Gly Thr Val Gly Ser
50 55 60
Ile Val Phe Trp Asn Tyr Xaa His Asp Xaa Glu Ala Lys Val Ala Lys
65 70 75 80
Glu Arg Ile Glu Xaa Val Glu Xaa Asp Lys Asn Leu Ile Thr Phe Arg
85 90 95
Val Ile Asp Gly Asp Leu Met Lys Glu Tyr Lys Ser Phe Leu Leu Thr
100 105 110
Ile Gln Val Thr Xaa Lys Xaa Gly Gly Pro Gly Ser Ile Val His Trp
115 120 125
His Leu Glu Tyr Glu Lys Xaa Ser Glu Glu Val Ala His Pro Glu Thr
130 135 140
Leu Leu Xaa Phe Cys Val Glu Val Ser Lys Glu Ile Asp Glu His Leu
145 150 155 160
Leu Ala Glu Glu

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..894

(D) OTHER INFORMATION: / Ceres Seq. ID 1498177

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

attttgaaaa gttttctaacc tctaggccac ccactcatgg ctactctgtt catgaagctg 60
gtgagctctt tcttaattct atctactttt tgtctcacta ctgtgaactc ggagccacag 120
tgccataaatt tcaaatcgat cattagtttc ggtgattcta ttgccgacac tggaaacttg 180
ctcgccctct ccgactoctac ccgttttctca aacggccgcc tcactatcga ttctattgct 240
ttcttccacc atccgaccgg ccgttttctca aacggccgcc tcactatcga ttctattgct 300
gaatttttgg gttttccgct tgtgcctcct ttttatggat ctcaaaaatgc aaatttttag 360
aaaggaggtta attttgcggt tggaggagca acggcactgg aacgttccct tcttgaagag 420
agaggcattc attttcctta caccaaagctt agtttagccg tacagcttag tagcttcaag 480
gagagtttgc ctaacttatg tgtctctcct tcagactgca gagatatgat agaaaaattct 540
ttgattctca tgggagaaat tggagggaat gactataact acgcattctg aaggagagac 600
acataaagta ggcaaacctc ccttgaagct acggtggttg aagacgtgag ggaggaggag 660

gatacgggtgg tgggtgaagga ggaggttacg gaggaagcgg tgggtggtgga ggaatggaat 720
tcctttaatt aggttttggga ttaccaatga atgttctctc tctcgcttgt tatgcttcta 780
cttggttttg ygtgttctct atttgttctt ggttctgctt tagatttgat gtaacagttc 840
gtgattaggt attttggtat ctggaaacgt aatgttaagt cacttgatcat tctc

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..184

(D) OTHER INFORMATION: / Ceres Seq. ID 1498178

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

Met Ala Thr Leu Phe Met Lys Leu Val Ser Phe Phe Leu Ile Leu Ser
1 5 10 15
Thr Phe Cys Leu Thr Thr Val Asn Ser Glu Pro Gln Cys His Asn Phe
20 25 30
Lys Ser Ile Ile Ser Phe Gly Asp Ser Ile Ala Asp Thr Gly Asn Leu
35 40 45
Leu Ala Leu Ser Asp Pro Thr Asn Leu Pro Lys Val Ala Phe Leu Pro
50 55 60
Tyr Gly Glu Thr Phe Phe His His Pro Thr Gly Arg Phe Ser Asn Gly
65 70 75 80
Arg Leu Ile Ile Asp Phe Ile Ala Glu Phe Leu Gly Phe Pro Leu Val
85 90 95
Pro Pro Phe Tyr Gly Ser Gln Asn Ala Asn Phe Glu Lys Gly Val Asn
100 105 110
Phe Ala Val Gly Gly Ala Thr Ala Leu Glu Arg Ser Phe Leu Glu Glu
115 120 125
Arg Gly Ile His Phe Pro Tyr Thr Asn Val Ser Leu Ala Val Gln Leu
130 135 140
Ser Ser Phe Lys Glu Ser Leu Pro Asn Leu Cys Val Ser Pro Ser Asp
145 150 155 160
Cys Arg Asp Met Ile Glu Asn Ser Leu Ile Leu Met Gly Glu Ile Gly
165 170 175
Gly Asn Asp Tyr Asn Tyr Ala Phe
180

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..179

(D) OTHER INFORMATION: / Ceres Seq. ID 1498179

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

Met Lys Leu Val Ser Phe Phe Leu Ile Leu Ser Thr Phe Cys Leu Thr
1 5 10 15
Thr Val Asn Ser Glu Pro Gln Cys His Asn Phe Lys Ser Ile Ile Ser
20 25 30
Phe Gly Asp Ser Ile Ala Asp Thr Gly Asn Leu Leu Ala Leu Ser Asp
35 40 45
Pro Thr Asn Leu Pro Lys Val Ala Phe Leu Pro Tyr Gly Glu Thr Phe
50 55 60
Phe His His Pro Thr Gly Arg Phe Ser Asn Gly Arg Leu Ile Ile Asp

65					70					75					80
Phe	Ile	Ala	Glu	Phe	Leu	Gly	Phe	Pro	Leu	Val	Pro	Pro	Phe	Tyr	Gly
				85					90				95		
Ser	Gln	Asn	Ala	Asn	Phe	Glu	Lys	Gly	Val	Asn	Phe	Ala	Val	Gly	Gly
			100					105					110		
Ala	Thr	Ala	Leu	Glu	Arg	Ser	Phe	Leu	Glu	Glu	Arg	Gly	Ile	His	Phe
			115				120					125			
Pro	Tyr	Thr	Asn	Val	Ser	Leu	Ala	Val	Gln	Leu	Ser	Ser	Phe	Lys	Glu
			130				135				140				
Ser	Leu	Pro	Asn	Leu	Cys	Val	Ser	Pro	Ser	Asp	Cys	Arg	Asp	Met	Ile
			145			150				155				160	
Glu	Asn	Ser	Leu	Ile	Leu	Met	Gly	Glu	Ile	Gly	Gly	Asn	Asp	Tyr	Asn
			165					170						175	

Tyr Ala Phe

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..723
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

agtcgtctag	ggtttgtttt	tcgtttcttc	tcgcattgtt	cagaggaatt	gcgaattaag	60
ataaagatga	ggccagtggt	cgctcgcaat	ttcgagtatg	aaactcgcca	gtcggatctg	120
gaacggtgtg	tcgacaagta	tgggagagtc	gaccgagtgg	acatgaaatc	tgatgatgct	180
tttgtgtact	ttgaggaatg	acgtgatgct	gaagacgcta	ttcgcaaaact	cgacaatttt	240
ccttttggtg	atgagaaaacg	caggttatca	gttgaatggg	caaagggtga	acgtggcagg	300
ccctcgtgtg	acgcgaaaagc	cccttcaaat	ctgaagccta	caaagacact	gtttgtcatt	360
aaacttgacc	ccattagaac	aaaagagcac	gacattgaaa	aacactttga	gcccatgggt	420
aaggtcacca	acgtgcgtat	cagacgcaac	ttctcatttg	ttcagtttga	aacacaagag	480
gatgctacaa	aaagcccttga	agctactcaa	agaagcaaaa	tattggatag	gggtgtttcc	540
gtggagtagt	cgttgaaaga	tgacgatgaa	agagatgata	gaaatgggtg	tcgtagcccg	600
agaaggtctc	ttagtctgtg	gtatcgtagg	cgctcatgta	tgatgtactg	tcgtattttt	660
aaagaaaatt	tggcaccttt	tgtataaaca	gaattcttta	tacctcgcat	tttgtgttta	720

cgt

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..228
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498181

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

Ser	Arg	Leu	Gly	Phe	Val	Phe	Arg	Phe	Phe	Ser	Asp	Cys	Ser	Glu	Glu
1			5						10				15		
Leu	Arg	Ile	Lys	Ile	Lys	Met	Arg	Pro	Val	Phe	Val	Gly	Asn	Phe	Glu
			20					25					30		
Tyr	Glu	Thr	Arg	Gln	Ser	Asp	Leu	Glu	Arg	Leu	Phe	Asp	Lys	Tyr	Gly
			35				40					45			
Arg	Val	Asp	Arg	Val	Asp	Met	Lys	Ser	Gly	Tyr	Ala	Phe	Val	Tyr	Phe
			50			55				60					
Glu	Asp	Glu	Arg	Asp	Ala	Glu	Asp	Ala	Ile	Arg	Lys	Leu	Asp	Asn	Phe

65					70					75					80
Pro	Phe	Gly	Tyr	Glu	Lys	Arg	Arg	Leu	Ser	Val	Glu	Trp	Ala	Lys	Gly
				85					90					95	
Glu	Arg	Gly	Arg	Pro	Arg	Gly	Asp	Ala	Lys	Ala	Pro	Ser	Asn	Leu	Lys
			100				105						110		
Pro	Thr	Lys	Thr	Leu	Phe	Val	Ile	Asn	Phe	Asp	Pro	Ile	Arg	Thr	Lys
		115					120					125			
Glu	His	Asp	Ile	Glu	Lys	His	Phe	Glu	Pro	Tyr	Gly	Lys	Val	Thr	Asn
						135					140				
Val	Arg	Ile	Arg	Arg	Asn	Phe	Ser	Phe	Val	Gln	Phe	Glu	Thr	Gln	Glu
					150					155				160	
Asp	Ala	Thr	Lys	Ala	Leu	Glu	Ala	Thr	Gln	Arg	Ser	Lys	Ile	Leu	Asp
				165					170					175	
Arg	Val	Val	Ser	Val	Glu	Tyr	Ala	Leu	Lys	Asp	Asp	Asp	Glu	Arg	Asp
			180					185					190		
Asp	Arg	Asn	Gly	Gly	Arg	Ser	Pro	Arg	Arg	Ser	Leu	Ser	Pro	Val	Tyr
		195					200					205			
Arg	Arg	Arg	His	Val	Met	Tyr	Cys	Arg	Tyr	Phe	Lys	Glu	Asn	Leu	
		210			215					220					
Ala	Pro	Phe	Val												
225															

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..206

(D) OTHER INFORMATION: / Ceres Seq. ID 1498182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

Met	Arg	Pro	Val	Phe	Val	Gly	Asn	Phe	Glu	Tyr	Glu	Thr	Arg	Gln	Ser
1			5						10					15	
Asp	Leu	Glu	Arg	Leu	Phe	Asp	Lys	Tyr	Gly	Arg	Val	Asp	Arg	Val	Asp
			20					25					30		
Met	Lys	Ser	Gly	Tyr	Ala	Phe	Val	Tyr	Phe	Glu	Asp	Glu	Arg	Asp	Ala
		35				40					45				
Glu	Asp	Ala	Ile	Arg	Lys	Leu	Asp	Asn	Phe	Pro	Phe	Gly	Tyr	Glu	Lys
	50					55					60				
Arg	Arg	Leu	Ser	Val	Glu	Trp	Ala	Lys	Gly	Glu	Arg	Gly	Arg	Pro	Arg
	65			70					75					80	
Gly	Asp	Ala	Lys	Ala	Pro	Ser	Asn	Leu	Lys	Pro	Thr	Lys	Thr	Leu	Phe
			85						90				95		
Val	Ile	Asn	Phe	Asp	Pro	Ile	Arg	Thr	Lys	Glu	His	Asp	Ile	Glu	Lys
		100						105				110			
His	Phe	Glu	Pro	Tyr	Gly	Lys	Val	Thr	Asn	Val	Arg	Ile	Arg	Arg	Asn
		115					120				125				
Phe	Ser	Phe	Val	Gln	Phe	Glu	Thr	Gln	Glu	Asp	Ala	Thr	Lys	Ala	Leu
	130					135					140				
Glu	Ala	Thr	Gln	Arg	Ser	Lys	Ile	Leu	Asp	Arg	Val	Val	Ser	Val	Glu
	145				150				155					160	
Tyr	Ala	Leu	Lys	Asp	Asp	Glu	Arg	Asp	Asp	Arg	Asn	Gly	Gly	Arg	
			165					170					175		
Ser	Pro	Arg	Arg	Ser	Leu	Ser	Pro	Val	Tyr	Arg	Arg	Arg	His	Val	Met
		180					185						190		
Met	Tyr	Cys	Arg	Tyr	Phe	Lys	Glu	Asn	Leu	Ala	Pro	Phe	Val		
	195					200					205				

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..174
(D) OTHER INFORMATION: / Ceres Seq. ID 1498183
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:
Met Lys Ser Gly Tyr Ala Phe Val Tyr Phe Glu Asp Glu Arg Asp Ala
1 5 10 15
Glu Asp Ala Ile Arg Lys Leu Asp Asn Phe Pro Phe Gly Tyr Glu Lys
20 25 30
Arg Arg Leu Ser Val Glu Trp Ala Lys Gly Glu Arg Gly Arg Pro Arg
35 40 45
Gly Asp Ala Lys Ala Pro Ser Asn Leu Lys Pro Thr Lys Thr Leu Phe
50 55 60
Val Ile Asn Phe Asp Pro Ile Arg Thr Lys Glu His Asp Ile Glu Lys
65 70 75 80
His Phe Glu Pro Tyr Gly Lys Val Thr Asn Val Arg Ile Arg Arg Asn
85 90 95
Phe Ser Phe Val Gln Phe Glu Thr Gln Glu Asp Ala Thr Lys Ala Leu
100 105 110
Glu Ala Thr Gln Arg Ser Lys Ile Leu Asp Arg Val Val Ser Val Glu
115 120 125
Tyr Ala Leu Lys Asp Asp Asp Glu Arg Asp Asp Arg Asn Gly Gly Arg
130 135 140
Ser Pro Arg Arg Ser Leu Ser Pro Val Tyr Arg Arg Arg His Val Met
145 150 155 160
Met Tyr Cys Arg Tyr Phe Lys Glu Asn Leu Ala Pro Phe Val
165 170
(2) INFORMATION FOR SEQ ID NO:256:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1051 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1051
(D) OTHER INFORMATION: / Ceres Seq. ID 1498190
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:
aaaaaacaga aaaaattcgt ggaaacgcc aataacgagat ctgacacaaa ctcgtagtgt 60
gggttagaag aagacaaaag caaggagcct cataataaaa ccctagagat attgtttct 120
ccaatttcaa aagacgagac gtgaagaaga cgatcgaga tgaacatttt cagattagct 180
ggtgatatga ctacacctagc cagtgttctt gtcttgcttc tcaagatcca caccatcaaa 240
tctctgcgtg gtgtttcatt gaagactcaa gaactctatg ccattgtctt tgcgacgcgt 300
tatttgata ttttcacgag ttttgtgtct ctgtacaaca cctctatgaa gtgtgtgttc 360
ttaggaaagt ctttttcgat tgttgggtac atgaagtatc ataaggccgt ccacagagact 420
taacacagag agcaagatac gtttcgtcat tggttccttg tgcttccttg cttctctcta 480
gtctctctga ttcatgaaaa gtttaccttt ctggaggtat tgtggacgtt ttcatgtac 540
ttggaggctg ttgcatatt accctcagctt gtcttgttgc aaaggactag aaatattgac 600
aaactgcacc gacaatatat atttctcctt ggggggtacc gtggattata catcctcaac 660
tggatctacc gttacttctac tgagccgcac ttgttccat ggataaacat gatgcgcggg 720
ttgtctcaaa cactgcctcta tgccgacttc ttctattatt ttctcctaag ctggaagaac 780
aacaataaac tccaattacc agcttaattt ctaaaagtct aatgctctgg aaacctcagg 840
attcgatttg gtgcccgcaca aaacatctac cggaatgtta ccaattacta ctgttgggtg 900
ttattagagg agaacgagca tagatgtgta aactccagca atctaacta ttacacttcc 960
tttagacttt ctgctctctc actctttttt ttggtcgact tagtgttact aaatatttcc 1020

acgcgacagt aatatattca ccacaattcg c

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..215

(D) OTHER INFORMATION: / Ceres Seq. ID 1498191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

Met	Asn	Ile	Phe	Arg	Leu	Ala	Gly	Asp	Met	Thr	His	Leu	Ala	Ser	Val
1			5					10						15	
Leu	Val	Leu	Leu	Leu	Lys	Ile	His	Thr	Ile	Lys	Ser	Cys	Ala	Gly	Val
			20					25					30		
Ser	Leu	Lys	Thr	Gln	Glu	Leu	Tyr	Ala	Ile	Val	Phe	Ala	Thr	Arg	Tyr
		35					40				45				
Leu	Asp	Ile	Phe	Thr	Ser	Phe	Val	Ser	Leu	Tyr	Asn	Thr	Ser	Met	Lys
	50					55					60				
Leu	Val	Phe	Leu	Gly	Ser	Ser	Phe	Ser	Ile	Val	Trp	Tyr	Met	Lys	Tyr
65					70					75				80	
His	Lys	Ala	Val	His	Arg	Thr	Tyr	Asp	Arg	Glu	Gln	Asp	Thr	Phe	Arg
				85					90				95		
His	Trp	Phe	Leu	Val	Leu	Pro	Cys	Phe	Leu	Leu	Ala	Leu	Leu	Ile	His
			100					105					110		
Glu	Lys	Phe	Thr	Phe	Leu	Glu	Val	Leu	Trp	Thr	Phe	Ser	Leu	Tyr	Leu
		115					120					125			
Glu	Ala	Val	Ala	Ile	Leu	Pro	Gln	Leu	Val	Leu	Leu	Gln	Arg	Thr	Arg
	130					135					140				
Asn	Ile	Asp	Asn	Leu	Thr	Gly	Gln	Tyr	Ile	Phe	Leu	Leu	Gly	Gly	Tyr
145				150						155				160	
Arg	Gly	Leu	Tyr	Ile	Leu	Asn	Trp	Ile	Tyr	Arg	Tyr	Phe	Thr	Glu	Pro
			165					170					175		
His	Phe	Val	His	Trp	Ile	Thr	Trp	Ile	Ala	Gly	Phe	Val	Gln	Thr	Leu
		180					185						190		
Leu	Tyr	Ala	Asp	Phe	Phe	Tyr	Tyr	Tyr	Phe	Leu	Ser	Trp	Lys	Asn	Asn
		195				200						205			
Lys	Lys	Leu	Gln	Leu	Pro	Ala									
	210					215									

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..206

(D) OTHER INFORMATION: / Ceres Seq. ID 1498192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

Met	Thr	His	Leu	Ala	Ser	Val	Leu	Val	Leu	Leu	Lys	Ile	His	Thr	
1				5					10				15		
Ile	Lys	Ser	Cys	Ala	Gly	Val	Ser	Leu	Lys	Thr	Gln	Glu	Leu	Tyr	Ala
			20					25					30		
Ile	Val	Phe	Ala	Thr	Arg	Tyr	Leu	Asp	Ile	Phe	Thr	Ser	Phe	Val	Ser
		35					40				45				
Leu	Tyr	Asn	Thr	Ser	Met	Lys	Leu	Val	Phe	Leu	Gly	Ser	Ser	Phe	Ser
	50					55					60				

Ile Val Trp Tyr Met Lys Tyr His Lys Ala Val His Arg Thr Tyr Asp
65 70 75 80
Arg Glu Gln Asp Thr Phe Arg His Trp Phe Leu Val Leu Pro Cys Phe
85 90 95
Leu Leu Ala Leu Leu Ile His Glu Lys Phe Thr Phe Leu Glu Val Leu
100 105 110
Trp Thr Phe Ser Leu Tyr Leu Glu Ala Val Ala Ile Leu Pro Gln Leu
115 120 125
Val Leu Leu Gln Arg Thr Arg Asn Ile Asp Asn Leu Thr Gly Gln Tyr
130 135 140
Ile Phe Leu Leu Gly Gly Tyr Arg Gly Leu Tyr Ile Leu Asn Trp Ile
145 150 155 160
Tyr Arg Tyr Phe Thr Glu Pro His Phe Val His Trp Ile Thr Trp Ile
165 170 175
Ala Gly Phe Val Gln Thr Leu Leu Tyr Ala Asp Phe Phe Tyr Tyr Tyr
180 185 190
Phe Leu Ser Trp Lys Asn Asn Lys Lys Leu Gln Leu Pro Ala
195 200 205

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1498193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

Met Lys Leu Val Phe Leu Gly Ser Ser Phe Ser Ile Val Trp Tyr Met
1 5 10 15
Lys Tyr His Lys Ala Val His Arg Thr Tyr Asp Arg Glu Gln Asp Thr
20 25 30
Phe Arg His Trp Phe Leu Val Leu Pro Cys Phe Leu Leu Ala Leu Leu
35 40 45
Ile His Glu Lys Phe Thr Phe Leu Glu Val Leu Trp Thr Phe Ser Leu
50 55 60
Tyr Leu Glu Ala Val Ala Ile Leu Pro Gln Leu Val Leu Leu Gln Arg
65 70 75 80
Thr Arg Asn Ile Asp Asn Leu Thr Gly Gln Tyr Ile Phe Leu Leu Gly
85 90 95
Gly Tyr Arg Gly Leu Tyr Ile Leu Asn Trp Ile Tyr Arg Tyr Phe Thr
100 105 110
Glu Pro His Phe Val His Trp Ile Thr Trp Ile Ala Gly Phe Val Gln
115 120 125
Thr Leu Leu Tyr Ala Asp Phe Phe Tyr Tyr Tyr Phe Leu Ser Trp Lys
130 135 140
Asn Asn Lys Lys Leu Gln Leu Pro Ala
145 150

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 947 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..947

(D) OTHER INFORMATION: / Ceres Seq. ID 1498194

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

aatgttgctt	taaaaccaat	gctcctcttc	ttgttcttca	tataaacacc	atatcctctc	60
ctccatattc	taacaatttc	atagcaaac	ctaaaattga	gaaagagata	gagagagaaa	120
gatgggtaga	ggaagatcg	agataaagag	gatagagaac	gcaacaaca	gagtggtgac	180
gttctcaaa	aggaggaatg	gattggtgaa	gaaggctaaa	gagatcacag	ttctttgtga	240
tgcaaaagtt	gcctcataaa	tccttgcaag	taatggtaag	atgattgatt	actgtgtgcc	300
ttccatggat	cttgggtgcta	tgttggaacca	ataccagaag	ttatctggca	agaaactatg	360
ggatgctaa	catgagaacc	ttagcaatga	gattgatagg	atcaagaaa	agaaatgata	420
cttacaaact	gagctcaggc	atttgaagg	agaagatata	cagtcctcca	acttgaaaaa	480
tctgatggct	gtcgagcagc	ccattgaaca	tgccctcgac	aaagtccgag	accaccagat	540
ggagatccct	atatcaaaaga	ggagaaatga	gaagatgatg	gcggaggagc	aacggcaact	600
cactttccac	ctgcaacaac	aggagatggc	tatagcaagc	aacgcaagag	gaatgatgat	660
gagagatcat	gatgggcagt	tcggatatag	agtgcaccc	attcagccaa	atcttcagga	720
aaagattatg	tccttggctca	tcgattgatc	atcgagattt	tataatctca	tcctgatcaa	780
ctccctatcta	taatatogtg	gtctttagtt	tgtctttatc	aatctgtgtg	tccttaactc	840
gagcaacata	tatactcgct	atcagacttt	ttacttaagc	tatatgtgtg	ttgtttgctt	900
atgacctcta	tgtattggtt	gtgttgtgtg	cttaaagctt	tcgmact		

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..208
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

Met	Gly	Arg	Gly	Lys	Ile	Glu	Ile	Lys	Arg	Ile	Glu	Asn	Ala	Asn	Asn	
1				5				10						15		
Arg	Val	Val	Thr	Phe	Ser	Lys	Arg	Arg	Asn	Gly	Leu	Val	Lys	Lys	Ala	
				20				25					30			
Lys	Glu	Ile	Thr	Val	Leu	Cys	Asp	Ala	Lys	Val	Ala	Leu	Ile	Ile	Phe	
				35				40					45			
Ala	Ser	Asn	Gly	Lys	Met	Ile	Asp	Tyr	Cys	Cys	Pro	Ser	Met	Asp	Leu	
				50				55					60			
Gly	Ala	Met	Leu	Asp	Gln	Tyr	Gln	Lys	Leu	Ser	Gly	Lys	Lys	Leu	Trp	
65					70					75					80	
Asp	Ala	Lys	His	Glu	Asn	Leu	Ser	Asn	Glu	Ile	Asp	Arg	Ile	Lys	Lys	
				85					90					95		
Glu	Asn	Asp	Ser	Leu	Gln	Leu	Glu	Leu	Arg	His	Leu	Lys	Gly	Glu	Asp	
				100				105					110			
Ile	Gln	Ser	Leu	Asn	Leu	Lys	Asn	Leu	Met	Ala	Val	Glu	His	Ala	Ile	
				115				120					125			
Glu	His	Gly	Leu	Asp	Lys	Val	Arg	Asp	His	Gln	Met	Glu	Ile	Leu	Ile	
				130				135				140				
Ser	Lys	Arg	Arg	Asn	Glu	Lys	Met	Met	Ala	Glu	Glu	Gln	Arg	Gln	Leu	
				145				150			155				160	
Thr	Phe	Gln	Leu	Gln	Gln	Gln	Glu	Met	Ala	Ile	Ala	Ser	Asn	Ala	Arg	
				165				170					175			
Gly	Met	Met	Met	Arg	Asp	His	Asp	Gly	Gln	Phe	Gly	Tyr	Arg	Val	Gln	
				180				185					190			
Pro	Ile	Gln	Pro	Asn	Leu	Gln	Glu	Lys	Ile	Met	Ser	Leu	Val	Ile	Asp	
				195				200					205			

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..155
(D) OTHER INFORMATION: / Ceres Seq. ID 1498196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

Met Ile Asp Tyr Cys Cys Pro Ser Met Asp Leu Gly Ala Met Leu Asp
1 5 10 15
Gln Tyr Gln Lys Leu Ser Gly Lys Lys Leu Trp Asp Ala Lys His Glu
20 25 30
Asn Leu Ser Asn Glu Ile Asp Arg Ile Lys Lys Glu Asn Asp Ser Leu
35 40 45
Gln Leu Glu Leu Arg His Leu Lys Gly Glu Asp Ile Gln Ser Leu Asn
50 55 60
Leu Lys Asn Leu Met Ala Val Glu His Ala Ile Glu His Gly Leu Asp
65 70 75 80
Lys Val Arg Asp His Gln Met Glu Ile Leu Ile Ser Lys Arg Arg Asn
85 90 95
Glu Lys Met Met Ala Glu Glu Gln Arg Gln Leu Thr Phe Gln Leu Gln
100 105 110
Gln Gln Glu Met Ala Ile Ala Ser Asn Ala Arg Gly Met Met Met Arg
115 120 125
Asp His Asp Gly Gln Phe Gly Tyr Arg Val Gln Pro Ile Gln Pro Asn
130 135 140
Leu Gln Glu Lys Ile Met Ser Leu Val Ile Asp
145 150 155

(2) INFORMATION FOR SEQ ID NO:263:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 147 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..147
(D) OTHER INFORMATION: / Ceres Seq. ID 1498197

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

Met Asp Leu Gly Ala Met Leu Asp Gln Tyr Gln Lys Leu Ser Gly Lys
1 5 10 15
Lys Leu Trp Asp Ala Lys His Glu Asn Leu Ser Asn Glu Ile Asp Arg
20 25 30
Ile Lys Lys Glu Asn Asp Ser Leu Gln Leu Glu Arg His Leu Lys
35 40 45
Gly Glu Asp Ile Gln Ser Leu Asn Leu Lys Asn Leu Met Ala Val Glu
50 55 60
His Ala Ile Glu His Gly Leu Asp Lys Val Arg Asp His Gln Met Glu
65 70 75 80
Ile Leu Ile Ser Lys Arg Arg Asn Glu Lys Met Met Ala Glu Glu Gln
85 90 95
Arg Gln Leu Thr Phe Gln Leu Gln Gln Glu Met Ala Ile Ala Ser
100 105 110
Asn Ala Arg Gly Met Met Met Arg Asp His Asp Gly Gln Phe Gly Tyr
115 120 125
Arg Val Gln Pro Ile Gln Pro Asn Leu Gln Glu Lys Ile Met Ser Leu
130 135 140
Val Ile Asp
145

(2) INFORMATION FOR SEQ ID NO:264:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1145 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1145

(D) OTHER INFORMATION: / Ceres Seq. ID 1498198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

```
atttcaaac acacattcaa actaactctg caaaagaaaa aaaaactcag agcagaggag 60
atcagagagag acaaaagagag acaaaagagag agagagagag agagagagag 120
agagatcttc aacaagcaat gtctatatcc atggcgttat tctctccgcc gatctcttcc 180
tcacttcaaa accetaatct catccccaag atctcaacct ctcttctctc caccaaacct 240
tctctctctaa tctccgtccc tagagcttcc tccgacaatg gtacgacttc ccccgctcgtg 300
aaaaattccga agcctgcgtc tgtagctgta gaggaagttc cgggtaaatc tccggcggaa 360
agctcctccg cttctgaaaa cggcgccggt ggaggtgaag cgactgattc gactactgag 420
acggtaatca aatatcaaaa tgcgaagtgg gttaatggaa cttgggattc gaacagttc 480
gagaaagatg gcaaaactga ttgggattct gttatcgttt ctgaggcaaa gaggagaaaa 540
tggcctgaag ataaccgccga aacaacgagt aacgacgagc ttgtgtctct cgactactcg 600
attattccat ggtgggcatg gatgaagaga taccatctac ctgaagctga acttctcaat 660
ggctcgtcgt cgatgatagg gttcttcatg gcttactttg ttgatagtct taccggagta 720
ggacttgttg atcaaatggg gaatttcttc tgcaaaacac tcttgtttgt ggctgtagct 780
ggagtctctc tcactccgtaa gaatgaagat ttatgcaaac gcatggaagc agccagattc atcaacagtt 900
actacgttat atgacaaaac atgcaaacgt ctttcaattt cctttttttg ttatgcaata 960
tcttcaaaag agtgaacaag ttcttacaat ctttcaattt cctttttttg ttatgcaata 1020
atctgtgaat cagtgaagt ttatctctac tgaactactg atcttcagat ttgttaactc 1080
tctctgttta aaaatctcta tgaagtatgc tcaaaagataa tgtatcgaag gtccttgact 1140
tgtaaacgac accattttcg ttttgacgtc tgataattta atcaataaga gatttttttt
ttaat
```

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 304 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..304

(D) OTHER INFORMATION: / Ceres Seq. ID 1498199

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

```
Ile Ser Asn His Thr Phe Lys Leu Thr Leu Gln Lys Lys Lys Lys Leu
1 5 10 15
Arg Ala Glu Glu Ile Glu Arg Asp Lys Glu Arg Gln Arg Glu Arg Glu
20 25 30
Arg Glu Arg Glu Arg Glu Arg Glu Arg Asp Leu Gln Gln Ala Met Ser
35 40 45
Ile Ser Met Ala Leu Phe Ser Pro Pro Ile Ser Ser Ser Leu Gln Asn
50 55 60
Pro Asn Leu Ile Pro Lys Ile Ser Thr Ser Leu Leu Ser Thr Lys Arg
65 70 75 80
Phe Ser Leu Ile Ser Val Pro Arg Ala Ser Ser Asp Asn Gly Thr Thr
85 90 95
Ser Pro Val Val Lys Ile Pro Lys Pro Ala Ser Val Ala Val Glu Glu
100 105 110
Val Pro Val Lys Ser Pro Ala Glu Ser Ser Ser Ala Ser Glu Asn Gly
115 120 125
Ala Val Gly Gly Glu Ala Thr Asp Ser Ser Thr Glu Thr Val Ile Lys
130 135 140
```

Tyr	Gln	Asn	Ala	Lys	Trp	Val	Asn	Gly	Thr	Trp	Asp	Leu	Lys	Gln	Phe	
145					150					155					160	
Glu	Lys	Asp	Gly	Lys	Thr	Asp	Trp	Asp	Ser	Val	Ile	Val	Ser	Glu	Ala	
				165					170					175		
Lys	Arg	Arg	Lys	Trp	Leu	Glu	Asp	Asn	Pro	Glu	Thr	Thr	Ser	Asn	Asp	
			180					185					190			
Glu	Leu	Val	Val	Phe	Asp	Thr	Ser	Ile	Ile	Pro	Trp	Trp	Ala	Trp	Met	
			195				200					205				
Lys	Arg	Tyr	His	Leu	Pro	Glu	Ala	Glu	Leu	Leu	Asn	Gly	Arg	Ala	Ala	
			210			215					220					
Met	Ile	Gly	Phe	Phe	Met	Ala	Tyr	Phe	Val	Asp	Ser	Leu	Thr	Gly	Val	
225					230					235					240	
Gly	Leu	Val	Asp	Gln	Met	Gly	Asn	Phe	Phe	Cys	Lys	Thr	Leu	Leu	Phe	
				245					250					255		
val	Ala	Val	Ala	Gly	Val	Leu	Phe	Ile	Arg	Lys	Asn	Glu	Asp	Leu	Asp	
			260					265					270			
Lys	Leu	Lys	Asp	Leu	Phe	Asp	Glu	Thr	Leu	Tyr	Asp	Lys	Gln	Trp		
			275				280				285					
Gln	Ala	Ala	Trp	Lys	Glu	Pro	Asp	Ser	Ser	Thr	Val	Ser	Ser	Lys	Lys	
			290			295					300					

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 258 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..258

(D) OTHER INFORMATION: / Ceres Seq. ID 1498200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

Met	Ser	Ile	Ser	Met	Ala	Leu	Phe	Ser	Pro	Pro	Ile	Ser	Ser	Ser	Leu	
1				5					10					15		
Gln	Asn	Pro	Asn	Leu	Ile	Pro	Lys	Ile	Ser	Thr	Ser	Leu	Leu	Ser	Thr	
				20				25					30			
Lys	Arg	Phe	Ser	Leu	Ile	Ser	Val	Pro	Arg	Ala	Ser	Ser	Asp	Asn	Gly	
		35					40				45					
Thr	Thr	Ser	Pro	Val	Val	Lys	Ile	Pro	Lys	Pro	Ala	Ser	Ser	Val	Ala	Val
		50				55					60					
Glu	Glu	Val	Pro	Val	Lys	Ser	Pro	Ala	Glu	Ser	Ser	Ser	Ala	Ser	Glu	
				70					75					80		
Asn	Gly	Ala	Val	Gly	Gly	Glu	Ala	Thr	Asp	Ser	Ser	Thr	Glu	Thr	Val	
				85					90				95			
Ile	Lys	Tyr	Gln	Asn	Ala	Lys	Trp	Val	Asn	Gly	Thr	Trp	Asp	Leu	Lys	
			100				105					110				
Gln	Phe	Glu	Lys	Asp	Gly	Lys	Thr	Asp	Trp	Asp	Ser	Val	Ile	Val	Ser	
			115				120					125				
Glu	Ala	Lys	Arg	Arg	Lys	Trp	Leu	Glu	Asp	Asn	Pro	Glu	Thr	Thr	Ser	
			130			135					140					
Asn	Asp	Glu	Leu	Val	Val	Phe	Asp	Thr	Ser	Ile	Ile	Pro	Trp	Trp	Ala	
145				150						155					160	
Trp	Met	Lys	Arg	Tyr	His	Leu	Pro	Glu	Ala	Glu	Leu	Leu	Asn	Gly	Arg	
				165					170				175			
Ala	Ala	Met	Ile	Gly	Phe	Phe	Met	Ala	Tyr	Phe	Val	Asp	Ser	Leu	Thr	
			180				185						190			
Gly	Val	Gly	Leu	Val	Asp	Gln	Met	Gly	Asn	Phe	Phe	Cys	Lys	Thr	Leu	
			195			200						205				
Leu	Phe	Val	Ala	Val	Ala	Gly	Val	Leu	Phe	Ile	Arg	Lys	Asn	Glu	Asp	

210					215										220
Leu	Asp	Lys	Leu	Lys	Asp	Leu	Phe	Asp	Glu	Thr	Thr	Leu	Tyr	Asp	Lys
225					230										240
Gln	Trp	Gln	Ala	Ala	Trp	Lys	Glu	Pro	Asp	Ser	Ser	Thr	Val	Ser	Ser
				245					250						255

Lys Lys

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..254
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

Met	Ala	Leu	Phe	Ser	Pro	Pro	Ile	Ser	Ser	Ser	Leu	Gln	Asn	Pro	Asn
1				5				10					15		
Leu	Ile	Pro	Lys	Ile	Ser	Thr	Ser	Leu	Ser	Thr	Lys	Arg	Phe	Ser	
			20				25					30			
Leu	Ile	Ser	Val	Pro	Arg	Ala	Ser	Ser	Asp	Asn	Gly	Thr	Ser	Pro	
			35			40					45				
Val	Val	Lys	Ile	Pro	Lys	Pro	Ala	Ser	Val	Ala	Val	Glu	Glu	Val	Pro
			50			55				60					
Val	Lys	Ser	Pro	Ala	Glu	Ser	Ser	Ser	Ala	Ser	Glu	Asn	Gly	Ala	Val
			65		70				75				80		
Gly	Gly	Glu	Ala	Thr	Asp	Ser	Ser	Thr	Glu	Thr	Val	Ile	Lys	Tyr	Gln
			85					90					95		
Asn	Ala	Lys	Trp	Val	Asn	Gly	Thr	Trp	Asp	Leu	Lys	Gln	Phe	Glu	Lys
			100				105					110			
Asp	Gly	Lys	Thr	Asp	Trp	Asp	Ser	Val	Ile	Val	Ser	Glu	Ala	Lys	Arg
			115			120					125				
Arg	Lys	Trp	Leu	Glu	Asp	Asn	Pro	Glu	Thr	Ser	Asn	Asp	Glu	Leu	
			130			135				140					
Val	Val	Phe	Asp	Thr	Ser	Ile	Ile	Pro	Trp	Trp	Ala	Trp	Met	Lys	Arg
			145		150					155				160	
Tyr	His	Leu	Pro	Glu	Ala	Glu	Leu	Leu	Asn	Gly	Arg	Ala	Ala	Met	Ile
			165					170					175		
Gly	Phe	Phe	Met	Ala	Tyr	Phe	Val	Asp	Ser	Leu	Thr	Gly	Val	Gly	Leu
			180				185					190			
Val	Asp	Gln	Met	Gly	Asn	Phe	Phe	Cys	Lys	Thr	Leu	Leu	Phe	Val	Ala
			195			200					205				
Val	Ala	Gly	Val	Leu	Phe	Ile	Arg	Lys	Asn	Glu	Asp	Leu	Asp	Lys	Leu
			210			215					220				
Lys	Asp	Leu	Phe	Asp	Glu	Thr	Leu	Tyr	Asp	Lys	Gln	Trp	Gln	Ala	
			225		230				235					240	
Ala	Trp	Lys	Glu	Pro	Asp	Ser	Ser	Thr	Val	Ser	Ser	Lys	Lys		
			245					250							

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 790 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..790

(B) LOCATION: 1..183

(D) OTHER INFORMATION: / Ceres Seq. ID 1498204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

Met Asp Gly Gly Asp Arg Leu Arg Val Thr Leu Leu Asp Arg Met Ser
1 5 10 15
Thr Val Glu Asn Gly Arg Ser Ser Val Thr Leu Glu Asp Ile Leu Met
20 25 30
Ala Glu Thr Ser Ser Phe Arg Ser Leu Thr Thr Pro Thr Thr Pro Val
35 40 45
Arg Asn His Ser Ser Ser Ser Leu Leu Asp Val Met Arg Arg Glu Arg
50 55 60
Arg Arg Asp Lys Thr Ala Trp Lys Ser Leu Arg Asp Xaa Leu Xaa Leu
65 70 75 80
Lys Arg Thr Ala Thr Gly Trp Ile Ser Ser Asn Pro Ile Pro Thr Leu
85 90 95
Asp Asn His Ile Leu Thr Pro Asp Asn Asp Ser His Arg Phe Asn Arg
100 105 110
Leu Gly Phe Leu Leu Thr Asn Ser Glu Thr Asn Arg Ser Ser Arg Asp
115 120 125
Val Ser Asp Ala Ala Glu Glu Val Ala Glu Arg Glu Gly Arg Leu Arg
130 135 140
Leu Gly Thr Val Leu Ala Ala Glu Arg Glu Glu Met Gln Pro Pro Arg
145 150 155 160
Met Ser Leu Met Glu Leu Leu Glu Pro Pro Ser Gln Pro Pro Pro Ile
165 170 175
Lys His Leu Val Asn Lys Phe
180

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..169

(D) OTHER INFORMATION: / Ceres Seq. ID 1498205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

Met Ser Thr Val Glu Asn Gly Arg Ser Ser Val Thr Leu Glu Asp Ile
1 5 10 15
Leu Met Ala Glu Thr Ser Ser Phe Arg Ser Leu Thr Thr Pro Thr Thr
20 25 30
Pro Val Arg Asn His Ser Ser Ser Ser Leu Leu Asp Val Met Arg Arg
35 40 45
Glu Arg Arg Arg Asp Lys Thr Ala Trp Lys Ser Leu Arg Asp Xaa Leu
50 55 60
Xaa Leu Lys Arg Thr Ala Thr Gly Trp Ile Ser Ser Asn Pro Ile Pro
65 70 75 80
Thr Leu Asp Asn His Ile Leu Thr Pro Asp Asn Asp Ser His Arg Phe
85 90 95
Asn Arg Leu Gly Phe Leu Leu Thr Asn Ser Glu Thr Asn Arg Ser Ser
100 105 110
Arg Asp Val Ser Asp Ala Ala Glu Glu Val Ala Glu Arg Glu Gly Arg
115 120 125
Leu Arg Leu Gly Thr Val Leu Ala Ala Glu Arg Glu Glu Met Gln Pro
130 135 140
Pro Arg Met Ser Leu Met Glu Leu Leu Glu Pro Pro Ser Gln Pro Pro
145 150 155 160
Pro Ile Lys His Leu Val Asn Lys Phe
165

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1609 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1609
(D) OTHER INFORMATION: / Ceres Seq. ID 1498206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

ccatagttcc	agttctgaaa	tctcacttct	acagtttgtg	tctgtgcgat	aatggccatg	60
gcagagctct	caaccoccaa	aacgacgtcg	cctttctcca	actcttctgc	tcggtcttgt	120
ctctcttcaa	aattgcacct	tccaaccac	tttcgccaat	ttctcttccc	acctctccac	180
acacacacat	ccaactccaa	aatctcttgc	tccgtttctc	aaaatagcca	agctcctgtt	240
gctgtgcaag	aaaaatggatt	ggtgaagacg	aagaaaagat	gttatggagt	gttctgcctc	300
acctatgac	ttaaagtga	agaagagaca	agatcatgga	agaagttaat	taatatgtca	360
gtttcagctg	ctgcaggaat	gatttctaac	catcttctct	tcaaaacttg	tcagggggaa	420
gtatttgctc	cagatcaacc	cattgcattg	aaactgctag	gatacagagag	atcaattcaa	480
gctcttgaa	gtgttgcaat	ggaaactggag	gattcatgtg	tcccattgtt	gagagaagtt	540
gatattagaa	cagatccaaa	tgaagtgttc	caagatgtgg	agtgggctat	tctgattgga	600
gcacaaacctc	gaggccctgg	aatggaacgt	gctgacttgt	tggacatcaa	tgcccaaatc	660
tttgctgagc	agggcaaaag	tctgaacaaa	gctgcctctc	ctaactgtca	ggctcttgta	720
gtgggaaacc	cttgcacaac	caatgccttg	atttgtctta	aaaatgctcc	caacattcct	780
gcaagaacct	tccatgccct	cacgaggtta	gacgaaaatc	gtgccaaatg	ccagcttgtgt	840
cttaaacccg	gtgttttcta	tgacaaaagt	tctaataatg	ccatattggg	aaatcactcc	900
acgactcagg	tgccagactt	cttaaatgcc	agaattaatg	gctgcctgtg	gaaggaggtt	960
attacagatc	acaaatggtt	agaagagggg	ttcactgaga	gtgtgcagaa	gagaggtggg	1020
ttattaattc	agaaatgggg	tcgatcttct	ctgctgttca	ctctgttttc	catgttgtat	1080
gctataaagt	ctcttgrtrc	tctactcctc	gaggktgatt	ggttttgcag	tggggtgtac	1140
acggatggaa	atccttatgg	tattgaagag	ggccttgctc	tcagtatgcc	atgccggtcg	1200
aaggagagat	gagattatga	acttgtcaag	gatgtagaaa	ttgatgacta	ccttcgcaaa	1260
cgaatcgcca	agtcggaagc	ggaactgttg	gctgagaaga	gatgtgttgc	acacctcact	1320
ggagagggca	ttgcctactg	tgatcttggt	cggtagataa	ctatgcttcc	tggggaagtt	1380
tgatttttgc	aggacgttga	acatctcaag	taagcattct	cttcgggttg	gttagctgta	1440
cagagcacag	ccacattact	tatgatgatt	gttcagaata	agaaaaagaa	actcttattt	1500
ctattttaca	tgcattctga	tgtgattttt	cttgagcaat	gctccaaaag	tcataacacg	1560
tagtatattg	aaacacttga	aacgtttcta	tgctttattc	cagtttcag		

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..443
(D) OTHER INFORMATION: / Ceres Seq. ID 1498207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

Met	Ala	Met	Ala	Glu	Leu	Ser	Thr	Pro	Lys	Thr	Thr	Ser	Pro	Phe	Leu
1				5				10						15	
Asn	Ser	Ser	Ser	Ser	Arg	Leu	Arg	Leu	Ser	Ser	Lys	Leu	His	Leu	Ser
				20				25						30	Asn
His	Phe	Arg	His	Leu	Leu	Leu	Pro	Pro	Leu	His	Thr	Thr	Thr	Pro	Asn
				35				40						45	
Ser	Lys	Ile	Ser	Cys	Ser	Val	Ser	Gln	Asn	Ser	Gln	Ala	Pro	Val	Ala
				50				55						60	
Val	Gln	Glu	Asn	Gly	Leu	Val	Lys	Thr	Lys	Lys	Glu	Cys	Tyr	Gly	Val
65				70				75						80	

Phe	Cys	Leu	Thr	Tyr	Asp	Leu	Lys	Ala	Glu	Glu	Glu	Thr	Arg	Ser	Trp	
				85					90					95		
Lys	Lys	Leu	Ile	Asn	Ile	Ala	Val	Ser	Gly	Ala	Ala	Gly	Met	Ile	Ser	
			100					105					110			
Asn	His	Leu	Leu	Phe	Lys	Leu	Ala	Ser	Gly	Glu	Val	Phe	Gly	Pro	Asp	
		115					120					125				
Gln	Pro	Ile	Ala	Leu	Lys	Leu	Leu	Gly	Ser	Glu	Arg	Ser	Ile	Gln	Ala	
		130				135					140					
Leu	Glu	Gly	Val	Ala	Met	Glu	Leu	Glu	Asp	Ser	Leu	Phe	Pro	Leu	Leu	
					150					155					160	
Arg	Glu	Val	Asp	Ile	Gly	Thr	Asp	Pro	Asn	Glu	Val	Phe	Gln	Asp	Val	
				165					170					175		
Glu	Trp	Ala	Ile	Leu	Ile	Gly	Ala	Lys	Pro	Arg	Gly	Pro	Gly	Met	Glu	
			180					185					190			
Arg	Ala	Asp	Leu	Leu	Asp	Ile	Asn	Gly	Gln	Ile	Phe	Ala	Glu	Gln	Gly	
		195					200				205					
Lys	Ala	Leu	Asn	Lys	Ala	Ala	Ser	Pro	Asn	Val	Lys	Val	Leu	Val	Val	
		210				215				220						
Gly	Asn	Pro	Cys	Asn	Thr	Asn	Ala	Leu	Ile	Cys	Leu	Lys	Asn	Ala	Pro	
		225				230				235					240	
Asn	Ile	Pro	Ala	Lys	Asn	Phe	His	Ala	Leu	Thr	Arg	Leu	Asp	Glu	Asn	
				245					250					255		
Arg	Ala	Lys	Cys	Gln	Leu	Ala	Leu	Lys	Ala	Gly	Val	Phe	Tyr	Asp	Lys	
			260				265						270			
Val	Ser	Asn	Met	Thr	Ile	Trp	Gly	Asn	His	Ser	Thr	Thr	Gln	Val	Pro	
		275					280					285				
Asp	Phe	Leu	Asn	Ala	Arg	Ile	Asn	Gly	Leu	Pro	Val	Lys	Glu	Val	Ile	
		290				295					300					
Thr	Asp	His	Lys	Trp	Leu	Glu	Glu	Gly	Phe	Thr	Glu	Ser	Val	Gln	Lys	
		305			310					315					320	
Arg	Gly	Gly	Leu	Leu	Ile	Gln	Lys	Trp	Gly	Arg	Ser	Ser	Ala	Ala	Ser	
			325						330					335		
Thr	Ala	Val	Ser	Ile	Val	Asp	Ala	Ile	Lys	Ser	Leu	Xaa	Thr	Pro	Thr	
			340				345						350			
Pro	Glu	Xaa	Asp	Trp	Phe	Ser	Thr	Gly	Val	Tyr	Thr	Asp	Gly	Asn	Pro	
		355					360				365					
Tyr	Gly	Ile	Glu	Glu	Gly	Leu	Val	Phe	Ser	Met	Pro	Cys	Arg	Ser	Lys	
		370				375					380					
Gly	Asp	Gly	Asp	Tyr	Glu	Leu	Val	Lys	Asp	Val	Glu	Ile	Asp	Asp	Tyr	
		385			390					395					400	
Leu	Arg	Gln	Arg	Ile	Ala	Lys	Ser	Glu	Ala	Glu	Leu	Leu	Ala	Glu	Lys	
				405					410					415		
Arg	Cys	Val	Ala	His	Leu	Thr	Gly	Glu	Gly	Ile	Ala	Tyr	Cys	Asp	Leu	
			420					425					430			
Gly	Pro	Val	Asp	Thr	Met	Leu	Pro	Gly	Glu	Val						
		435				440										

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..441
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

Met	Ala	Glu	Leu	Ser	Thr	Pro	Lys	Thr	Ser	Pro	Phe	Leu	Asn	Ser	
1				5				10					15		
Ser	Ser	Arg	Leu	Arg	Leu	Ser	Ser	Lys	Leu	His	Leu	Ser	Asn	His	Phe

Arg	His	Leu	Leu	Pro	Pro	Leu	His	Thr	Thr	Thr	Pro	Asn	Ser	Lys
Ile	Ser	Cys	Ser	Val	Ser	Gln	Asn	Ser	Gln	Ala	Pro	Val	Ala	Val
Glu	Asn	Gly	Leu	Val	Lys	Thr	Lys	Lys	Glu	Cys	Tyr	Gly	Val	Phe
Leu	Thr	Tyr	Asp	Leu	Lys	Ala	Glu	Glu	Glu	Thr	Arg	Ser	Trp	Lys
Leu	Ile	Asn	Ile	Ala	Val	Ser	Gly	Ala	Ala	Gly	Met	Ile	Ser	Asn
Leu	Leu	Phe	Lys	Leu	Ala	Ser	Gly	Glu	Val	Phe	Gly	Pro	Asp	Gln
Ile	Ala	Leu	Lys	Leu	Leu	Gly	Ser	Glu	Arg	Ser	Ile	Gln	Ala	Leu
Gly	Val	Ala	Met	Glu	Leu	Glu	Asp	Ser	Leu	Phe	Pro	Leu	Leu	Arg
Val	Asp	Ile	Gly	Thr	Asp	Pro	Asn	Glu	Val	Phe	Gln	Asp	Val	Glu
Ala	Ile	Leu	Ile	Gly	Ala	Lys	Pro	Arg	Gly	Pro	Gly	Met	Glu	Arg
Asp	Leu	Leu	Asp	Ile	Asn	Gly	Gln	Ile	Phe	Ala	Glu	Gln	Gly	Lys
Leu	Asn	Lys	Ala	Ala	Ser	Pro	Asn	Val	Lys	Val	Leu	Val	Val	Gly
Pro	Cys	Asn	Thr	Asn	Ala	Leu	Ile	Cys	Leu	Lys	Asn	Ala	Pro	Asn
Pro	Ala	Lys	Asn	Phe	His	Ala	Leu	Thr	Arg	Leu	Asp	Glu	Asn	Arg
Lys	Cys	Gln	Leu	Ala	Leu	Lys	Ala	Gly	Val	Phe	Tyr	Asp	Lys	Val
Asn	Met	Thr	Ile	Trp	Gly	Asn	His	Ser	Thr	Thr	Gln	Val	Pro	Asp
Leu	Asn	Ala	Arg	Ile	Asn	Gly	Leu	Pro	Val	Lys	Glu	Val	Ile	Thr
His	Lys	Trp	Leu	Glu	Glu	Gly	Phe	Thr	Glu	Ser	Val	Gln	Lys	Arg
Gly	Leu	Leu	Ile	Gln	Lys	Trp	Gly	Arg	Ser	Ser	Ala	Val	Ser	Thr
Val	Ser	Ile	Val	Asp	Ala	Ile	Lys	Ser	Leu	Xaa	Thr	Pro	Thr	Pro
Xaa	Asp	Trp	Phe	Ser	Thr	Gly	Val	Tyr	Thr	Asp	Gly	Asn	Pro	Tyr
Ile	Glu	Glu	Gly	Leu	Val	Phe	Ser	Met	Pro	Cys	Arg	Ser	Lys	Gly
Gly	Asp	Tyr	Glu	Leu	Val	Lys	Asp	Val	Glu	Ile	Asp	Asp	Tyr	Leu
Gln	Arg	Ile	Ala	Lys	Ser	Glu	Ala	Glu	Leu	Leu	Ala	Glu	Lys	Arg
Val	Ala	His	Leu	Thr	Gly	Glu	Gly	Ile	Ala	Tyr	Cys	Asp	Leu	Gly
Val	Asp	Thr	Met	Leu	Pro	Gly	Glu	Val						

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..334
(D) OTHER INFORMATION: / Ceres Seq. ID 1498209

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

Met	Ile	Ser	Asn	His	Leu	Leu	Phe	Lys	Leu	Ala	Ser	Gly	Glu	Val	Phe
1				5				10						15	
Gly	Pro	Asp	Gln	Pro	Ile	Ala	Leu	Lys	Leu	Leu	Gly	Ser	Glu	Arg	Ser
			20					25						30	
Ile	Gln	Ala	Leu	Glu	Gly	Val	Ala	Met	Glu	Leu	Glu	Asp	Ser	Leu	Phe
		35					40					45			
Pro	Leu	Leu	Arg	Glu	Val	Asp	Ile	Gly	Thr	Asp	Pro	Asn	Glu	Val	Phe
	50					55					60				
Gln	Asp	Val	Glu	Trp	Ala	Ile	Leu	Ile	Gly	Ala	Lys	Pro	Arg	Gly	Pro
65				70						75				80	
Gly	Met	Glu	Arg	Ala	Asp	Leu	Leu	Asp	Ile	Asn	Gly	Gln	Ile	Phe	Ala
				85					90					95	
Glu	Gln	Gly	Lys	Ala	Leu	Asn	Lys	Ala	Ala	Ser	Pro	Asn	Val	Lys	Val
			100					105					110		
Leu	Val	Val	Gly	Asn	Pro	Cys	Asn	Thr	Asn	Ala	Leu	Ile	Cys	Leu	Lys
			115				120					125			
Asn	Ala	Pro	Asn	Ile	Pro	Ala	Lys	Asn	Phe	His	Ala	Leu	Thr	Arg	Leu
			130				135					140			
Asp	Glu	Asn	Arg	Ala	Lys	Cys	Gln	Leu	Ala	Leu	Lys	Ala	Gly	Val	Phe
145				150						155				160	
Tyr	Asp	Lys	Val	Ser	Asn	Met	Thr	Ile	Trp	Gly	Asn	His	Ser	Thr	Thr
				165					170					175	
Gln	Val	Pro	Asp	Phe	Leu	Asn	Ala	Arg	Ile	Asn	Gly	Leu	Pro	Val	Lys
			180					185					190		
Glu	Val	Ile	Thr	Asp	His	Lys	Trp	Leu	Glu	Glu	Gly	Phe	Thr	Glu	Ser
			195					200				205			
Val	Gln	Lys	Arg	Gly	Gly	Leu	Leu	Ile	Gln	Lys	Trp	Gly	Arg	Ser	Ser
			210				215					220			
Ala	Ala	Ser	Thr	Ala	Val	Ser	Ile	Val	Asp	Ala	Ile	Lys	Ser	Leu	Xaa
225				230						235				240	
Thr	Pro	Thr	Pro	Glu	Xaa	Asp	Trp	Phe	Ser	Thr	Gly	Val	Tyr	Thr	Asp
				245					250					255	
Gly	Asn	Pro	Tyr	Gly	Ile	Glu	Glu	Gly	Leu	Val	Phe	Ser	Met	Pro	Cys
				260				265					270		
Arg	Ser	Lys	Gly	Asp	Gly	Asp	Tyr	Glu	Leu	Val	Lys	Asp	Val	Glu	Ile
			275				280					285			
Asp	Asp	Tyr	Leu	Arg	Gln	Arg	Ile	Ala	Lys	Ser	Glu	Ala	Glu	Leu	Leu
			290				295				300				
Ala	Glu	Lys	Arg	Cys	Val	Ala	His	Leu	Thr	Gly	Glu	Gly	Ile	Ala	Tyr
305				310						315				320	
Cys	Asp	Leu	Gly	Pro	Val	Asp	Thr	Met	Leu	Pro	Gly	Glu	Val		
			325					330							

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1500 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1500
(D) OTHER INFORMATION: / Ceres Seq. ID 1498210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

atctcttggt	ctctccgcc	atctctgtc	tcttttatt	tccagaaag	ttttttttt	60
tttcccgaa	tccgttaac	tcattgggt	ttccattgat	agcaatggc	acggttttg	120
ctccactaa	gtcactgcc	acggttcct	tgcatggat	ccatgagaat	cgtctcttg	180

tcccgatcgc	attggtcctc	cctctctctt	tccctggatc	caccgcgttc	ctctcccttc	240
gcagactcaa	tcaactccaac	gccaccgcgc	gatctcccgct	cgtctctgtc	cagggaagttg	300
tcaaggagaa	gcaatccacc	aataatacca	gcctgttgat	aaccaagag	gaaggattgg	360
agttgtatga	agatatgata	ctaggttagat	ctttcgaaaga	catgtgtgct	caaatgtatt	420
accgaggcaa	gatgtttgg	ttgtttcact	tgtacaatgg	ccaagagct	gtttctactg	480
gctttatcaa	gctccttacc	aagtctgact	ctgtcgttag	tacctaccgt	gaccatgtcc	540
atgcccctag	caaaaggtgtc	tctgtctgtg	ctgttatgat	cgagctcttc	ggcaaggtta	600
ctggatgctg	cagaaggccaa	gggtgatcca	tgcacatgtt	ctccaaagaa	caacaatgac	660
tgtgtggcct	tgccttttatt	gggtgaaggca	ttcctgtcgc	cactggtgct	gctctttagct	720
ccaagtacag	gaggggaagtc	ttgaaacagg	attgtgatga	tgtcaactgtc	gctcttttgc	780
gagatgggaa	ttgtatacaac	ggacagttct	tgcagtgctc	caacatggct	gctctctata	840
aactgcctat	tatctttgtt	gtcgagaata	actgtggggc	cattggggatg	tctcaactgt	900
gagccacttc	tgaccocagg	atttgaaga	aaggtcctgc	cttggggatg	cctgggtgttc	960
atgttgacgg	tatggatgtc	ttgaaggtca	gggaagtcgc	taaagagctc	gtcactagag	1020
ctagaagagg	agaaggtcca	acctgtggtg	aatgtgagac	ttatagattt	agaggacact	1080
ctctgggtga	tcccgtatgag	ctccgtgatg	ctgctgagaa	agccaaatag	gcggctagag	1140
acccaatcgc	agcattgaag	aagtatttga	tagagaacaa	gcttgcaaa	gagcagagac	1200
taaagtcaat	agagaaaaag	atagacgagt	tgggtggagga	agcggttgag	tttgacagac	1260
ctagtccaca	gcccggtcgc	agtcagttgc	tagagaaatg	gtttgctgat	ccaaaaggat	1320
ttggaattgg	acctgatgga	cggtagacat	gtgaggacc	caagtttacc	gaaggcacag	1380
ctcaagctcg	agaagacaag	tttaaccata	agctgtctac	tgtctctctc	atgtatttcta	1440
tatatcttat	taagttaaat	gctacagaga	atcagtttga	atcatttgca	ctttttgtcg	1500

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..462
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498211

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

Leu	Leu	Phe	Ser	Pro	Pro	Ile	Ser	Ala	Leu	Phe	Tyr	Phe	Pro	Gly	Leu	Ser
1			5					10					15			
Phe	Phe	Phe	Phe	Ser	Arg	Ile	Pro	Leu	Ile	Ser	Leu	Gly	Phe	Pro	Leu	
			20					25					30			
Ile	Ala	Met	Ala	Thr	Ala	Phe	Ala	Pro	Thr	Lys	Leu	Thr	Ala	Thr	Val	
		35					40					45				
Pro	Leu	His	Gly	Ser	His	Glu	Asn	Arg	Leu	Leu	Leu	Pro	Ile	Arg	Leu	
		50					55				60					
Ala	Pro	Pro	Ser	Ser	Phe	Leu	Gly	Ser	Thr	Arg	Ser	Leu	Ser	Leu	Arg	
		65					70				75				80	
Arg	Leu	Asn	His	Ser	Asn	Ala	Thr	Arg	Arg	Ser	Pro	Val	Val	Ser	Val	
			85							90					95	
Gln	Glu	Val	Val	Lys	Glu	Lys	Gln	Ser	Thr	Asn	Asn	Thr	Ser	Leu	Leu	
			100							105				110		
Ile	Thr	Lys	Glu	Glu	Gly	Leu	Glu	Leu	Tyr	Glu	Asp	Met	Ile	Leu	Gly	
		115					120					125				
Arg	Ser	Phe	Glu	Asp	Met	Cys	Ala	Gln	Met	Tyr	Tyr	Arg	Gly	Lys	Met	
		130					135					140				
Phe	Gly	Phe	Val	His	Leu	Tyr	Asn	Gly	Gln	Glu	Ala	Val	Ser	Thr	Gly	
					150					155					160	
Phe	Ile	Lys	Leu	Leu	Thr	Lys	Ser	Asp	Ser	Val	Val	Ser	Thr	Tyr	Arg	
					165					170					175	
Asp	His	Val	His	Ala	Leu	Ser	Lys	Gly	Val	Ser	Ala	Arg	Ala	Val	Met	
					180					185					190	
Ser	Glu	Leu	Phe	Gly	Lys	Val	Thr	Gly	Cys	Cys	Arg	Gly	Gln	Gly	Gly	
			195				200							205		

Ser Met His Met Phe Ser Lys Glu His Asn Met Leu Gly Gly Phe Ala
210 215 220
Phe Ile Gly Glu Gly Ile Pro Val Ala Thr Gly Ala Ala Phe Ser Ser
225 230 235 240
Lys Tyr Arg Arg Glu Val Leu Lys Gln Asp Cys Asp Val Thr Val
245 250 255
Ala Phe Phe Gly Asp Gly Thr Cys Asn Asn Gly Gln Phe Phe Glu Cys
260 265 270
Leu Asn Met Ala Ala Leu Tyr Lys Leu Pro Ile Ile Phe Val Val Glu
275 280 285
Asn Asn Leu Trp Ala Ile Gly Met Ser His Leu Arg Ala Thr Ser Asp
290 295 300
Pro Glu Ile Trp Lys Lys Gly Pro Ala Phe Gly Met Pro Gly Val His
305 310 315 320
Val Asp Gly Met Asp Val Leu Lys Val Arg Glu Val Ala Lys Glu Ala
325 330 335
Val Thr Arg Ala Arg Arg Gly Glu Gly Pro Thr Leu Val Glu Cys Glu
340 345 350
Thr Tyr Arg Phe Arg Gly His Ser Leu Ala Asp Pro Asp Glu Leu Arg
355 360 365
Asp Ala Ala Glu Lys Ala Lys Tyr Ala Ala Arg Asp Pro Ile Ala Ala
370 375 380
Leu Lys Lys Tyr Leu Ile Glu Asn Lys Leu Ala Lys Glu Ala Glu Leu
385 390 395 400
Lys Ser Ile Glu Lys Lys Ile Asp Glu Leu Val Glu Glu Ala Val Glu
405 410 415
Phe Ala Asp Ala Ser Pro Gln Pro Gly Arg Ser Gln Leu Leu Glu Asn
420 425 430
Val Phe Ala Asp Pro Lys Gly Phe Gly Ile Gly Pro Asp Gly Arg Tyr
435 440 445
Arg Cys Glu Asp Pro Lys Phe Thr Glu Gly Thr Ala Gln Val
450 455 460

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..428
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

Met Ala Thr Ala Phe Ala Pro Thr Lys Leu Thr Ala Thr Val Pro Leu
1 5 10 15
His Gly Ser His Glu Asn Arg Leu Leu Pro Ile Arg Leu Ala Pro
20 25 30
Pro Ser Ser Phe Leu Gly Ser Thr Arg Ser Leu Ser Leu Arg Arg Leu
35 40 45
Asn His Ser Asn Ala Thr Arg Arg Ser Pro Val Val Ser Val Gln Glu
50 55 60
Val Val Lys Glu Lys Gln Ser Thr Asn Asn Thr Ser Leu Leu Ile Thr
65 70 75 80
Lys Glu Glu Gly Leu Glu Leu Tyr Glu Asp Met Ile Leu Gly Arg Ser
85 90 95
Phe Glu Asp Met Cys Ala Gln Met Tyr Tyr Arg Gly Lys Met Phe Gly
100 105 110
Phe Val His Leu Tyr Asn Gly Gln Glu Ala Val Ser Thr Gly Phe Ile
115 120 125
Lys Leu Leu Thr Lys Ser Asp Ser Val Val Ser Thr Tyr Arg Asp His

130	135	140
Val His Ala Leu Ser Lys Gly Val Ser Ala Arg Ala Val Met Ser Glu		
145	150	155
Leu Phe Gly Lys Val Thr Gly Cys Cys Arg Gly Gln Gly Gly Ser Met		
165	170	175
His Met Phe Ser Lys Glu His Asn Met Leu Gly Gly Phe Ala Phe Ile		
180	185	190
Gly Glu Gly Ile Pro Val Ala Thr Gly Ala Ala Phe Ser Ser Lys Tyr		
195	200	205
Arg Arg Glu Val Leu Lys Gln Asp Cys Asp Asp Val Thr Val Ala Phe		
210	215	220
Phe Gly Asp Gly Thr Cys Asn Asn Gly Gln Phe Phe Glu Cys Leu Asn		
225	230	235
Met Ala Ala Leu Tyr Lys Leu Pro Ile Ile Phe Val Val Glu Asn Asn		
245	250	255
Leu Trp Ala Ile Gly Met Ser His Leu Arg Ala Thr Ser Asp Pro Glu		
260	265	270
Ile Trp Lys Lys Gly Pro Ala Phe Gly Met Pro Gly Val His Val Asp		
275	280	285
Gly Met Asp Val Leu Lys Val Arg Glu Val Ala Lys Glu Ala Val Thr		
290	295	300
Arg Ala Arg Arg Gly Glu Gly Pro Thr Leu Val Glu Cys Glu Thr Tyr		
305	310	315
Arg Phe Arg Gly His Ser Leu Ala Asp Pro Asp Glu Leu Arg Asp Ala		
325	330	335
Ala Glu Lys Ala Lys Tyr Ala Ala Arg Asp Pro Ile Ala Ala Leu Lys		
340	345	350
Lys Tyr Leu Ile Glu Asn Lys Leu Ala Lys Glu Ala Glu Leu Lys Ser		
355	360	365
Ile Glu Lys Lys Ile Asp Glu Leu Val Glu Glu Ala Val Glu Phe Ala		
370	375	380
Asp Ala Ser Pro Gln Pro Gly Arg Ser Gln Leu Leu Glu Asn Val Phe		
385	390	395
Ala Asp Pro Lys Gly Phe Gly Ile Gly Pro Asp Gly Arg Tyr Arg Cys		
405	410	415
Glu Asp Pro Lys Phe Thr Glu Gly Thr Ala Gln Val		
420	425	

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..338

(D) OTHER INFORMATION: / Ceres Seq. ID 1498213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

Met Ile Leu Gly Arg Ser Phe Glu Asp Met Cys Ala Gln Met Tyr Tyr		
1	5	10
Arg Gly Lys Met Phe Gly Phe Val His Leu Tyr Asn Gly Gln Glu Ala		
20	25	30
Val Ser Thr Gly Phe Ile Lys Leu Leu Thr Lys Ser Asp Ser Val Val		
35	40	45
Ser Thr Tyr Arg Asp His Val His Ala Leu Ser Lys Gly Val Ser Ala		
50	55	60
Arg Ala Val Met Ser Glu Leu Phe Gly Lys Val Thr Gly Cys Cys Arg		
65	70	75
Gly Gln Gly Gly Ser Met His Met Phe Ser Lys Glu His Asn Met Leu		
85	90	95

Gly Gly Phe Ala Phe Ile Gly Glu Gly Ile Pro Val Ala Thr Gly Ala
100 105 110
Ala Phe Ser Ser Lys Tyr Arg Arg Glu Val Leu Lys Gln Asp Cys Asp
115 120 125
Asp Val Thr Val Ala Phe Phe Gly Asp Gly Thr Cys Asn Asn Gly Gln
130 135 140
Phe Phe Glu Cys Leu Asn Met Ala Ala Leu Tyr Lys Leu Pro Ile Ile
145 150 155 160
Phe Val Val Glu Asn Asn Leu Trp Ala Ile Gly Met Ser His Leu Arg
165 170 175
Ala Thr Ser Asp Pro Glu Ile Trp Lys Lys Gly Pro Ala Phe Gly Met
180 185 190
Pro Gly Val His Val Asp Gly Met Asp Val Leu Lys Val Arg Glu Val
195 200 205
Ala Lys Glu Ala Val Thr Arg Ala Arg Arg Gly Glu Gly Pro Thr Leu
210 215 220
Val Glu Cys Glu Thr Tyr Arg Phe Arg Gly His Ser Leu Ala Asp Pro
225 230 235 240
Asp Glu Leu Arg Asp Ala Ala Glu Lys Ala Lys Tyr Ala Ala Arg Asp
245 250 255
Pro Ile Ala Ala Leu Lys Lys Tyr Leu Ile Glu Asn Lys Leu Ala Lys
260 265 270
Glu Ala Glu Leu Lys Ser Ile Glu Lys Lys Ile Asp Glu Leu Val Glu
275 280 285
Glu Ala Val Glu Phe Ala Asp Ala Ser Pro Gln Pro Gly Arg Ser Gln
290 295 300
Leu Leu Glu Asn Val Phe Ala Asp Pro Lys Gly Phe Gly Ile Gly Pro
305 310 315 320
Asp Gly Arg Tyr Arg Cys Glu Asp Pro Lys Phe Thr Glu Gly Thr Ala
325 330 335
Gln Val

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1126 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1126
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498214

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

aaaataattt	gaaaggaata	tgaatatctc	gttgaagaag	acttgctcct	gaaatcccttt	60
ggaccgaaac	togtaaaatt	atttccccttc	aatttctctg	aaatctattc	accgtctcct	120
ttgtctctcc	ctccaaaatc	atcgttctct	gtcgtcgtct	gattttctct	acgattgtct	180
tttctgtcta	gctcgataag	aaaaaacaaa	actaattttt	gaagagtttt	tttttttggt	240
tttgggagcg	atgggtcaag	cttttcgtaa	gctattcgat	actttctctg	gcaatcaaga	300
aatgagggtc	gttatgcttg	ggctggatgc	tgctggcaaa	acaactattc	ttcacaagct	360
tcataattggg	gaagttttgt	ctactgttcc	caccattgga	ttcaatgttg	agaaagtcca	420
gtacaagaat	gtgatgttca	cagtttggtg	tggttggtgc	caagagaaaac	tgagacctct	480
tttgaggcat	tacttcaata	atactgatgg	acttatatac	gtggtggatt	ccttagatog	540
agagaggtac	gggaaagcaa	agcaagaatt	tcaggagatc	ataaaagacc	cattcatgct	600
aaacagtatc	attctgttgt	ttgcaaacaa	acaggacatg	agaggagcca	tgtaaccagg	660
agaagtatgt	gaagggttag	gottatttga	ttccaagaac	aggaatagcg	acatacaagg	720
tacttgtgtc	cttcgtggag	acgggcttta	tgaaggcttg	gactgtgtat	catctactct	780
taaggtatgt	aaagccgctg	gattcacatc	ggttggccac	tcgtttttaa	tcttccaggt	840
atactttgat	atcaatggcc	agtgctctct	tcttggctct	atcacgaaat	cagaactctc	900
gaagactttt	ttgtttaagg	aaagaatgat	cttctcattg	tggaatattt	agactccatt	960
agactatttt	tgaattttga	tcattgctgc	atgaaaagctt	cttgttatat	tcgtgtgatg	1020

aagagtgtga tcactctgaaa aacctctctct ttgggggtcat cttgtccga ttaagacttt 1080
ggtagatgta tatacatctcc ttccgaatca tgatatattt ttttat

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..192

(D) OTHER INFORMATION: / Ceres Seq. ID 1498215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

Met	Gly	Gln	Ala	Phe	Arg	Lys	Leu	Phe	Asp	Thr	Phe	Phe	Gly	Asn	Gln	
1															15	
Glu	Met	Arg	Val	Val	Met	Leu	Gly	Leu	Asp	Ala	Ala	Gly	Lys	Thr	Thr	
			20							25					30	
Ile	Leu	Tyr	Lys	Leu	His	Ile	Gly	Glu	Val	Leu	Ser	Thr	Val	Pro	Thr	
			35					40					45			
Ile	Gly	Phe	Asn	Val	Glu	Lys	Val	Gln	Tyr	Lys	Asn	Val	Met	Phe	Thr	
			50					55				60				
Val	Trp	Asp	Val	Gly	Gly	Gln	Glu	Lys	Leu	Arg	Pro	Leu	Trp	Arg	His	
						70				75					80	
Tyr	Phe	Asn	Asn	Thr	Asp	Gly	Leu	Ile	Tyr	Val	Val	Asp	Ser	Leu	Asp	
						85				90					95	
Arg	Glu	Arg	Ile	Gly	Lys	Ala	Lys	Gln	Glu	Phe	Gln	Glu	Ile	Ile	Lys	
						100				105				110		
Asp	Pro	Phe	Met	Leu	Asn	Ser	Ile	Ile	Leu	Val	Phe	Ala	Asn	Lys	Gln	
						115				120				125		
Asp	Met	Arg	Gly	Ala	Met	Ser	Pro	Arg	Glu	Val	Cys	Glu	Gly	Leu	Gly	
						130				135				140		
Leu	Phe	Asp	Leu	Lys	Asn	Arg	Lys	Trp	His	Ile	Gln	Gly	Thr	Cys	Ala	
						145				150				155		160
Leu	Arg	Gly	Asp	Gly	Leu	Tyr	Glu	Gly	Leu	Asp	Trp	Leu	Ser	Ser	Thr	
						165				170				175		
Leu	Lys	Asp	Val	Lys	Ala	Ala	Gly	Phe	Thr	Ser	Val	Gly	His	Ser	Phe	
						180			185					190		

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1498216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

Met	Arg	Val	Val	Met	Leu	Gly	Leu	Asp	Ala	Ala	Gly	Lys	Thr	Thr	Ile	
1															15	
Leu	Tyr	Lys	Leu	His	Ile	Gly	Glu	Val	Leu	Ser	Thr	Val	Pro	Thr	Ile	
															30	
Gly	Phe	Asn	Val	Glu	Lys	Val	Gln	Tyr	Lys	Asn	Val	Met	Phe	Thr	Val	
															45	
Trp	Asp	Val	Gly	Gly	Gln	Glu	Lys	Leu	Arg	Pro	Leu	Trp	Arg	His	Tyr	
															60	
Phe	Asn	Asn	Thr	Asp	Gly	Leu	Ile	Tyr	Val	Val	Asp	Ser	Leu	Asp	Arg	

65				70				75				80			
Glu	Arg	Ile	Gly	Lys	Ala	Lys	Gln	Glu	Phe	Gln	Glu	Ile	Ile	Lys	Asp
				85				90						95	
Pro	Phe	Met	Leu	Asn	Ser	Ile	Ile	Leu	Val	Phe	Ala	Asn	Lys	Gln	Asp
				100				105						110	
Met	Arg	Gly	Ala	Met	Ser	Pro	Arg	Glu	Val	Cys	Glu	Gly	Leu	Gly	Leu
				115				120						125	
Phe	Asp	Leu	Lys	Asn	Arg	Lys	Trp	His	Ile	Gln	Gly	Thr	Cys	Ala	Leu
				130				135						140	
Arg	Gly	Asp	Gly	Leu	Tyr	Glu	Gly	Leu	Asp	Trp	Leu	Ser	Ser	Thr	Leu
				145				150						155	
Lys	Asp	Val	Lys	Ala	Ala	Gly	Phe	Thr	Ser	Val	Gly	His	Ser	Phe	
				165				170						175	

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..171
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

Met	Leu	Gly	Leu	Asp	Ala	Ala	Gly	Lys	Thr	Thr	Ile	Leu	Tyr	Lys	Leu
1				5				10						15	
His	Ile	Gly	Glu	Val	Leu	Ser	Thr	Val	Pro	Thr	Ile	Gly	Phe	Asn	Val
				20				25						30	
Glu	Lys	Val	Gln	Tyr	Lys	Asn	Val	Met	Phe	Thr	Val	Trp	Asp	Val	Gly
				35				40						45	
Gly	Gln	Glu	Lys	Leu	Arg	Pro	Leu	Trp	Arg	His	Tyr	Phe	Asn	Asn	Thr
				50				55						60	
Asp	Gly	Leu	Ile	Tyr	Val	Val	Asp	Ser	Leu	Asp	Arg	Glu	Arg	Ile	Gly
				65				70						75	
Lys	Ala	Lys	Gln	Glu	Phe	Gln	Glu	Ile	Ile	Lys	Asp	Pro	Phe	Met	Leu
				85				90						95	
Asn	Ser	Ile	Ile	Leu	Val	Phe	Ala	Asn	Lys	Gln	Asp	Met	Arg	Gly	Ala
				100				105						110	
Met	Ser	Pro	Arg	Glu	Val	Cys	Glu	Gly	Leu	Gly	Leu	Phe	Asp	Leu	Lys
				115				120						125	
Asn	Arg	Lys	Trp	His	Ile	Gln	Gly	Thr	Cys	Ala	Leu	Arg	Gly	Asp	Gly
				130				135						140	
Leu	Tyr	Glu	Gly	Leu	Asp	Trp	Leu	Ser	Ser	Thr	Leu	Lys	Asp	Val	Lys
				145				150						155	
Ala	Ala	Gly	Phe	Thr	Ser	Val	Gly	His	Ser	Phe					
				165				170							

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1056 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1056
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498218

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

aaaaaaaaa accaaagcaa aaaaatggct ttgaaactca cttctccgcc ttcagttttc
tcacatacaa ggagattatc ttcttcttcg ttaattccga taaggtcmaa atccacattc

60
120

```

accggatttc gatcgagac cgggtgtttat ttaagcaaaa cgacggcgct tcaactcgctc 180
acaaaactga gtgtggcgcc ggagagtcct gcggcgacaa ttgcgacgga tgattgggggg 240
aaagtatcgg cgtgttctgtt tgatatggac ggtgtgcttt gtaacagtga agatctttct 300
agacgcgcgc cgtgtggtgt ttttacggag atgggagttg aagtcactgt ggacgatttc 360
gttcctttta tgggaacagg tgaagccaa gttttaggag gtgttgcttc agtcaaaagaa 420
gttaaaggat ttgatccaga tgcagctaaa aagagattct ttgaaatata tctcgataag 480
tatgcgaagc cagaatctgg gattggattt ccaggagcat tggagcttgt tactgagttg 540
aagaacaaa gctctaaagt cgtgtttgca tctagtgtc accgtatcaa agttgatggc 600
aatctgaaag ctgctgtgtt gtctttgacc atgtttgatg ccattgtttc agcagatgcc 660
tttgagaatt tgaaccagc tccagatatt ttcttgctg ctgcaaaagt cttaggtgtg 720
cctaccagcg agtgtgtgtt tattgaagat gcgcttgctg gagtccaagc cgcacaagct 780
gcgacatga gatgtatagc cgtaaaaact actttatctg aagcaattct taaggatgct 840
ggctcttcaa tgataccaga cgataattga aacatctcaa tcaatgacat tctcactggt 900
ggctcagatt ctaccagtat gtagtctcaa agaaattcga tggaaaatat cggtcttttc 960
atgtgtattt tttttttt ttactccttt tgaaaacttt tgaataaagg ggctttcttt 1020
gtaacgagat tacacatta aaacaattct tctgt

```

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..307
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

```

Lys Lys Lys Asn Gln Ser Lys Lys Met Ala Leu Lys Leu Thr Ser Pro
1      5      10      15
Pro Ser Val Phe Ser Gln Ser Arg Arg Leu Ser Ser Ser Ser Leu Ile
20     25     30
Pro Ile Arg Ser Lys Ser Thr Phe Thr Gly Phe Arg Ser Arg Thr Gly
35     40     45
Val Tyr Leu Ser Lys Thr Thr Ala Leu Gln Ser Ser Thr Lys Leu Ser
50     55     60
Val Ala Ala Glu Ser Pro Ala Ala Thr Ile Ala Thr Asp Asp Trp Gly
65     70     75
Lys Val Ser Ala Val Leu Phe Asp Met Asp Gly Val Leu Cys Asn Ser
85     90     95
Glu Asp Leu Ser Arg Arg Ala Ala Val Asp Val Phe Thr Glu Met Gly
100    105    110
Val Glu Val Thr Val Asp Asp Phe Val Pro Phe Met Gly Thr Gly Glu
115    120    125
Ala Lys Phe Leu Gly Gly Val Ala Ser Val Lys Glu Val Lys Gly Phe
130    135    140
Asp Pro Asp Ala Ala Lys Lys Arg Phe Phe Glu Ile Tyr Leu Asp Lys
145    150    155
Tyr Ala Lys Pro Glu Ser Gly Ile Gly Phe Pro Gly Ala Leu Glu Leu
165    170    175
Val Thr Glu Cys Lys Asn Lys Gly Leu Lys Val Ala Val Ala Ser Ser
180    185    190
Ala Asp Arg Ile Lys Val Asp Ala Asn Leu Lys Ala Ala Gly Leu Ser
195    200    205
Leu Thr Met Phe Asp Ala Ile Val Ser Ala Asp Ala Phe Glu Asn Leu
210    215    220
Lys Pro Ala Pro Asp Ile Phe Leu Ala Ala Ala Lys Ile Leu Gly Val
225    230    235
Pro Thr Ser Glu Cys Val Val Ile Glu Asp Ala Leu Ala Gly Val Gln
245    250    255
Ala Ala Gln Ala Ala Asn Met Arg Cys Ile Ala Val Lys Thr Thr Leu

```


	260		265		270
Ser	Glu	Ala	Ile	Leu	Lys
	275		280		285
Ile	Gly	Asn	Ile	Ser	Ile
	290		295		300
Thr	Ser	Met			
305					

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..299
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498220

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

Met	Ala	Leu	Lys	Leu	Thr	Ser	Pro	Pro	Ser	Val	Phe	Ser	Gln	Ser	Arg
1			5					10					15		
Arg	Leu	Ser	Ser	Ser	Leu	Ile	Pro	Ile	Arg	Ser	Lys	Ser	Thr	Phe	
			20				25					30			
Thr	Gly	Phe	Arg	Ser	Arg	Thr	Gly	Val	Tyr	Leu	Ser	Lys	Thr	Thr	Ala
		35					40					45			
Leu	Gln	Ser	Ser	Thr	Lys	Leu	Ser	Val	Ala	Ala	Glu	Ser	Pro	Ala	Ala
	50					55					60				
Thr	Ile	Ala	Thr	Asp	Asp	Trp	Gly	Lys	Val	Ser	Ala	Val	Leu	Phe	Asp
	65				70				75					80	
Met	Asp	Gly	Val	Leu	Cys	Asn	Ser	Glu	Asp	Leu	Ser	Arg	Arg	Ala	Ala
			85					90					95		
Val	Asp	Val	Phe	Thr	Glu	Met	Gly	Val	Glu	Val	Thr	Val	Asp	Asp	Phe
		100					105						110		
Val	Pro	Phe	Met	Gly	Thr	Gly	Glu	Ala	Lys	Phe	Leu	Gly	Gly	Val	Ala
		115					120					125			
Ser	Val	Lys	Glu	val	Lys	Gly	Phe	Asp	Pro	Asp	Ala	Ala	Lys	Lys	Arg
		130				135					140				
Phe	Phe	Glu	Ile	Tyr	Leu	Asp	Lys	Tyr	Ala	Lys	Pro	Glu	Ser	Gly	Ile
	145				150				155					160	
Gly	Phe	Pro	Gly	Ala	Leu	Glu	Leu	Val	Thr	Glu	Cys	Lys	Asn	Lys	Gly
			165					170					175		
Leu	Lys	Val	Ala	Val	Ala	Ser	Ser	Ala	Asp	Arg	Ile	Lys	Val	Asp	Ala
		180					185						190		
Asn	Leu	Lys	Ala	Ala	Gly	Leu	Ser	Leu	Thr	Met	Phe	Asp	Ala	Ile	Val
	195						200					205			
Ser	Ala	Asp	Ala	Phe	Glu	Asn	Leu	Lys	Pro	Ala	Pro	Asp	Ile	Phe	Leu
	210					215					220				
Ala	Ala	Ala	Lys	Ile	Leu	Gly	Val	Pro	Thr	Ser	Glu	Cys	Val	Val	Ile
	225					230				235				240	
Glu	Asp	Ala	Leu	Ala	Gly	Val	Gln	Ala	Ala	Gln	Ala	Ala	Asn	Met	Arg
		245						250					255		
Cys	Ile	Ala	Val	Lys	Thr	Thr	Leu	Ser	Glu	Ala	Ile	Leu	Lys	Asp	Ala
	260						265						270		
Gly	Pro	Ser	Met	Ile	Arg	Asp	Asp	Ile	Gly	Asn	Ile	Ser	Ile	Asn	Asp
	275						280					285			
Ile	Leu	Thr	Gly	Gly	Ser	Asp	Ser	Thr	Ser	Met					
	290					295									

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..219
(D) OTHER INFORMATION: / Ceres Seq. ID 1498221
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:
Met Asp Gly Val Leu Cys Asn Ser Glu Asp Leu Ser Arg Arg Ala Ala
1 5 10 15
Val Asp Val Phe Thr Glu Met Gly Val Glu Val Thr Val Asp Asp Phe
20 25 30
Val Pro Phe Met Gly Thr Gly Glu Ala Lys Phe Leu Gly Gly Val Ala
35 40 45
Ser Val Lys Glu Val Lys Gly Phe Asp Pro Asp Ala Ala Lys Lys Arg
50 55 60
Phe Phe Glu Ile Tyr Leu Asp Lys Tyr Ala Lys Pro Glu Ser Gly Ile
65 70 75 80
Gly Phe Pro Gly Ala Leu Glu Leu Val Thr Glu Cys Lys Asn Lys Gly
85 90 95
Leu Lys Val Ala Val Ala Ser Ser Ala Asp Arg Ile Lys Val Asp Ala
100 105 110
Asn Leu Lys Ala Ala Gly Leu Ser Leu Thr Met Phe Asp Ala Ile Val
115 120 125
Ser Ala Asp Ala Phe Glu Asn Leu Lys Pro Ala Pro Asp Ile Phe Leu
130 135 140
Ala Ala Ala Lys Ile Leu Gly Val Pro Thr Ser Glu Cys Val Val Ile
145 150 155 160
Glu Asp Ala Leu Ala Gly Val Gln Ala Ala Gln Ala Ala Asn Met Arg
165 170 175
Cys Ile Ala Val Lys Thr Thr Leu Ser Glu Ala Ile Leu Lys Asp Ala
180 185 190
Gly Pro Ser Met Ile Arg Asp Asp Ile Gly Asn Ile Ser Ile Asn Asp
195 200 205
Ile Leu Thr Gly Gly Ser Asp Ser Thr Ser Met
210 215

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 643 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..643

(D) OTHER INFORMATION: / Ceres Seq. ID 1498223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

aaaaaaaaatca aaccaccat tcaaaaaa caaaaaaca aaaaaaaaaa catttcccc 60
aaaaaaaaaaaa aacagaggat gaaacaaaac cagagcaagt ttttgagaat aatctcaagc 120
cctctagaag ctttaggcaa ggcacgtgat ttctacgtga gaagcatcac cgttgtcgca 180
gctcggactc aatattctc ctccgcctcc gtctccgctc ctttccaag aagccggagc 240
tcctctccgc cccgcttctc ctctcccgca tcatcccgga gaaccaccga tttcgggata 300
gatgaagatt acagcgagct agtgagagct gcgtcggtga ggagttagg gcacaagaat 360
gagatagaca tgttgatata agagaagctg caacagcaga agcaacagaa gcaaggaggg 420
ttgcctaaga gctcgagtcg tgggatggcg aggatagagg aagaggaaga aacagaggaa 480
ggatctgtga atccgaagg gaagaagact aagaaaagtct ctgatctttt gtatcctcgt 540
agcaaatctt acgcggttac tactagtacc cctatcttgt aacttctctt cttatttttt 600
cttctcttta atttttagt ttgtggagt gattatcatt ttc

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..193
(D) OTHER INFORMATION: / Ceres Seq. ID 1498224
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:
Lys Lys Ile Lys Pro Thr Ile Gln Thr Lys His Lys Asn Lys Lys Lys
1 5 10 15
Asn Ile Ser Pro Lys Lys Lys Lys Lys Arg Met Lys Gln Asn Gln Ser
20 25 30
Lys Phe Leu Arg Ile Ile Ser Thr Pro Leu Arg Ala Leu Gly Lys Ala
35 40 45
Arg Asp Phe Tyr Val Arg Ser Ile Thr Gly Cys Ala Ala Arg Thr Gln
50 55 60
Tyr Ser Ser Ser Ala Ser Val Ser Ala Pro Phe Pro Arg Ser Arg Ser
65 70 75 80
Ser Ser Ser Ala Ala Phe Ser Ser Ser Ala Ser Arg Arg Thr Thr
85 90 95
Asp Phe Gly Ile Asp Glu Asp Tyr Ser Glu Leu Val Arg Ala Ala Ser
100 105 110
Val Arg Ser Leu Gly His Lys Asn Glu Ile Asp Met Leu Ile Gln Glu
115 120 125
Lys Leu Gln Gln Gln Lys Gln Gln Lys Gln Gly Gly Leu Pro Lys Ser
130 135 140
Ser Ser Ala Gly Met Ala Arg Ile Glu Glu Glu Glu Thr Glu Glu
145 150 155 160
Gly Ser Val Asn Pro Lys Val Lys Lys Thr Lys Lys Val Ser Asp Leu
165 170 175
Leu Tyr Pro Arg Ser Lys Ser Tyr Ala Val Thr Thr Ser Thr Pro Ile
180 185 190
Leu

(2) INFORMATION FOR SEQ ID NO:290:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 167 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..167
(D) OTHER INFORMATION: / Ceres Seq. ID 1498225
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:
Met Lys Gln Asn Gln Ser Lys Phe Leu Arg Ile Ile Ser Thr Pro Leu
1 5 10 15
Arg Ala Leu Gly Lys Ala Arg Asp Phe Tyr Val Arg Ser Ile Thr Gly
20 25 30
Cys Ala Ala Arg Thr Gln Tyr Ser Ser Ala Ser Val Ser Ala Pro
35 40 45
Phe Pro Arg Ser Arg Ser Ser Ser Ser Ala Ala Phe Ser Ser Ser Ala
50 55 60
Ser Ser Arg Arg Thr Thr Asp Phe Gly Ile Asp Glu Asp Tyr Ser Glu
65 70 75 80
Leu Val Arg Ala Ala Ser Val Arg Ser Leu Gly His Lys Asn Glu Ile
85 90 95
Asp Met Leu Ile Gln Glu Lys Leu Gln Gln Lys Gln Gln Lys Gln

	100		105		110										
Gly	Gly	Leu	Pro	Lys	Ser	Ser	Ser	Ala	Gly	Met	Ala	Arg	Ile	Glu	Glu
	115				120					125					
Glu	Glu	Glu	Thr	Glu	Glu	Gly	Ser	Val	Asn	Pro	Lys	Val	Lys	Lys	Thr
	130				135					140					
Lys	Lys	Val	Ser	Asp	Leu	Leu	Tyr	Pro	Arg	Ser	Lys	Ser	Tyr	Ala	Val
	145				150					155					160
Thr	Thr	Ser	Thr	Pro	Ile	Leu									
					165										

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..501

(D) OTHER INFORMATION: / Ceres Seq. ID 1498226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

attacttctc	cactgaatgc	atttactctc	ctaatagcata	tcgtgggttt	gcccgtagt	60
tcataaaga	tttggaaga	ataaggccaa	ggcgattct	ggacatcata	aagtctgggtg	120
aagattttag	aattgcaaca	accacaaaga	tgccctgagca	agggacgtgt	gagcgatgctg	180
ggatattttc	tagccagaaa	tggtgtataag	cttgtgtttt	gctggaagga	ctgaaccgtg	240
gtttgcctaa	gatgggtatt	ggaagacctc	gagcgataaa	tggtgatcat	aataaggaaa	300
caaagaagcc	tgatctgtga	gcaaaatcta	tagagagcaa	acaatgtgga	tctctggatt	360
tctaaaattt	tgagaaaaaa	gctacaaaat	cgtatgagtc	atagtgaatg	atttgattat	420
atagaaaaag	aaaagatttt	tttttccct	tcataaactt	ctttagaac	ttaattgtac	480
ttttggtttt	cttttttgt	t				

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1498227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

Tyr	Phe	Ser	Thr	Glu	Cys	Ile	Tyr	Ser	Pro	Asn	Ala	Tyr	Arg	Gly	Phe
1				5					10					15	
Ala	Arg	Glu	Phe	Ile	Lys	Asp	Leu	Glu	Arg	Ile	Arg	Pro	Arg	Ala	Ile
				20				25					30		
Leu	Asp	Ile	Ile	Lys	Ser	Gly	Glu	Asp	Phe	Arg	Ile	Ala	Thr	Thr	
				35				40					45		
Lys	Met	Pro	Glu	Gln	Gly	Thr	Cys	Glu	Arg	Cys	Gly	Tyr	Ile	Ser	Ser
				50				55					60		
Gln	Lys	Trp	Cys	Lys	Ala	Cys	Val	Leu	Leu	Glu	Gly	Leu	Asn	Arg	Gly
				65				70					75		80
Leu	Pro	Lys	Met	Gly	Ile	Gly	Arg	Pro	Arg	Gly	Val	Asn	Gly	Asp	His
				85				90					95		
Asn	Lys	Glu	Thr	Lys	Lys	Pro	Gly	Ser	Val	Ala	Lys	Ser	Ile	Glu	Ser
				100				105					110		
Lys	Gln	Cys	Gly	Ser	Leu	Asp	Phe								
				115				120							

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..71
(D) OTHER INFORMATION: / Ceres Seq. ID 1498228
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:
Met Pro Glu Gln Gly Thr Cys Glu Arg Cys Gly Tyr Ile Ser Ser Gln
1 5 10 15
Lys Trp Cys Lys Ala Cys Val Leu Leu Gly Gly Leu Asn Arg Gly Leu
20 25 30
Pro Lys Met Gly Ile Gly Arg Pro Arg Gly Val Asn Gly Asp His Asn
35 40 45
Lys Glu Thr Lys Lys Pro Gly Ser Val Ala Lys Ser Ile Glu Ser Lys
50 55 60
Gln Cys Gly Ser Leu Asp Phe
65 70

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..567

(D) OTHER INFORMATION: / Ceres Seq. ID 1498244

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

aaaaacacaa caaatggga aactcatat gcgtaacgga aaaaacgacg acgtcgtggn 60
tcaggagacg ataattggatc atataacaag agaaggagaa gaagaagatc caccgtggtt 120
cacgacgaca acgacgacgg agagaagctg ctcggagaaa caagcaacgt tacgtcaaca 180
agttcgtcat cgtcttctga gagaagagag attaagataa ggataacgaa aaaggaaactt 240
gaagatctca tgagaaacat tgggttgaag agtttaacgg cggaagagat tctttctaag 300
ttaattttcg aaggtggaga ccaaatcgga ttctctcggt tcgatgtgac gaatcaccac 360
caaccatgga aaccggtgtt gcaaaagcata ccggagatgg attagtgtta ttttttttat 420
ttttcttata aaaaaataga taaaaaaatc tgagtgatgc gtgtgtctaa acttgacctt 480
ctcgacaggt gattttagct ttttaaaaagt atgtacatgt ttggttttgt aattaatttt 540
tttattgaaa tttttattga aattttt

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1498245

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

Lys Thr Gln Asn Gly Lys Leu His Met Arg Asn Gly Lys Asn Asp
1 5 10 15
Asp Val Val Xaa Gln Glu Thr Ile Met Asp His Ile Thr Arg Glu Gly
20 25 30
Glu Glu Glu Asp Pro Pro Trp Phe Thr Thr Thr Thr Thr Glu Arg
35 40 45
Ser Cys Ser Glu Lys Gln Ala Thr Leu Arg Gln Gln Val Arg His Arg
50 55 60

Leu Leu Arg Glu Glu Arg Leu Arg
65 70

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..63
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

Met	Arg	Asn	Gly	Lys	Asn	Asp	Asp	Val	Val	Xaa	Gln	Glu	Thr	Ile	Met
1				5					10					15	
Asp	His	Ile	Thr	Arg	Glu	Gly	Glu	Glu	Glu	Asp	Pro	Pro	Trp	Phe	Thr
			20					25					30		
Thr	Thr	Thr	Thr	Thr	Glu	Arg	Ser	Cys	Ser	Glu	Lys	Gln	Ala	Thr	Leu
			35				40					45			
Arg	Gln	Gln	Val	Arg	His	Arg	Leu	Leu	Arg	Glu	Glu	Arg	Leu	Arg	
			50			55						60			

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..51
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498247

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

Met	Arg	Asn	Ile	Gly	Leu	Lys	Ser	Leu	Thr	Ala	Glu	Glu	Ile	Leu	Ser
1				5					10					15	
Lys	Leu	Ile	Phe	Glu	Gly	Gly	Asp	Gln	Ile	Gly	Phe	Ser	Ala	Val	Asp
			20				25						30		
Val	Thr	Asn	His	His	Gln	Pro	Trp	Lys	Pro	Val	Leu	Gln	Ser	Ile	Pro
			35				40					45			
Glu	Met	Asp													
		50													

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1632 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1632
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

tcttctctct	acacacacac	acacacacac	acacacacac	tggtattcttc	gaatgttgaa	60
gaaaacctaa	accagagaac	aaaatccgca	gaagaacaaa	accacttgc	cattttocat	120
tcttctctac	caatcgcatc	tcttctctct	acctgtgtcc	catctctgac	tcaatttctc	180
aaattgtttg	ctatcatctc	aaacaaggtt	aagatcccta	cgcaggcttc	tctctctca	240
catctctctc	tcttctctct	ctctctctct	ctctctctct	gaatctctct	caaatccacc	300
atcgctgcta	accctcttca	atccccctct	tcctctctct	ctctctctct	cgtgtgacct	360
tctctcgccg	ccgtctctcg	ccgtctctct	gtctctctgt	tccgcgaatga	cctccgtgtc	420

(2) INFORMATION FOR SEQ ID NO:299:

(A) LENGTH: 460 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..460

SEQUENCE DESCRIPTION:

Ser	Ser	Leu	Tyr	Thr	His	Thr	His	Thr	His	Thr	His	Lys	Met	Asp	Ser
1				5					10					15	
Ser	Asn	Val	Glu	Glu	Asn	Leu	Asn	Pro	Glu	Thr	Lys	Ser	Ala	Glu	Glu
			20					25					30		
Gln	Asn	Pro	Leu	Ala	Ile	Phe	His	Ser	Ser	Leu	Pro	Ile	Ala	Ser	Leu
		35				40						45			
Ser	Leu	Thr	Leu	Phe	Pro	Ser	Ser	Thr	Gln	Phe	Leu	Lys	Leu	Phe	Ala
	50					55				60					
His	His	Pro	Asn	Lys	Val	Lys	Ile	Pro	Thr	Gln	Ala	Ser	Ser	Leu	Thr
65					70					75					80
His	Leu	Ser	Leu	Ser	Ser	Val	Ser	Pro	Phe	Pro	Ser	Ser	Arg	Ile	Ser
				85					90					95	
Phe	Lys	Ser	Thr	Ile	Ala	Ala	Asn	Pro	Leu	Gln	Ser	Pro	Leu	Ser	Ile
			100					105					110		
Val	Pro	Arg	Arg	Pro	Val	Asp	Pro	Ser	Ser	Ala	Ala	Ala	Leu	Arg	Arg
		115					120					125			
Ala	Ala	Val	Val	Trp	Phe	Arg	Asn	Asp	Leu	Arg	Val	His	Asp	Asn	Glu
		130				135					140				
Cys	Leu	Asn	Ser	Ala	Asn	Asp	Glu	Cys	Val	Ser	Val	Leu	Pro	Val	Tyr
145					150					155					160
Cys	Phe	Asp	Pro	Arg	Asp	Tyr	Gly	Lys	Ser	Ser	Ser	Gly	Phe	Asp	Lys
			165					170						175	
Thr	Gly	Pro	Phe	Arg	Ala	Gln	Phe	Leu	Ile	Glu	Ser	Val	Ser	Glu	Leu
			180					185					190		
Arg	Lys	Asn	Leu	Gln	Ala	Arg	Gly	Ser	Asn	Leu	Val	Val	Arg	Val	Gly
		195					200					205			
Lys	Pro	Glu	Ala	Val	Leu	Val	Glu	Leu	Ala	Lys	Glu	Ile	Gly	Ala	Asp
	210					215					220				

Ala Val Tyr Ala His Arg Glu Val Ser His Asp Glu Val Lys Ala Glu
225 230 235 240
Gly Lys Ile Glu Thr Ala Met Lys Glu Glu Gly Val Glu Val Lys Tyr
245 250 255
Phe Trp Gly Ser Thr Leu Tyr His Leu Asp Asp Leu Pro Phe Lys Ile
260 265 270
Glu Asp Leu Pro Ser Asn Tyr Gly Ala Phe Lys Asp Lys Val Gln Lys
275 280 285
Leu Glu Ile Arg Lys Thr Ile Ala Ala Leu Asp Gln Leu Lys Ser Leu
290 295 300
Pro Ser Arg Gly Asp Val Glu Leu Gly Asp Ile Pro Ser Leu Leu Asp
305 310 315 320
Leu Gly Ile Ser Pro Thr Pro Arg Thr Ser Gln Glu Gly Lys Pro Thr
325 330 335
Met Val Gly Gly Glu Thr Glu Ala Leu Thr Arg Leu Lys Ser Phe Ala
340 345 350
Ala Asp Cys Gln Ala Arg Leu Ser Lys Gly Asn Gln Lys Gly Gly Asn
355 360 365
Asn Ser Val Phe Gly Ala Asn Phe Ser Cys Lys Ile Ser Pro Trp Leu
370 375 380
Ala Met Gly Ser Ile Ser Pro Arg Ser Met Phe Asp Glu Leu Lys Lys
385 390 395 400
Thr Ile Ser Ala Ser Thr Thr Ser Thr Thr Pro Arg Asn Gly Pro Gly
405 410 415
Asp Thr Gly Leu Asn Trp Leu Met Tyr Glu Leu Leu Trp Arg Asp Phe
420 425 430
Phe Arg Phe Ile Thr Lys Lys Tyr Ser Ser Ala Lys Thr Gln Val Glu
435 440 445
Ala Gly Pro Ala Thr Ala Cys Thr Gly Ala Phe Ala
450 455 460

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..447
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498253

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

Met Asp Ser Ser Asn Val Glu Glu Asn Leu Asn Pro Glu Thr Lys Ser
1 5 10 15
Ala Glu Glu Gln Asn Pro Leu Ala Ile Phe His Ser Ser Leu Pro Ile
20 25 30
Ala Ser Leu Ser Leu Thr Leu Phe Pro Ser Ser Thr Gln Phe Leu Lys
35 40 45
Leu Phe Ala His His Pro Asn Lys Val Lys Ile Pro Thr Gln Ala Ser
50 55 60
Ser Leu Thr His Leu Ser Leu Ser Ser Val Ser Pro Phe Pro Ser Ser
65 70 75 80
Arg Ile Ser Phe Lys Ser Thr Ile Ala Ala Asn Pro Leu Gln Ser Pro
85 90 95
Leu Ser Ile Val Pro Arg Arg Pro Val Asp Pro Ser Ser Ala Ala Ala
100 105 110
Leu Arg Arg Ala Ala Val Val Trp Phe Arg Asn Asp Leu Arg Val His
115 120 125
Asp Asn Glu Cys Leu Asn Ser Ala Asn Asp Glu Cys Val Ser Val Leu
130 135 140
Pro Val Tyr Cys Phe Asp Pro Arg Asp Tyr Gly Lys Ser Ser Ser Gly

145 150 155 160
Phe Asp Lys Thr Gly Pro Phe Arg Ala Gln Phe Leu Ile Glu Ser Val
165 170 175
Ser Glu Leu Arg Lys Asn Leu Gln Ala Arg Gly Ser Asn Leu Val Val
180 185 190
Arg Val Gly Lys Pro Glu Ala Val Leu Val Glu Leu Ala Lys Glu Ile
195 200 205
Gly Ala Asp Ala Val Tyr Ala His Arg Glu Val Ser His Asp Glu Val
210 215 220
Lys Ala Glu Gly Lys Ile Glu Thr Ala Met Lys Glu Glu Gly Val Glu
225 230 235 240
Val Lys Tyr Phe Trp Gly Ser Thr Leu Tyr His Leu Asp Asp Leu Pro
245 250 255
Phe Lys Ile Glu Asp Leu Pro Ser Asn Tyr Gly Ala Phe Lys Asp Lys
260 265 270
Val Gln Lys Leu Glu Ile Arg Lys Thr Ile Ala Ala Leu Asp Gln Leu
275 280 285
Lys Ser Leu Pro Ser Arg Gly Asp Val Glu Leu Gly Asp Ile Pro Ser
290 295 300
Leu Leu Asp Leu Gly Ile Ser Pro Thr Pro Arg Thr Ser Gln Glu Gly
305 310 315 320
Lys Pro Thr Met Val Gly Gly Glu Thr Glu Ala Leu Thr Arg Leu Lys
325 330 335
Ser Phe Ala Ala Asp Cys Gln Ala Arg Leu Ser Lys Gly Asn Gln Lys
340 345 350
Gly Gly Asn Asn Ser Val Phe Gly Ala Asn Phe Ser Cys Lys Ile Ser
355 360 365
Pro Trp Leu Ala Met Gly Ser Ile Ser Pro Arg Ser Met Phe Asp Glu
370 375 380
Leu Lys Lys Thr Ile Ser Ala Ser Thr Thr Ser Thr Thr Pro Arg Asn
385 390 395 400
Gly Pro Gly Asp Thr Gly Leu Asn Trp Leu Met Tyr Glu Leu Leu Trp
405 410 415
Arg Asp Phe Phe Arg Phe Ile Thr Lys Lys Tyr Ser Ser Ala Lys Thr
420 425 430
Gln Val Glu Ala Gly Pro Ala Thr Ala Cys Thr Gly Ala Phe Ala
435 440 445

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 859 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..859
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498254

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

atcggtattaa	aaataaaaaag	cctctctttt	tttrctcag	tgagacaatc	gactttcttaa	60
aatcgatggc	gactgagaaa	ccgattacga	cggagactgt	tgctctcaact	gagaagaaaa	120
tgacatctc	tttagatgag	attatcaaga	tggaaaaagag	caataaccaat	gtgaataagg	180
gcaagaacac	gagagatttg	aataaaaaag	agaaatttag	tggtgctgcg	aagaataagt	240
cggtgaaagc	acagcggttat	atggactctc	ggctctgatgt	tagacagggg	gcttttgcta	300
agaagaggct	taatttccaa	ggaaccaggt	ttcctgtaac	aaaacaaccg	ttgctcgtaa	360
agccgcttct	gctactccgc	tggttagacc	ttataatggg	ggaaggatga	ctaatacgaa	420
tcaatcaagg	tttattgctc	caccagctca	gaatagagct	tcacaagaag	ggtttgctcg	480
aaagcagcag	cagcagcaaa	gggagaagat	agtgcagcag	caggcaaatg	gaggagaggag	540
agggcaaaag	caatggcctc	agacactgga	ttctcggttt	gcaaacatga	aggaagagag	600
aatgagaatg	agaaggtttg	cagacaatag	aagcaatgta	ggcaacaagt	gagctggatc	660
gcatacagcag	cagcggttcga	tggtcccgtg	ggtgagaaga	gctacaagat	tccccaactg	720

atattatgacc tgcagaatag tcttgtttca agggtagggg gaacatatatt gctacttatg 780
tagtttgggtt tggattcatt gatatcaagt tagaacattc gtatgtgaag ctctaaaacc 840
ttgaatcttt tcttggcc

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..135

(D) OTHER INFORMATION: / Ceres Seq. ID 1498255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

Arg Ile Lys Asn Lys Lys Pro Leu Phe Phe Xaa Leu Ser Glu Thr Ile
1 5 10 15
Asp Phe Leu Lys Ser Met Ala Thr Glu Lys Pro Ile Thr Thr Glu Thr
20 25 30
Val Ala Leu Thr Glu Lys Lys Met Asp Ile Ser Leu Asp Glu Ile Ile
35 40 45
Lys Met Glu Lys Ser Asn Thr Asn Val Asn Lys Gly Lys Lys Gln Arg
50 55 60
Val Leu Asn Lys Lys Glu Lys Phe Ser Gly Ala Ala Lys Asn Ser Ala
65 70 75 80
Val Lys Ala Gln Arg Tyr Met Asp Ser Arg Ser Asp Val Arg Gln Gly
85 90 95
Ala Phe Ala Lys Lys Arg Ser Asn Phe Gln Gly Asn Gln Phe Pro Val
100 105 110
Thr Lys Gln Pro Leu Leu Val Lys Pro Leu Leu Leu Leu Arg Val Val
115 120 125
Asp Leu Ile Met Val Glu Gly
130 135

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1498256

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

Met Ala Thr Glu Lys Pro Ile Thr Thr Glu Thr Val Ala Leu Thr Glu
1 5 10 15
Lys Lys Met Asp Ile Ser Leu Asp Glu Ile Ile Lys Met Glu Lys Ser
20 25 30
Asn Thr Asn Val Asn Lys Gly Lys Lys Gln Arg Val Leu Asn Lys Lys
35 40 45
Glu Lys Phe Ser Gly Ala Ala Lys Asn Ser Ala Val Lys Ala Gln Arg
50 55 60
Tyr Met Asp Ser Arg Ser Asp Val Arg Gln Gly Ala Phe Ala Lys Lys
65 70 75 80
Arg Ser Asn Phe Gln Gly Asn Gln Phe Pro Val Thr Lys Gln Pro Leu
85 90 95
Leu Val Lys Pro Leu Leu Leu Leu Arg Val Val Asp Leu Ile Met Val
100 105 110
Glu Gly

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

Met Thr Asn Thr Asn Gln Ser Arg Phe Ile Ala Pro Pro Ala Gln Asn
1 5 10 15
Arg Ala Ser Gln Arg Gly Phe Val Ala Lys Gln Gln Gln Gln Arg
20 25 30
Glu Lys Ile Val Gln Gln Gln Ala Asn Gly Gly Gly Gly Gln Arg
35 40 45
Gln Trp Pro Gln Thr Leu Asp Ser Arg Phe Ala Asn Met Lys Glu Glu
50 55 60
Arg Met Arg Met Arg Arg Phe Ala Asp Asn Arg Ser Asn Val Gly Asn
65 70 75 80
Asn Gly Ala Gly Ser His Gln Gln Gln Arg Ser Met Val Pro Trp Val
85 90 95
Arg Arg Ala Thr Arg Phe Pro Asn
100

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 988 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..988
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

aaaagaagac ttttgaagg aaataaacac acaactaaag agatgtcgtc aaccttgagc 60
aacgaagagt caggactcgg tgattcaaat cggtcgacgg aagtagatag cgggcagcga 120
ggaacttcaa cggtttacga gtctcgattc cagtcgcagc ggtttgactc ttcttctctc 180
aattttgact cccaaccgga gaagagtgca gaattaccag gcgcgcatcc atctcctcga 240
cccgaactc aatctccgcc gtcgataaat agtttcgatg atacaaacgg ttcgattctg 300
ccgcaccat cgcccatgga gaagagggaa ggtttcgctc tttagagagt gcgaaggcta 360
aatgtctcga gattggaaga gaaagaaaag aaatggttca acaaatctta 420
gaagcagcag agcaaatataa ggcgtgagtc tatagcaagc gtaacgttac tattgaaaac 480
aacaagaaac taaccgcgga gaaagagaag ttttttttgg agaactcaag aaagttttac 540
gctgaagctg acaaaaaacaa ttggaaggcg attgcagaac tcattctctg tgaagtgcga 600
gttatagaga atagagggaa caagaagaaa acagcaacca taactgtaat ccaggggacca 660
aagccaggga agccctactga tctgtgctcg tatgcgtcaa gtgctcaaga aactcaagca 720
caatccgcca actcatatga agccaaaact gccctcacca tctggagctg acccgaaagt 780
gagtgtgagt gaacaggtca cagttacaga gaagttgtag ttgtgtatgt gacaagttaa 840
cttcttcttg attgatgtta aaccgtcttt actttgttag cttccctcat gtccagtcctc 900
gactattggt tgttttgatt tgcgtcttgg tcttaccatt gttgggtttcc cacacagttt 960
tctacttga tgatatata atatattc

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..242

(D) OTHER INFORMATION: / Ceres Seq. ID 1498262

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

Met	Ser	Ser	Thr	Leu	Ser	Asn	Glu	Glu	Ser	Gly	Leu	Gly	Asp	Ser	Asn	
1				5				10					15			
Arg	Ser	Thr	Glu	Val	Asp	Ser	Gly	Asp	Gly	Gly	Asn	Phe	Thr	Ala	Tyr	
			20				25				30					
Glu	Ser	Arg	Phe	Gln	Ser	Gln	Arg	Phe	Asp	Ser	Ser	Phe	Ser	Asn	Phe	
		35					40				45					
Asp	Ser	Gln	Pro	Glu	Lys	Glu	Ser	Asp	Leu	Pro	Gly	Gly	Asp	Ser	Ser	
	50					55					60					
Pro	Arg	Pro	Glu	Thr	Gln	Ser	Pro	Pro	Ser	Ile	Asn	Ser	Phe	Asp	Asp	
	65			70					75					80		
Thr	Asn	Gly	Ser	Ile	Leu	Pro	Pro	Pro	Ser	Ala	Met	Glu	Lys	Glu	Glu	
			85						90				95			
Gly	Phe	Ala	Leu	Arg	Glu	Trp	Arg	Arg	Leu	Asn	Ala	Leu	Arg	Leu	Glu	
		100					105						110			
Glu	Lys	Glu	Lys	Glu	Glu	Lys	Glu	Met	Val	Gln	Gln	Ile	Leu	Glu	Ala	
	115					120					125					
Ala	Glu	Gln	Tyr	Lys	Ala	Glu	Phe	Tyr	Ser	Lys	Arg	Asn	Val	Thr	Ile	
	130				135						140					
Glu	Asn	Asn	Lys	Lys	Leu	Asn	Arg	Glu	Lys	Glu	Lys	Phe	Phe	Leu	Glu	
	145			150					155						160	
Asn	Gln	Glu	Lys	Phe	Tyr	Ala	Glu	Ala	Asp	Lys	Asn	Asn	Trp	Lys	Ala	
		165					170						175			
Ile	Ala	Glu	Leu	Ile	Pro	Arg	Glu	Val	Pro	Val	Ile	Glu	Asn	Arg	Gly	
		180					185					190				
Asn	Lys	Lys	Lys	Thr	Ala	Thr	Ile	Thr	Val	Ile	Gln	Gly	Pro	Lys	Pro	
	195					200					205					
Gly	Lys	Pro	Thr	Asp	Leu	Cys	Ser	Tyr	Ala	Ser	Ser	Ala	His	Glu	Thr	
	210				215						220					
Gln	Ala	Gln	Ser	Ala	Asn	Ser	Tyr	Glu	Ala	Lys	Thr	Ala	Leu	Thr	Ile	
	225				230				235					240		
Trp	Ser															

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 151 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1498263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

Met	Glu	Lys	Glu	Glu	Gly	Phe	Ala	Leu	Arg	Glu	Trp	Arg	Arg	Leu	Asn	
1			5					10					15			
Ala	Leu	Arg	Leu	Glu	Glu	Lys	Glu	Lys	Glu	Met	Val	Gln				
		20					25			30						
Gln	Ile	Leu	Glu	Ala	Ala	Glu	Gln	Tyr	Lys	Ala	Glu	Phe	Tyr	Ser	Lys	
	35					40				45						
Arg	Asn	Val	Thr	Ile	Glu	Asn	Asn	Lys	Lys	Leu	Asn	Arg	Glu	Lys	Glu	
	50				55					60						
Lys	Phe	Phe	Leu	Glu	Asn	Gln	Glu	Lys	Phe	Tyr	Ala	Glu	Ala	Asp	Lys	
	65			70					75				80			
Asn	Asn	Trp	Lys	Ala	Ile	Ala	Glu	Leu	Ile	Pro	Arg	Glu	Val	Pro	Val	

(2) INFORMATION FOR SEQ ID NO:308:

(A) LENGTH: 122 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1498264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

Met	Val	Gln	Gln	Ile	Leu	Glu	Ala	Ala	Glu	Gln	Tyr	Lys	Ala	Glu	Phe
1			5						10					15	
Tyr	Ser	Lys	Arg	Asn	Val	Thr	Ile	Glu	Asn	Asn	Lys	Lys	Leu	Asn	Arg
			20					25					30		
Glu	Lys	Glu	Lys	Phe	Phe	Leu	Glu	Asn	Gln	Glu	Lys	Phe	Tyr	Ala	Glu
		35					40					45			
Ala	Asp	Lys	Asn	Asn	Trp	Lys	Ala	Ile	Ala	Glu	Leu	Ile	Pro	Arg	Glu
	50					55					60				
Val	Pro	Val	Ile	Glu	Asn	Arg	Gly	Asn	Lys	Lys	Lys	Thr	Ala	Thr	Ile
65				70						75					80
Thr	Val	Ile	Gln	Gly	Pro	Lys	Pro	Gly	Lys	Pro	Thr	Asp	Leu	Cys	Ser
			85					90					95		
Tyr	Ala	Ser	Ser	Ala	His	Glu	Thr	Gln	Ala	Gln	Ser	Ala	Asn	Ser	Tyr
			100					105					110		
Glu	Ala	Lys	Thr	Ala	Leu	Thr	Ile	Trp	Ser						
		115				120									

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 601 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

```
(ix) FEATURE:
```

(A) NAME/KEY: -

(B) LOCATION: 1..601

(D) OTHER INFORMATION: / Ceres Seq. ID 1498268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

tccaacaaa	ctcgcgatgaa	gaatatactgt	ctctctctgtg	atggacgcgtc	gaatcgaaac	60
gagcagtcac	gtttattgac	ctcagacagt	tctcggctccc	ctcgggggaag	cgagccttttg	120
ctctctttatc	ggcgcaaaa	ggcataattt	ctcaaatggt	tgagacaaa	gcgaacattc	180
cgtaacaagat	gtctttctct	tgtgggacag	cagggggcaca	gtgtaaagg	ccctttgggtg	240
taatggctgt	tgtctggagat	caagcacaca	ctcttcaata	tatggcgcaa	cgaaacctga	300
gtttcgaag	atcgcaggatt	aactctcaag	cgaaagctga	acgtacagg	atcgcctctt	360
acagactatta	ttacaataacg	aggacacagc	atatgacttc	tattgttgga	ccctgtgatgt	420
atgacgcttaa	tgttttggttc	ctctggctcta	gtagaattgt	attatgattt	ccgcttttta	480
ttctctcttc	tttgtgttttc	atctagattg	ttccggttca	gaaatgtgat	tgttgagacg	540
ggaattaa	cgggattcca	cgttgtatga	tgtatcgttg	tatgatggat	cggttcaagg	600
t						

(2) INFORMATION FOR SEQ ID NO:310:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 167 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..167
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:
Pro Thr Asn Leu Asp Glu Glu Ile Ser Ser Leu Pro Gly Trp Thr Val
1 5 10 15
Glu Ser Asn Arg Ala Val Arg Phe Ile Asp Ser Asp His Phe Ser Val
 20 25 30
Pro Glu Gly Lys Arg Ala Leu Glu Leu Ser Gly Lys Glu Gly Ile
 35 40 45
Ile Ser Gln Met Val Glu Thr Lys Ala Asn Ile Pro Tyr Lys Met Ser
 50 55 60
Phe Ser Leu Gly His Ala Gly Asp Lys Cys Lys Glu Pro Leu Ala Val
65 70 75 80
Met Ala Phe Ala Gly Asp Gln Ala Gln Asn Phe His Tyr Met Ala Gln
 85 90 95
Ala Asn Ser Ser Phe Glu Arg Ser Glu Leu Asn Phe Thr Ala Lys Ala
 100 105 110
Glu Arg Thr Arg Ile Ala Phe Tyr Ser Ile Tyr Tyr Asn Thr Arg Thr
 115 120 125
Asp Asp Met Thr Ser Leu Cys Gly Pro Val Ile Asp Asp Val Lys Val
 130 135 140
Trp Phe Ser Gly Ser Ser Arg Ile Gly Phe Ser Phe Pro Leu Phe Ile
145 150 155 160
Leu Leu Ser Leu Val Phe Ile
 165

- (2) INFORMATION FOR SEQ ID NO:311:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 116 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..116
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:
Met Val Glu Thr Lys Ala Asn Ile Pro Tyr Lys Met Ser Phe Ser Leu
1 5 10 15
Gly His Ala Gly Asp Lys Cys Lys Glu Pro Leu Ala Val Met Ala Phe
 20 25 30
Ala Gly Asp Gln Ala Gln Asn Phe His Tyr Met Ala Gln Ala Asn Ser
 35 40 45
Ser Phe Glu Arg Ser Glu Leu Asn Phe Thr Ala Lys Ala Glu Arg Thr
 50 55 60
Arg Ile Ala Phe Tyr Ser Ile Tyr Tyr Asn Thr Arg Thr Asp Asp Met
65 70 75 80
Thr Ser Leu Cys Gly Pro Val Ile Asp Asp Val Lys Val Trp Phe Ser
 85 90 95
Gly Ser Ser Arg Ile Gly Phe Ser Phe Pro Leu Phe Ile Leu Leu Ser
 100 105 110
Leu Val Phe Ile
 115

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..105

- (D) OTHER INFORMATION: / Ceres Seq. ID 1498271

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

(2) INFORMATION FOR SEQ ID NO:313:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1143 base pairs

- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- ```
(ix) FEATURE:
```

- (A) NAME/KEY: -

- (B) LOCATION: 1..1143

- (D) OTHER INFORMATION: / Ceres Seq. ID 1498272

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

(2) INFORMATION FOR SEQ ID NO:314:

- (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..337  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498273  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:  
Asn Pro Lys Asn Arg Pro His Leu Ser Arg Leu Leu Tyr Ser Leu Arg  
1 5 10 15  
Ser Leu Ile Ser Asn Ser Asn Leu Leu Cys Phe Ala Leu Met Glu Lys  
20 25 30  
Ile Ala Pro Glu Leu Phe Leu Val Ala Gly Asn Pro Asp Ser Phe Val  
35 40 45  
Val Asp Asp Leu Leu Asp Phe Ser Asn Asp Asp Gly Glu Val Asp Asp  
50 55 60  
Gly Leu Asn Thr Leu Pro Asp Ser Ser Thr Leu Ser Thr Gly Thr Leu  
65 70 75 80  
Thr Asp Ser Ser Asn Ser Ser Ser Leu Phe Thr Asp Gly Thr Gly Phe  
85 90 95  
Ser Asp Leu Tyr Ile Pro Asn Asp Asp Ile Ala Glu Leu Glu Trp Leu  
100 105 110  
Ser Asn Phe Val Glu Glu Ser Phe Ala Gly Glu Asp Gln Xaa Lys Xaa  
115 120 125  
His Leu Phe Ser Xaa Leu Lys Asn Pro Gln Thr Xaa Gly Ser Thr Leu  
130 135 140  
Thr His Leu Ile Lys Pro Glu Xaa Glu Leu Asp His Gln Phe Ile Asp  
145 150 155 160  
Ile Asp Glu Ser Asn Val Ala Val Pro Ala Lys Xaa Arg Xaa Lys Arg  
165 170 175  
Xaa Arg Xaa Ala Ala Ser Thr Trp Ala Ser Arg Xaa Leu Ser Leu Ala  
180 185 190  
Asp Ser Asp Glu Thr Asn Pro Lys Lys Lys Arg Arg Val Lys Glu  
195 200 205  
Gln Asp Phe Ala Gly Asp Met Asp Val Asp Cys Gly Glu Ser Gly Gly  
210 215 220  
Gly Arg Arg Cys Leu His Cys Ala Thr Glu Lys Thr Pro Gln Trp Arg  
225 230 235 240  
Thr Gly Pro Met Gly Pro Lys Thr Leu Cys Asn Ala Cys Gly Val Arg  
245 250 255  
Tyr Lys Ser Gly Arg Leu Val Pro Glu Tyr Arg Pro Ala Ser Ser Pro  
260 265 270  
Thr Phe Val Met Ala Arg His Ser Asn Ser His Arg Lys Val Met Glu  
275 280 285  
Leu Arg Arg Gln Lys Glu Met Arg Asp Glu His Leu Leu Ser Gln Leu  
290 295 300  
Arg Cys Glu Asn Leu Leu Met Asp Ile Arg Ser Asn Gly Glu Asp Phe  
305 310 315 320  
Leu Met His Asn Asn Thr Asn His Val Ala Pro Asp Phe Arg His Leu  
325 330 335  
Ile

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 308 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:



|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| aatcaaaacc | aaaagcccaa | aaccagagaa | agaaaaatct | ctcttttgaa | aattctctct | 60  |
| ttgcaaatca | ttcaagttaa | ggaaatcat  | ctctcttctc | ttctctctca | gcttcattca | 120 |
| ttctcttcta | actcttttcg | tttacctga  | aaactgtttt | tcgcggaaga | actcgatcac | 180 |
| ttctgatgtt | ctgtcgaact | agattaccgt | ttactctcga | tgaccctctc | catcttcttc | 240 |
| cacttttttt | ccccagtttt | ctgataactt | ttctcagatg | agaaacttga | cgttactctt | 300 |

|             |             |             |             |             |            |      |
|-------------|-------------|-------------|-------------|-------------|------------|------|
| tctcaagttc  | ttcttcttct  | tcttcaatct  | gacttcgctt  | gagtatcaag  | ttgatggagc | 360  |
| atttgttggg  | acatatggga  | taaattatgg  | aaggatagct  | gacaacatcc  | catctccggg | 420  |
| gaaagttagt  | ttactttctaa | agcaagctaa  | aattcgggaat | gtgcgtatat  | acgatgtaga | 480  |
| tcacactgtt  | cttgaagcct  | ttagtggaac  | tggtttagac  | cttggtgttg  | gacttcctaa | 540  |
| tggtgtttta  | aaagagatga  | gttcaaatgc  | tgatcatgct  | ttcacttggg  | ttaaagaaaa | 600  |
| tttccagctt  | ttcttaccga  | agactcggat  | tcgcggtatc  | gctatagtag  | acgaagttct | 660  |
| tggaagcggt  | gattctgagc  | tcgcggggag  | tttacttggg  | gctgctaaaa  | atgtgtacaa | 720  |
| tgctgtgaag  | aaaatgaatc  | tggaagacac  | tgtagcagac  | actacggctc  | attcacaggg | 780  |
| tggtttttct  | gattcctacc  | cgcttctcgt  | ttgtgtgttt  | aaagagaagt  | ttgttcagtt | 840  |
| catgaagcca  | ttgttggagt  | tttttcagca  | gattgggtct  | cccttttggg  | tgaatgctta | 900  |
| cccttttttg  | gcgtacactt  | ataatccgaa  | ggagattgat  | atcaactatg  | ctcttttcaa | 960  |
| gcacaagcaa  | gggatatatg  | accgcaaaac  | cgatttgcat  | tacgataaca  | tgctgtatgc | 1020 |
| tcagattgat  | gctgcttaca  | tgccgttgca  | agatgtcggg  | tttaagaaga  | tggaagttat | 1080 |
| gatcactgaa  | actcgggtgg  | cttctaaaag  | ggattcagat  | gaacctgcag  | caacaccaga | 1140 |
| gaacgcaaga  | acgtataact  | ataacccctc  | gaagaggcct  | gctaagaaga  | aaggagacac | 1200 |
| tccttagacca | aaaacgggtg  | ttaaagccta  | tatctttgca  | ttgttcaatg  | aaaactcaaa | 1260 |
| acggggcgaag | agttctgaga  | cacactttgg  | acttttttaa  | ccctgatggaa | ccatatcata | 1320 |
| tgacattgga  | ttcaacagtc  | taaagtctga  | ttctcccaag  | tcactcattt  | catcatcaaa | 1380 |
| gtcagctcgt  | tactatgtgg  | cattggctcat | ctctgtctcg  | gctttcctct  | tgatgatata | 1440 |
| aatgcggaaa  | tggtgtgagc  | tttgacgatc  | ctcggaattg  | gtcgtacatt  | cgtagcacta | 1500 |
| taatatatat  | tactagggtt  | gggacgctaa  | cgaaatggta  | ggagcacaaa  | tttactgcaa | 1560 |
| ttctcatata  | tgtagccaag  | agatatccag  | aaaagatatc  | accagacact  | atcatatata | 1620 |
| cacatctttat | gtaaaaaaca  | tctaatacat  | aaatttgggc  | c           |            |      |

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..387
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498280

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Ser | Ser | Thr | Leu | Leu | Leu | Leu | Lys | Phe | Phe | Phe | Phe | Phe | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Leu | Thr | Ser | Leu | Glu | Tyr | Gln | Val | Asp | Gly | Ala | Phe | Val | Gly | Thr |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |
| Tyr | Gly | Ile | Asn | Tyr | Gly | Arg | Ile | Ala | Asp | Asn | Ile | Pro | Ser | Pro | Glu |
|     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |
| Lys | Val | Val | Leu | Leu | Lys | Gln | Ala | Lys | Ile | Arg | Asn | Val | Arg | Ile |     |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     |     |     |
| Tyr | Asp | Val | Asp | His | Thr | Val | Leu | Glu | Ala | Phe | Ser | Gly | Thr | Gly | Leu |
| 65  |     |     |     |     |     |     |     |     | 70  |     |     |     |     | 75  |     |
| Asp | Leu | Val | Val | Gly | Leu | Pro | Asn | Gly | Phe | Leu | Lys | Glu | Met | Ser | Ser |
|     |     |     |     |     |     |     |     |     | 85  |     |     |     |     | 90  |     |
| Asn | Ala | Asp | His | Ala | Phe | Thr | Trp | Val | Lys | Glu | Asn | Ile | Gln | Ser | Phe |
|     |     |     |     |     |     |     |     |     | 100 |     |     |     |     | 105 |     |
| Leu | Pro | Lys | Thr | Arg | Ile | Arg | Gly | Ile | Ala | Ile | Gly | Asn | Glu | Val | Leu |
|     |     |     |     |     |     |     |     |     | 115 |     |     |     |     | 120 |     |
| Gly | Gly | Gly | Asp | Ser | Glu | Leu | Ala | Gly | Ala | Leu | Leu | Gly | Ala | Ala | Lys |
|     |     |     |     |     |     |     |     |     | 130 |     |     |     |     | 135 |     |
| Asn | Val | Tyr | Asn | Ala | Leu | Lys | Lys | Met | Asn | Leu | Glu | Asp | Thr | Val | Gln |
| 145 |     |     |     |     |     |     |     |     | 150 |     |     |     |     | 155 |     |
| Ile | Thr | Thr | Ala | His | Ser | Gln | Ala | Val | Phe | Ser | Asp | Ser | Tyr | Pro | Pro |
|     |     |     |     |     |     |     |     |     | 165 |     |     |     |     | 170 |     |
| Ser | Ser | Cys | Val | Phe | Lys | Glu | Asn | Val | Val | Gln | Phe | Met | Lys | Pro | Leu |
|     |     |     |     |     |     |     |     |     | 180 |     |     |     |     | 185 |     |
| Leu | Glu | Phe | Phe | Gln | Gln | Ile | Gly | Ser | Pro | Phe | Cys | Leu | Asn | Ala | Tyr |
|     |     |     |     |     |     |     |     |     | 195 |     |     |     |     | 200 |     |

Pro Phe Leu Ala Tyr Thr Tyr Asn Pro Lys Glu Ile Asp Ile Asn Tyr  
210 215 220  
Ala Leu Phe Lys Pro Thr Glu Gly Ile Tyr Asp Pro Lys Thr Asp Leu  
225 230 235 240  
His Tyr Asp Asn Met Leu Asp Ala Gln Ile Asp Ala Ala Tyr Met Ala  
245 250 255  
Leu Gln Asp Ala Gly Phe Lys Lys Met Glu Val Met Ile Thr Glu Thr  
260 265 270  
Gly Trp Ala Ser Lys Gly Asp Ser Asp Glu Pro Ala Ala Thr Pro Glu  
275 280 285  
Asn Ala Arg Thr Tyr Asn Tyr Asn Leu Arg Lys Arg Leu Ala Lys Lys  
290 295 300  
Lys Gly Thr Pro Leu Arg Pro Lys Thr Val Leu Lys Ala Tyr Ile Phe  
305 310 315 320  
Ala Leu Phe Asn Glu Asn Ser Lys Pro Gly Lys Ser Ser Glu Thr His  
325 330 335  
Phe Gly Leu Phe Lys Pro Asp Gly Thr Ile Ser Tyr Asp Ile Gly Phe  
340 345 350  
Asn Ser Leu Lys Ser Asp Ser Pro Lys Ser Leu Ile Ser Ser Ser Lys  
355 360 365  
Ser Ala Arg Tyr Tyr Val Ala Leu Val Ile Ser Val Ser Ala Phe Leu  
370 375 380  
Leu Met Ile

385

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 294 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..294

(D) OTHER INFORMATION: / Ceres Seq. ID 1498281

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

Met Ser Ser Asn Ala Asp His Ala Phe Thr Trp Val Lys Glu Asn Ile  
1 5 10 15  
Gln Ser Phe Leu Pro Lys Thr Arg Ile Arg Gly Ile Ala Ile Gly Asn  
20 25 30  
Glu Val Leu Gly Gly Asp Ser Glu Leu Ala Gly Ala Leu Leu Gly  
35 40 45  
Ala Ala Lys Asn Val Tyr Asn Ala Leu Lys Lys Met Asn Leu Glu Asp  
50 55 60  
Thr Val Gln Ile Thr Thr Ala His Ser Gln Ala Val Phe Ser Asp Ser  
65 70 75 80  
Tyr Pro Pro Ser Ser Cys Val Phe Lys Glu Asn Val Val Gln Phe Met  
85 90 95  
Lys Pro Leu Leu Glu Phe Phe Gln Ile Gly Ser Pro Phe Cys Leu  
100 105 110  
Asn Ala Tyr Pro Phe Leu Ala Tyr Thr Tyr Asn Pro Lys Glu Ile Asp  
115 120 125  
Ile Asn Tyr Ala Leu Phe Lys Pro Thr Glu Gly Ile Tyr Asp Pro Lys  
130 135 140  
Thr Asp Leu His Tyr Asp Asn Met Leu Asp Ala Gln Ile Asp Ala Ala  
145 150 155 160  
Tyr Met Ala Leu Gln Asp Ala Gly Phe Lys Lys Met Glu Val Met Ile  
165 170 175  
Thr Glu Thr Gly Trp Ala Ser Lys Gly Asp Ser Asp Glu Pro Ala Ala  
180 185 190  
Thr Pro Glu Asn Ala Arg Thr Tyr Asn Tyr Asn Leu Arg Lys Arg Leu

195 200 205  
Ala Lys Lys Lys Gly Thr Pro Leu Arg Pro Lys Thr Val Leu Lys Ala  
210 215 220  
Tyr Ile Phe Ala Leu Phe Asn Glu Asn Ser Lys Pro Gly Lys Ser Ser  
225 230 235 240  
Glu Thr His Phe Gly Leu Phe Lys Pro Asp Gly Thr Ile Ser Tyr Asp  
245 250 255  
Ile Gly Phe Asn Ser Leu Lys Ser Asp Ser Pro Lys Ser Leu Ile Ser  
260 265 270  
Ser Ser Lys Ser Ala Arg Tyr Tyr Val Ala Leu Val Ile Ser Val Ser  
275 280 285  
Ala Phe Leu Leu Met Ile  
290

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..235
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

Met Asn Leu Glu Asp Thr Val Gln Ile Thr Thr Ala His Ser Gln Ala  
1 5 10 15  
Val Phe Ser Asp Ser Tyr Pro Pro Ser Ser Cys Val Phe Lys Glu Asn  
20 25 30  
Val Val Gln Phe Met Lys Pro Leu Leu Glu Phe Phe Gln Gln Ile Gly  
35 40 45  
Ser Pro Phe Cys Leu Asn Ala Tyr Pro Phe Leu Ala Tyr Thr Tyr Asn  
50 55 60  
Pro Lys Glu Ile Asp Ile Asn Tyr Ala Leu Phe Lys Pro Thr Glu Gly  
65 70 75 80  
Ile Tyr Asp Pro Lys Thr Asp Leu His Tyr Asp Asn Met Leu Asp Ala  
85 90 95  
Gln Ile Asp Ala Ala Tyr Met Ala Leu Gln Asp Ala Gly Phe Lys Lys  
100 105 110  
Met Glu Val Met Ile Thr Glu Thr Gly Trp Ala Ser Lys Gly Asp Ser  
115 120 125  
Asp Glu Pro Ala Ala Thr Pro Glu Asn Ala Arg Thr Tyr Asn Tyr Asn  
130 135 140  
Leu Arg Lys Arg Leu Ala Lys Lys Lys Gly Thr Pro Leu Arg Pro Lys  
145 150 155 160  
Thr Val Leu Lys Ala Tyr Ile Phe Ala Leu Phe Asn Glu Asn Ser Lys  
165 170 175  
Pro Gly Lys Ser Ser Glu Thr His Phe Gly Leu Phe Lys Pro Asp Gly  
180 185 190  
Thr Ile Ser Tyr Asp Ile Gly Phe Asn Ser Leu Lys Ser Asp Ser Pro  
195 200 205  
Lys Ser Leu Ile Ser Ser Ser Lys Ser Ala Arg Tyr Tyr Val Ala Leu  
210 215 220  
Val Ile Ser Val Ser Ala Phe Leu Leu Met Ile  
225 230 235

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 690 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..690

(D) OTHER INFORMATION: / Ceres Seq. ID 1498283

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

|             |            |            |             |            |             |     |
|-------------|------------|------------|-------------|------------|-------------|-----|
| aaaatcgctcg | ctctctgcct | ctctcgcctc | tccaaatcga  | aatcgctctc | cgctccgctc  | 60  |
| tcgctctccg  | tctccgctct | cgctccgctc | tcgctctccg  | tctccatctc | tctctccggt  | 120 |
| aagtgactga  | aagatggggc | gtgttagaac | caagacgggtg | aagaaatctt | caagctcragt | 180 |
| cattgagaag  | tactactctc | gcctgactct | tgactttcac  | actaacaaga | agatccttga  | 240 |
| agaggttgcc  | atcatcccat | caaagagact | ccgcaacaag  | attgtggtag | tctccaccga  | 300 |
| cttgatgaaa  | cgatatcaga | akkgaccagt | ccgtggmatc  | tcactcaagc | ttcaagaaga  | 360 |
| agagcgtgaa  | cgccgatgag | actttgttcc | cgatgagtct  | gctatcaaga | ctgatgagat  | 420 |
| caagctgac   | aaagagactc | ttgagatgct | tgtctctcta  | ggaatgtctg | acactctcgg  | 480 |
| catctctgca  | gtcgaccac  | aacaagctat | ggcaccaatc  | cctgctttcg | gcgcggcgag  | 540 |
| ggcaccacga  | agatactaag | atggacgatt | ggctctcttt  | tttcaacagt | agggaacaaga | 600 |
| aagacttttg  | tgggttttta | ttgtttcttt | tgattatgct  | ttaaactcaa | tgtgagactc  | 660 |
| tttcgtatta  | atggtttttg | agttatgtgg |             |            |             |     |

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..141

(D) OTHER INFORMATION: / Ceres Seq. ID 1498284

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Gly | Arg | Val | Arg | Thr | Lys | Thr | Val | Lys | Lys | Ser | Ser | Arg | Xaa | Val |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Ile | Glu | Lys | Tyr | Tyr | Ser | Arg | Met | Thr | Leu | Asp | Phe | His | Thr | Asn | Lys |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Lys | Ile | Leu | Glu | Glu | Val | Ala | Ile | Ile | Pro | Ser | Lys | Arg | Leu | Arg | Asn |  |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |  |
| Lys | Ile | Ala | Gly | Phe | Ser | Thr | His | Leu | Met | Lys | Arg | Ile | Gln | Xaa | Xaa |  |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |  |
| Pro | Val | Arg | Xaa | Ile | Ser | Leu | Lys | Leu | Gln | Glu | Glu | Arg | Glu | Arg |     |  |
| 65  |     |     |     |     |     |     |     | 70  |     |     |     | 75  |     |     | 80  |  |
| Arg | Met | Asp | Phe | Val | Pro | Asp | Glu | Ser | Ala | Ile | Lys | Thr | Asp | Glu | Ile |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 95  |  |
| Lys | Val | Asp | Lys | Glu | Thr | Leu | Glu | Met | Leu | Ala | Ser | Leu | Gly | Met | Ser |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 110 |  |
| Asp | Thr | Leu | Gly | Ile | Ser | Ala | Val | Asp | Pro | Gln | Gln | Ala | Met | Ala | Pro |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 125 |  |
| Ile | Pro | Ala | Phe | Gly | Gly | Gly | Arg | Ala | Pro | Arg | Arg | Tyr |     |     |     |  |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 140 |  |

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..118

(D) OTHER INFORMATION: / Ceres Seq. ID 1498285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

Met Thr Leu Asp Phe His Thr Asn Lys Lys Ile Leu Glu Val Ala

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| 1                                                               | 5   | 10  | 15  |
| Ile Ile Pro Ser Lys Arg Leu Arg Asn Lys Ile Ala Gly Phe Ser Thr |     |     |     |
|                                                                 | 20  | 25  | 30  |
| His Leu Met Lys Arg Ile Gln Xaa Xaa Pro Val Arg Xaa Ile Ser Leu |     |     |     |
|                                                                 | 35  | 40  | 45  |
| Lys Leu Gln Glu Glu Glu Arg Glu Arg Arg Met Asp Phe Val Pro Asp |     |     |     |
|                                                                 | 50  | 55  | 60  |
| Glu Ser Ala Ile Lys Thr Asp Glu Ile Lys Val Asp Lys Glu Thr Leu |     |     |     |
|                                                                 | 65  | 70  | 75  |
| Glu Met Leu Ala Ser Leu Gly Met Ser Asp Thr Leu Gly Ile Ser Ala |     |     |     |
|                                                                 | 85  | 90  | 95  |
| Val Asp Pro Gln Gln Ala Met Ala Pro Ile Pro Ala Phe Gly Gly Gly |     |     |     |
|                                                                 | 100 | 105 | 110 |
| Arg Ala Pro Arg Arg Tyr                                         |     |     |     |
|                                                                 | 115 |     |     |

(2) INFORMATION FOR SEQ ID NO:323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

|                                                                 |             |
|-----------------------------------------------------------------|-------------|
| Met Lys Arg Ile Gln Xaa Xaa Pro Val Arg Xaa Ile Ser Leu Lys Leu |             |
| 1                                                               | 5 10 15     |
| Gln Glu Glu Glu Arg Glu Arg Arg Met Asp Phe Val Pro Asp Glu Ser |             |
|                                                                 | 20 25 30    |
| Ala Ile Lys Thr Asp Glu Ile Lys Val Asp Lys Glu Thr Leu Glu Met |             |
|                                                                 | 35 40 45    |
| Leu Ala Ser Leu Gly Met Ser Asp Thr Leu Gly Ile Ser Ala Val Asp |             |
|                                                                 | 50 55 60    |
| Pro Gln Gln Ala Met Ala Pro Ile Pro Ala Phe Gly Gly Gly Arg Ala |             |
|                                                                 | 65 70 75 80 |
| Pro Arg Arg Tyr                                                 |             |

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1264
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

|                                                |     |
|------------------------------------------------|-----|
| attatgagaa agaattctcac ctaaatgatgt tctaggtta   | 60  |
| acgagactat accacctaac atctccgaga aagaagctgc    | 120 |
| cagcggtgaga ggaggaaaaa gagcgtagaa cgcattgcaat  | 180 |
| ctgctcagc tgacgcagcg gtgctggcggt ctaaaagcggc   | 240 |
| aaggtcgaag caaagagtgggt ccgttaggag gtggcgaagg  | 300 |
| tgcatgatcca atgtgccttt agaggctact tggcgagaaa   | 360 |
| gagtgtgtgaa gattcacaagt ttatgtgagag gttttttggt | 420 |
| ctctccggag tatggaaagca ctgttttagag ctcagaaaaac | 480 |
| tccgtcgtaa cggaaatgct gctccggcga gaaaatccac    | 540 |
| tggagaatcg aaacaacggc gaagagacag ctaagatagt    | 600 |
| ggaggtagat acagggaaccc                         |     |

|            |            |             |             |            |            |      |
|------------|------------|-------------|-------------|------------|------------|------|
| gaccgggac  | ttacagaatc | cgagcaccgc  | ttttatccgc  | gtcggaattc | ttagacaacc | 660  |
| cggttcgacg | tacgctttct | tcaccgctct  | cggttcgag   | cccaccgcgt | ctatcaatgc | 720  |
| ctaaacctga | atgggaagag | tgcaagtagc  | agttcccgac  | ggcgagagc  | acacctcggt | 780  |
| ttttctgtgg | gtctccggcg | aggagcgtgt  | gctgctctgg  | tgccggagta | gagcgaggag | 840  |
| tggtatagca | ggctgatgct | aaccggttct  | gtttcttctg  | gggggaattt | aactcggggt | 900  |
| acatggcgga | tacaacgtcg | tttagggcga  | aactgagggtc | gcatagtgca | ccgagacaga | 960  |
| gaccagagag | taatgcttca | gctggcggtat | ggaggaggag  | tatcgccggc | gggtggtgta | 1020 |
| ggatcagag  | acagtcgtgt | tcgggtgtca  | gagaagctgt  | ggcggggaat | atcgagaggc | 1080 |
| gtaggatgcg | ttggtgatct | ttatttccat  | aattattatc  | cgtttagttt | tggttaatta | 1140 |
| ggggagtaat | gttattaatt | taatatagtt  | tgatattatt  | atagttttct | aagtttcaat | 1200 |
| gacaaaattt | aaaattgttg | tttcttgat   | gctacatatt  | ctatttctat | gtaagttttt | 1260 |

tgcc

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..352

(D) OTHER INFORMATION: / Ceres Seq. ID 1498292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Ser | Leu | Cys | Asp | Ser | Tyr | Glu | Thr | Ile | Pro | Pro | Asn | Ile | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Lys | Glu | Ala | Ala | Trp | Leu | Arg | Ser | Phe | Tyr | Ala | Ala | Gly | Glu | Glu |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Glu | Lys | Glu | Arg | Arg | Thr | His | Ala | Ile | Ala | Val | Ala | Ala | Ala | Thr | Ala |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Ala | Ala | Asp | Ala | Ala | Val | Ala | Ala | Lys | Ala | Ala | Ala | Ala | Val |     |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Val | Met | Leu | Gln | Gly | Gln | Gly | Lys | Ser | Gly | Pro | Leu | Gly | Gly | Gly | Lys |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     | 80  |     |
| Ser | Arg | Glu | His | Arg | Ala | Ala | Met | Gln | Ile | Gln | Cys | Ala | Phe | Arg | Gly |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Tyr | Leu | Ala | Arg | Lys | Ala | Leu | Arg | Ala | Leu | Arg | Gly | Val | Val | Lys | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gln | Ala | Leu | Val | Arg | Gly | Phe | Leu | Val | Arg | Asn | Gln | Ala | Ala | Ala | Thr |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Arg | Ser | Met | Glu | Ala | Leu | Val | Arg | Ala | Gln | Lys | Thr | Val | Lys | Ile |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Gln | Arg | Ala | Leu | Arg | Arg | Asn | Gly | Asn | Ala | Ala | Pro | Ala | Arg | Lys | Ser |
|     |     |     | 145 |     |     |     | 150 |     |     | 155 |     |     |     | 160 |     |
| Thr | Glu | Arg | Phe | Ser | Gly | Ser | Leu | Glu | Asn | Arg | Asn | Asn | Gly | Glu | Glu |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Thr | Ala | Lys | Ile | Val | Glu | Val | Asp | Thr | Gly | Thr | Arg | Pro | Gly | Thr | Tyr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Arg | Ile | Arg | Ala | Pro | Val | Leu | Ser | Gly | Ser | Asp | Phe | Leu | Asp | Asn | Pro |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Phe | Arg | Arg | Thr | Leu | Ser | Ser | Pro | Leu | Ser | Gly | Arg | Val | Pro | Pro | Arg |
|     |     |     | 210 |     |     |     | 215 |     |     |     | 220 |     |     |     |     |
| Leu | Ser | Met | Pro | Lys | Pro | Glu | Trp | Glu | Glu | Cys | Ser | Ser | Lys | Phe | Pro |
|     |     |     | 225 |     |     |     | 230 |     |     | 235 |     |     |     | 240 |     |
| Thr | Ala | Gln | Ser | Thr | Pro | Arg | Phe | Ser | Gly | Gly | Ser | Pro | Ala | Arg | Ser |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Val | Cys | Cys | Ser | Gly | Gly | Gly | Val | Glu | Ala | Glu | Val | Asp | Thr | Glu | Ala |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Asp | Ala | Asn | Arg | Phe | Cys | Phe | Leu | Ser | Gly | Glu | Phe | Asn | Ser | Gly | Tyr |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Met | Ala | Asp | Thr | Thr | Ser | Phe | Arg | Ala | Lys | Leu | Arg | Ser | His | Ser | Ala |

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| 290                                                             | 295 | 300 |     |
| Pro Arg Gln Arg Pro Glu Ser Asn Ala Ser Ala Gly Gly Trp Arg Arg |     |     |     |
| 305                                                             | 310 | 315 | 320 |
| Ser Ile Gly Gly Gly Gly Val Arg Met Gln Arg Gln Ser Cys Ser Gly |     |     |     |
|                                                                 | 325 | 330 | 335 |
| Val Arg Glu Ala Val Val Gly Asn Ile Glu Arg Arg Arg Met Arg Trp |     |     |     |
|                                                                 | 340 | 345 | 350 |

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 287 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..287

(D) OTHER INFORMATION: / Ceres Seq. ID 1498293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Gln | Gly | Gln | Gly | Lys | Ser | Gly | Pro | Leu | Gly | Gly | Gly | Lys | Ser |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Arg | Glu | His | Arg | Ala | Ala | Met | Gln | Ile | Gln | Cys | Ala | Phe | Arg | Gly | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Ala | Arg | Lys | Ala | Leu | Arg | Ala | Leu | Arg | Gly | Val | Val | Lys | Ile | Gln |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Leu | Val | Arg | Gly | Phe | Leu | Val | Arg | Asn | Gln | Ala | Ala | Ala | Thr | Leu |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Arg | Ser | Met | Glu | Ala | Leu | Val | Arg | Ala | Gln | Lys | Thr | Val | Lys | Ile | Gln |
|     |     |     | 65  |     |     | 70  |     |     | 75  |     |     |     | 80  |     |     |
| Arg | Ala | Leu | Arg | Arg | Asn | Gly | Asn | Ala | Ala | Pro | Ala | Arg | Lys | Ser | Thr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Glu | Arg | Phe | Ser | Gly | Ser | Leu | Glu | Asn | Arg | Asn | Asn | Gly | Glu | Glu | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Lys | Ile | Val | Glu | Val | Asp | Thr | Gly | Thr | Arg | Pro | Gly | Thr | Tyr | Arg |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Arg | Ala | Pro | Val | Leu | Ser | Gly | Ser | Asp | Phe | Leu | Asp | Asn | Pro | Phe |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Arg | Arg | Thr | Leu | Ser | Ser | Pro | Leu | Ser | Gly | Arg | Val | Pro | Pro | Arg | Leu |
|     |     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     | 160 |     |
| Ser | Met | Pro | Lys | Pro | Glu | Trp | Glu | Glu | Cys | Ser | Ser | Lys | Phe | Pro | Thr |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     | 175 |     |     |
| Ala | Gln | Ser | Thr | Pro | Arg | Phe | Ser | Gly | Gly | Ser | Pro | Ala | Arg | Ser | Val |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Cys | Cys | Ser | Gly | Gly | Gly | Val | Glu | Ala | Glu | Val | Asp | Thr | Glu | Ala | Asp |
|     |     |     | 195 |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Ala | Asn | Arg | Phe | Cys | Phe | Leu | Ser | Gly | Glu | Phe | Asn | Ser | Gly | Tyr | Met |
|     |     |     | 210 |     |     | 215 |     |     |     | 220 |     |     |     |     |     |
| Ala | Asp | Thr | Thr | Ser | Phe | Arg | Ala | Lys | Leu | Arg | Ser | His | Ser | Ala | Pro |
|     |     |     | 225 |     |     | 230 |     |     |     | 235 |     |     |     | 240 |     |
| Arg | Gln | Arg | Pro | Glu | Ser | Asn | Ala | Ser | Ala | Gly | Gly | Trp | Arg | Arg | Ser |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Ile | Gly | Gly | Gly | Gly | Val | Arg | Met | Gln | Arg | Gln | Ser | Cys | Ser | Gly | Val |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Arg | Glu | Ala | Val | Val | Gly | Asn | Ile | Glu | Arg | Arg | Arg | Met | Arg | Trp |     |
|     |     |     | 275 |     |     | 280 |     |     |     |     |     | 285 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 265 amino acids

(B) TYPE: amino acid



(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..265  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498294  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:  
Met Gln Ile Gln Cys Ala Phe Arg Gly Tyr Leu Ala Arg Lys Ala Leu  
1 5 10 15  
Arg Ala Leu Arg Gly Val Val Lys Ile Gln Ala Leu Val Arg Gly Phe  
20 25 30  
Leu Val Arg Asn Gln Ala Ala Ala Thr Leu Arg Ser Met Glu Ala Leu  
35 40 45  
Val Arg Ala Gln Lys Thr Val Lys Ile Gln Arg Ala Leu Arg Arg Asn  
50 55 60  
Gly Asn Ala Ala Pro Ala Arg Lys Ser Thr Glu Arg Phe Ser Gly Ser  
65 70 75 80  
Leu Glu Asn Arg Asn Asn Gly Glu Glu Thr Ala Lys Ile Val Glu Val  
85 90 95  
Asp Thr Gly Thr Arg Pro Gly Thr Tyr Arg Ile Arg Ala Pro Val Leu  
100 105 110  
Ser Gly Ser Asp Phe Leu Asp Asn Pro Phe Arg Arg Thr Leu Ser Ser  
115 120 125  
Pro Leu Ser Gly Arg Val Pro Pro Arg Leu Ser Met Pro Lys Pro Glu  
130 135 140  
Trp Glu Glu Cys Ser Ser Lys Phe Pro Thr Ala Gln Ser Thr Pro Arg  
145 150 155 160  
Phe Ser Gly Gly Ser Pro Ala Arg Ser Val Cys Cys Ser Gly Gly Gly  
165 170 175  
Val Glu Ala Glu Val Asp Thr Glu Ala Asp Ala Asn Arg Phe Cys Phe  
180 185 190  
Leu Ser Gly Glu Phe Asn Ser Gly Tyr Met Ala Asp Thr Thr Ser Phe  
195 200 205  
Arg Ala Lys Leu Arg Ser His Ser Ala Pro Arg Gln Arg Pro Glu Ser  
210 215 220  
Asn Ala Ser Ala Gly Gly Trp Arg Arg Ser Ile Gly Gly Gly Gly Val  
225 230 235 240  
Arg Met Gln Arg Gln Ser Cys Ser Gly Val Arg Glu Ala Val Val Gly  
245 250 255  
Asn Ile Glu Arg Arg Met Arg Trp  
260 265

- (2) INFORMATION FOR SEQ ID NO:328:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 727 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..727  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498295  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:  
aagtagagagg aagacgatgg cgtagagaaa gcacatagag aaggctactct tcagcgatga 60  
agtaattgcg caccgggtga atcagcttgg aatcgatatt acttctgatt tctcgggtga 120  
ctcggaggaa actcctctatt ttgtcggcgt agccactggt gcttgctctt tcttggccga 180  
tctcgttagg cgaattgact tgccaatagc tatagatttc attagagctg agtcttaacg 240  
ctctggtact gtatccagtg gaggttccag agtatcattt gacttaaaagc ttgacatcac 300  
gaacaagcac gttgtctctgg tcgaggacat tgtggatact ggcaatacac ttagtgcctc 360  
gattgagcac atgaagcaa aaaaggcgctc atctgtttcg gtttgcactc tctctgacaa 420

|             |             |            |            |            |            |     |
|-------------|-------------|------------|------------|------------|------------|-----|
| gccatcgaga  | agaaagggttc | attataagct | ggttggaag  | gggaattct  | acagtgttt  | 480 |
| tgaatgtcca  | gatgaatttg  | tcgtgggcta | tggcatggat | tttgcagaac | aataccgcaa | 540 |
| cctatcttac  | attggcgat   | tgaagcctga | atattacatg | tgacaatatt | gcatgaactg | 600 |
| gtcaaatcatg | acatcttttg  | atgacttgca | cctctgttag | gtgttcaaag | cagtagcacc | 660 |
| aatgtttatac | tacaatttga  | cagtgtttct | gatgtaaaag | ctaattgaaa | ttgtgttatg | 720 |
| atatgtt     |             |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..193
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Arg | Lys | Thr | Met | Ala | Leu | Glu | Lys | His | Ile | Glu | Lys | Val | Leu |     |
| 1   |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |     |
| Phe | Ser | Asp | Glu | Val | Ile | Ala | His | Arg | Val | Asn | Gln | Leu | Gly | Ile | Asp |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Ile | Thr | Ser | Asp | Phe | Ser | Gly | Asp | Ser | Glu | Glu | Thr | Pro | Ile | Phe | Val |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Gly | Val | Ala | Thr | Gly | Ala | Cys | Leu | Phe | Leu | Ala | Asp | Leu | Val | Arg | Arg |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ile | Asp | Leu | Pro | Ile | Ala | Ile | Asp | Phe | Ile | Arg | Ala | Glu | Ser | Tyr | Gly |
| 65  |     |     | 70  |     |     |     | 75  |     |     |     |     |     |     | 80  |     |
| Ser | Gly | Thr | Val | Ser | Ser | Gly | Val | Pro | Arg | Val | Ser | Phe | Asp | Leu | Lys |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |     |
| Leu | Asp | Ile | Thr | Asn | Lys | His | Val | Val | Leu | Val | Glu | Asp | Ile | Val | Asp |
|     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |     |
| Thr | Gly | Asn | Thr | Leu | Ser | Cys | Leu | Ile | Glu | His | Met | Lys | Ala | Lys | Lys |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Ala | Ser | Ser | Val | Ser | Val | Cys | Thr | Leu | Leu | Asp | Lys | Pro | Ser | Arg | Arg |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Val | His | Tyr | Lys | Leu | Val | Gly | Lys | Gly | Lys | Phe | Tyr | Ser | Gly | Phe |
|     |     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     | 160 |     |
| Glu | Cys | Pro | Asp | Glu | Phe | Val | Val | Gly | Tyr | Gly | Met | Asp | Phe | Ala | Glu |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     | 175 |     |     |
| Gln | Tyr | Arg | Asn | Leu | Ser | Tyr | Ile | Gly | Val | Leu | Lys | Pro | Glu | Tyr | Tyr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |

Met

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..188
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Leu | Glu | Lys | His | Ile | Glu | Lys | Val | Leu | Phe | Ser | Asp | Glu | Val |
| 1   |     | 5   |     |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Ala | His | Arg | Val | Asn | Gln | Leu | Gly | Ile | Asp | Ile | Thr | Ser | Asp | Phe |
|     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |     |
| Ser | Gly | Asp | Ser | Glu | Glu | Thr | Pro | Ile | Phe | Val | Gly | Val | Ala | Thr | Gly |

|                                     |                                     |                     |
|-------------------------------------|-------------------------------------|---------------------|
| 35                                  | 40                                  | 45                  |
| Ala Cys Leu Phe Leu                 | Ala Asp Leu Val Arg Arg             | Ile Asp Leu Pro Ile |
| 50                                  | 55                                  | 60                  |
| Ala Ile Asp Phe Ile Arg             | Glu Ser Tyr Gly Ser Gly Thr Val Ser |                     |
| 65                                  | 70                                  | 75                  |
| Ser Gly Val Pro Arg Val Ser         | Phe Asp Leu Lys Leu Asp Ile Thr Asn |                     |
| 85                                  | 90                                  | 95                  |
| Lys His Val Val Leu Val Glu Asp     | Ile Val Asp Thr Gly Asn Thr Leu     |                     |
| 100                                 | 105                                 | 110                 |
| Ser Cys Leu Ile Glu His Met         | Lys Ala Lys Lys Ala Ser Ser Val Ser |                     |
| 115                                 | 120                                 | 125                 |
| Val Cys Thr Leu Leu Asp Lys         | Pro Ser Arg Arg Lys Val His Tyr Lys |                     |
| 130                                 | 135                                 | 140                 |
| Leu Val Gly Lys Gly Lys Phe Tyr Ser | Gly Phe Glu Cys Pro Asp Glu         |                     |
| 145                                 | 150                                 | 155                 |
| Phe Val Val Gly Tyr Gly Met Asp     | Phe Ala Glu Gln Tyr Arg Asn Leu     |                     |
| 165                                 | 170                                 | 175                 |
| Ser Tyr Ile Gly Val Leu Lys Pro     | Glu Tyr Tyr Met                     |                     |
| 180                                 | 185                                 |                     |

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1795 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1795

(D) OTHER INFORMATION: / Ceres Seq. ID 1498309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| aaaataactta | gaaagaaaaa  | gagctctcagc | agcatcagct  | cgctccttaaa | tctgatccat  | 60   |
| catcgctcact | ttctcccgcc  | gaattccggt  | ttatcgattt  | aagtaacgag  | attatgtgcaa | 120  |
| agatgactca  | ggacgtggag  | atgaaagata  | ataacacccc  | ttctcaatcg  | attatctcttt | 180  |
| cttcgacctc  | tactatgcag  | aatttgaagg  | agattgcagc  | actcatcgat  | actgggtcttt | 240  |
| acacgaagga  | ggttcgtcgt  | attgctcgtg  | ctgtgcgtct  | cactataggg  | cttaggcaga  | 300  |
| aactcacggg  | ctctgtgctc  | ttctccttcc  | tggattttgc  | tttggttcca  | ggatccgaag  | 360  |
| ctcaactctcg | ctctctcttcc | tttgttctca  | agggtgatga  | acatgacatg  | gaagttgata  | 420  |
| ctgcctcatc  | ggccacacaa  | gctgctcctt  | ctaagcatct  | acctgcagag  | ctcgagatct  | 480  |
| actgctactct | cattgtttctt | ctttttctga  | ttgatcagaa  | gaagtacaac  | gaggctaaaag | 540  |
| cttgtttctt  | agcaagcatt  | gctcgtctca  | agaacgtcaa  | ccgaaggacc  | attgatgtga  | 600  |
| tagcatcaag  | actctacttt  | tactattctt  | tgagttatga  | gcaaacccgt  | gatctgtcgt  | 660  |
| aaattcgccg  | tactctttctt | gcggtgcctc  | attctgcaac  | gctaaggcac  | cttagctgtgg | 720  |
| gtcaggaaac  | ctctctgtaac | ctgtgtgtac  | gtaactattt  | gcattacaac  | ctctatgatc  | 780  |
| aggcagagaa  | gctaagatca  | aaggcacctc  | gctttgaggg  | tcattcaaac  | caacagctttt | 840  |
| gtaggctacc  | ttctatcttc  | gggaagatcc  | gtactattca  | gctcgaatat  | acggagcga   | 900  |
| aagagagcct  | tcttcaggcg  | gccaggaaaa  | cccctatagc  | agctttgggg  | ttcaggatcc  | 960  |
| aattgtaata  | attggcaatt  | ctggttcgtc  | ttagctgtgg  | tgagatacca  | gagcgtttca  | 1020 |
| tcttcaactca | aaagggtgat  | gagaaggccc  | tcagacccta  | cttcgagcta  | acaaattgcgg | 1080 |
| ttaggattgg  | ggaattggag  | ttgtttagga  | gactccagga  | gaagttcttg  | gacacatttg  | 1140 |
| ctcaagacag  | aacgcacaa   | ctcatcgtgc  | gactccgcca  | caatgtcatc  | aggactggac  | 1200 |
| tgcggaaact  | aagtatcttc  | tactcgagaa  | ctcttttacc  | cgatgttgcc  | aaaaagctga  | 1260 |
| ggctcaactc  | tgaaaaccc   | ggctgatgag  | gaaagcatcg  | tgccaaaggc  | catcgcgcac  | 1320 |
| ggagctatcg  | atgctacaa   | cgatcacaaa  | aacggatgca  | tggtctccaa  | agaaactggg  | 1380 |
| gacatctact  | cgacgaatga  | gccacaaa    | gcgttcaact  | caagaattgc  | tttctgcctc  | 1440 |
| aacatgcata  | acgaagctgt  | cagagacattg | aggtttcttc  | ctaacactca  | caagagagaa  | 1500 |
| gaaagcgatg  | agaagagag   | agagaggaag  | caacaggaag  | aagagcttgc  | taagcatatg  | 1560 |
| gctgaggaag  | acgatgatga  | cttttagaca  | aaggtcatct  | atttcttata  | agagttgact  | 1620 |
| ctccatctgt  | ctcaactttt  | ttatgttcc   | aagtttactt  | ggatctctta  | tcactgtctc  | 1680 |
| taagtgtttc  | tttattgagg  | atttttatcc  | tcaggaaacct | ttttattact  | ctggtttcac  | 1740 |
| tttaggaaaa  | gatatttatc  | ttgttggttt  | cagaagatca  | aattcaagtt  | cgttt       |      |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(ix) FEATURE:

(B) LOCATION: 1..387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Gln | Asp | Ala | Glu | Met | Lys | Asp | Asn | Asn | Thr | Pro | Ser | Gln | Ser |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ile | Ile | Ser | Ser | Ser | Thr | Ser | Thr | Met | Gln | Asn | Leu | Lys | Glu | Ile | Ala |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Leu | Ile | Asp | Thr | Gly | Ser | Tyr | Thr | Lys | Glu | Val | Arg | Arg | Ile | Ala |
|     |     |     |     | 35  |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Ala | Val | Arg | Leu | Thr | Ile | Gly | Leu | Arg | Gln | Lys | Leu | Thr | Gly | Ser |
|     |     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Val | Leu | Ser | Ser | Phe | Leu | Asp | Phe | Ala | Leu | Val | Pro | Gly | Ser | Glu | Ala |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| His | Ser | Arg | Leu | Ser | Ser | Phe | Val | Pro | Lys | Gly | Asp | Glu | His | Asp | Met |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Val | Asp | Thr | Ala | Ser | Ser | Ala | Thr | Gln | Ala | Ala | Pro | Ser | Lys | His |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Pro | Ala | Glu | Leu | Glu | Ile | Tyr | Cys | Tyr | Phe | Ile | Val | Leu | Leu | Phe |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     | 125 |     |     |     |
| Leu | Ile | Asp | Gln | Lys | Lys | Tyr | Asn | Glu | Ala | Lys | Ala | Cys | Ser | Ser | Ala |
|     |     |     |     | 130 |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Ser | Ile | Ala | Arg | Leu | Lys | Asn | Val | Asn | Arg | Arg | Thr | Ile | Asp | Val | Ile |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Ala | Ser | Arg | Leu | Tyr | Phe | Tyr | Tyr | Ser | Leu | Ser | Tyr | Glu | Gln | Thr | Gly |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Asp | Leu | Ala | Glu | Ile | Arg | Gly | Thr | Leu | Leu | Ala | Leu | His | His | Ser | Ala |
|     |     |     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Thr | Leu | Arg | His | Asp | Glu | Leu | Gly | Gln | Glu | Thr | Leu | Leu | Asn | Leu | Leu |
|     |     |     |     | 195 |     |     |     | 200 |     |     |     | 205 |     |     |     |
| Leu | Arg | Asn | Tyr | Leu | His | Tyr | Asn | Leu | Tyr | Asp | Gln | Ala | Glu | Lys | Leu |
|     |     |     |     | 210 |     |     | 215 |     |     |     | 220 |     |     |     |     |
| Arg | Ser | Lys | Ala | Pro | Arg | Phe | Glu | Ala | His | Ser | Asn | Gln | Gln | Phe | Cys |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     | 240 |
| Arg | Tyr | Leu | Phe | Tyr | Leu | Gly | Lys | Ile | Arg | Thr | Ile | Gln | Leu | Glu | Tyr |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Thr | Asp | Ala | Lys | Glu | Ser | Leu | Leu | Gln | Ala | Ala | Arg | Lys | Ala | Pro | Ile |
|     |     |     |     | 260 |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ala | Ala | Leu | Gly | Phe | Arg | Ile | Gln | Cys | Asn | Lys | Trp | Ala | Ile | Leu | Val |
|     |     |     |     | 275 |     |     |     | 280 |     |     |     | 285 |     |     |     |
| Arg | Leu | Leu | Leu | Gly | Glu | Ile | Pro | Glu | Arg | Ser | Ile | Phe | Thr | Gln | Lys |
|     |     |     |     | 290 |     |     | 295 |     |     |     | 300 |     |     |     |     |
| Gly | Met | Glu | Lys | Ala | Leu | Arg | Pro | Tyr | Phe | Glu | Leu | Thr | Asn | Ala | Val |
| 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     |     | 320 |
| Arg | Ile | Gly | Asp | Leu | Glu | Leu | Phe | Arg | Thr | Val | Gln | Glu | Lys | Phe | Leu |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Asp | Thr | Phe | Ala | Gln | Asp | Arg | Thr | His | Asn | Leu | Ile | Val | Arg | Leu | Arg |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

385

(2) INFORMATION FOR SEQ ID NO:333:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 381 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..381  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Asp | Asn | Asn | Thr | Pro | Ser | Gln | Ser | Ile | Ile | Ser | Ser | Ser | Thr |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ser | Thr | Met | Gln | Asn | Leu | Lys | Glu | Ile | Ala | Ala | Leu | Ile | Asp | Thr | Gly |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Ser | Tyr | Thr | Lys | Glu | Val | Arg | Arg | Ile | Ala | Arg | Ala | Val | Arg | Leu | Thr |
|     |     |     | 35  |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Ile | Gly | Leu | Arg | Gln | Lys | Leu | Thr | Gly | Ser | Val | Leu | Ser | Ser | Phe | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Phe | Ala | Leu | Val | Pro | Gly | Ser | Glu | Ala | His | Ser | Arg | Leu | Ser | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Phe | Val | Pro | Lys | Gly | Asp | Glu | His | Asp | Met | Glu | Val | Asp | Thr | Ala | Ser |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ser | Ala | Thr | Gln | Ala | Ala | Pro | Ser | Lys | His | Leu | Pro | Ala | Glu | Leu | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Tyr | Cys | Tyr | Phe | Ile | Val | Leu | Leu | Phe | Leu | Ile | Asp | Gln | Lys | Lys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Tyr | Asn | Glu | Ala | Lys | Ala | Cys | Ser | Ser | Ala | Ser | Ile | Ala | Arg | Leu | Lys |
|     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Asn | Val | Asn | Arg | Arg | Thr | Ile | Asp | Val | Ile | Ala | Ser | Arg | Leu | Tyr | Phe |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Tyr | Tyr | Ser | Leu | Ser | Tyr | Glu | Gln | Thr | Gly | Asp | Leu | Ala | Glu | Ile | Arg |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Gly | Thr | Leu | Leu | Ala | Leu | His | His | Ser | Ala | Thr | Leu | Arg | His | Asp | Glu |
|     |     | 180 |     |     |     | 185 |     |     |     |     |     |     | 190 |     |     |
| Leu | Gly | Gln | Glu | Thr | Leu | Leu | Asn | Leu | Leu | Leu | Arg | Asn | Tyr | Leu | His |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Tyr | Asn | Leu | Tyr | Asp | Gln | Ala | Glu | Lys | Leu | Arg | Ser | Lys | Ala | Pro | Arg |
|     |     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |
| Phe | Glu | Ala | His | Ser | Asn | Gln | Gln | Phe | Cys | Arg | Tyr | Leu | Phe | Tyr | Leu |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Gly | Lys | Ile | Arg | Thr | Ile | Gln | Leu | Glu | Tyr | Thr | Asp | Ala | Lys | Glu | Ser |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Leu | Leu | Gln | Ala | Ala | Arg | Lys | Ala | Pro | Ile | Ala | Ala | Leu | Gly | Phe | Arg |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Ile | Gln | Cys | Asn | Lys | Trp | Ala | Ile | Leu | Val | Arg | Leu | Leu | Leu | Gly | Glu |
|     |     | 275 |     |     |     | 280 |     |     |     |     |     | 285 |     |     |     |
| Ile | Pro | Glu | Arg | Ser | Ile | Phe | Thr | Gln | Lys | Gly | Met | Glu | Lys | Ala | Leu |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Arg | Pro | Tyr | Phe | Glu | Leu | Thr | Asn | Ala | Val | Arg | Ile | Gly | Asp | Leu | Glu |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Leu | Phe | Arg | Thr | Val | Gln | Glu | Lys | Phe | Leu | Asp | Thr | Phe | Ala | Gln | Asp |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |     |
| Arg | Thr | His | Asn | Leu | Ile | Val | Arg | Leu | Arg | His | Asn | Val | Ile | Arg | Thr |
|     |     | 340 |     |     |     | 345 |     |     |     |     |     |     | 350 |     |     |
| Gly | Leu | Arg | Asn | Ile | Ser | Ile | Ser | Tyr | Ser | Arg | Ile | Ser | Leu | Pro | Asp |
|     |     | 355 |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |
| Val | Ala | Lys | Lys | Leu | Arg | Leu | Asn | Ser | Glu | Asn | Pro | Gly |     |     |     |
|     |     | 370 |     |     |     | 375 |     |     |     |     |     | 380 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 363 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..363

(D) OTHER INFORMATION: / Ceres Seq. ID 1498312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

Met Gln Asn Leu Lys Glu Ile Ala Ala Leu Ile Asp Thr Gly Ser Tyr  
1 5 10 15  
Thr Lys Glu Val Arg Arg Ile Ala Arg Ala Val Arg Leu Thr Ile Gly  
20 25 30  
Leu Arg Gln Lys Leu Thr Gly Ser Val Leu Ser Ser Phe Leu Asp Phe  
35 40 45  
Ala Leu Val Pro Gly Ser Glu Ala His Ser Arg Leu Ser Ser Phe Val  
50 55 60  
Pro Lys Gly Asp Glu His Asp Met Glu Val Asp Thr Ala Ser Ser Ala  
65 70 75 80  
Thr Gln Ala Ala Pro Ser Lys His Leu Pro Ala Glu Leu Glu Ile Tyr  
85 90 95  
Cys Tyr Phe Ile Val Leu Leu Phe Lys Ile Asp Gln Lys Lys Tyr Asn  
100 105 110  
Glu Ala Lys Ala Cys Ser Ser Ala Ser Ile Ala Arg Leu Lys Asn Val  
115 120 125  
Asn Arg Arg Thr Ile Asp Val Ile Ala Ser Arg Leu Tyr Phe Tyr Tyr  
130 135 140  
Ser Leu Ser Tyr Glu Gln Thr Gly Asp Leu Ala Glu Ile Arg Gly Thr  
145 150 155 160  
Leu Leu Ala Leu His His Ser Ala Thr Leu Arg His Asp Glu Leu Gly  
165 170 175  
Gln Glu Thr Leu Leu Asn Leu Leu Leu Arg Asn Tyr Leu His Tyr Asn  
180 185 190  
Leu Tyr Asp Gln Ala Glu Lys Leu Arg Ser Lys Ala Pro Arg Phe Glu  
195 200 205  
Ala His Ser Asn Gln Gln Phe Cys Arg Tyr Leu Phe Tyr Leu Gly Lys  
210 215 220  
Ile Arg Thr Ile Gln Leu Glu Tyr Thr Asp Ala Lys Glu Ser Leu Leu  
225 230 235 240  
Gln Ala Ala Arg Lys Ala Pro Ile Ala Ala Leu Gly Phe Arg Ile Gln  
245 250 255  
Cys Asn Lys Trp Ala Ile Leu Val Arg Leu Leu Leu Gly Glu Ile Pro  
260 265 270  
Glu Arg Ser Ile Phe Thr Gln Lys Gly Met Glu Lys Ala Leu Arg Pro  
275 280 285  
Tyr Phe Glu Leu Thr Asn Ala Val Arg Ile Gly Asp Leu Glu Leu Phe  
290 295 300  
Arg Thr Val Gln Glu Lys Phe Leu Asp Thr Phe Ala Gln Asp Arg Thr  
305 310 315 320  
His Asn Leu Ile Val Arg Leu Arg His Asn Val Ile Arg Thr Gly Leu  
325 330 335  
Arg Asn Ile Ser Ile Ser Tyr Ser Arg Ile Ser Leu Pro Asp Val Ala  
340 345 350  
Lys Lys Leu Arg Leu Asn Ser Glu Asn Pro Gly  
355 360

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1905 base pairs

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1905  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| acactgttac  | tctctctctc  | tctctctctt  | cttctctctc  | tcttgcattc  | catcgacatc  | 60   |
| atcctttccc  | atggctgatg  | catacgagcc  | ttaatcatgtt | cttcaacaaa  | gcgcgcgaga  | 120  |
| caaaactctg  | attccatctc  | tgcattccca  | cttccacttt  | caccctctct  | ctctctcttc  | 180  |
| ctccggcgcc  | ggagggtggc  | cttttctctc  | cgctgattcc  | gatttctctg  | cagccgggtg  | 240  |
| ctttcaactc  | aacaacaaca  | acaaccacat  | atctaaccct  | agctacagta  | atttcatggg  | 300  |
| atttttcggt  | ggcccttctt  | ctttctctc   | caccgcagtc  | gccgtgcgcg  | gagatcattc  | 360  |
| cttttaacgcc | ggactttctt  | cgggagacgt  | tcttgtcttc  | aaacccgagc  | ctctatctct  | 420  |
| atctttgtct  | tctcacccta  | gaactcgctta | cgatctagtc  | gttcccgggt  | ctctatctct  | 480  |
| cggatttctg  | agatctgcgc  | gtgaagccaa  | cgccgcgcgc  | gtcaccatcg  | cgcttagaag  | 540  |
| ctctggctgc  | ctcggacott  | tcacggcgta  | cgctgcgatt  | cttaaaagat  | caaggttctt  | 600  |
| gaaaccagca  | gacgatcttc  | ttgatgagtt  | ttgtaatgtg  | ggctggtgga  | ttacacacga  | 660  |
| caaaagtcat  | cagcagcatg  | attcttctct  | cgcttttgat  | ccgacgggtg  | agaatctctg  | 720  |
| cggtgtttct  | gatggcgccg  | gaggagataa  | tggaaagaaa  | aaatcaaaac  | tcacttccat  | 780  |
| gctcgcagcg  | gtttacaaga  | ggtataagca  | atactatgag  | cagctacaag  | ctgtgatggg  | 840  |
| atcattcgaa  | tgcgtgtcag  | gtctcgggca  | cgctgtctcg  | tacgtctaac  | tagccttgaa  | 900  |
| agcgttgtct  | aagcatttca  | agtgtttgaa  | gaatgctata  | acggaccagc  | tccaatctag  | 960  |
| ccacaacaac  | aagatcccaa  | aacaacaaca  | atgtggctcat | ccgatgaact  | ctgagaataa  | 1020 |
| gactgattct  | ttaagatttg  | gaggaagtga  | tagttctaga  | ggcttatggt  | ctgcttggtca | 1080 |
| aagacatgga  | tttctctgac  | atcatgtctc  | tggttgagga  | ccgcaccgtg  | gcctacccca  | 1140 |
| acgtgtctgt  | actgtttctaa | gggcttggtc  | cttctgcatc  | tcttctgcatc | cttatccaac  | 1200 |
| agatcacagc  | aaactcatgc  | tggctaagca  | gacaggtctc  | tccaagaatc  | aggtatcgaa  | 1260 |
| ttggttcata  | aacgcgaagtg | ttagggtttg  | gaagccgatg  | gtgggaagga  | ttcacatgct  | 1320 |
| ggagactcga  | caattctaga  | gatcttcttc  | tctctcttgg  | agagacgaac  | ctcatagcac  | 1380 |
| cacccgtctc  | cctgacaaca  | acaacaacaa  | cccatctctg  | tctctggcga  | agcaaaagacc | 1440 |
| taacaactca  | ttccgcgcta  | gacgggcacg  | aaacgacgac  | gttcatggtc  | caacaacaaa  | 1500 |
| caacagctat  | gtaaacagtg  | ggagcggcgg  | cggtagtgcg  | gttggtttct  | cgtatggaat  | 1560 |
| tgggtctgct  | aatgtgcggg  | tgatgaatag  | cagcacaac   | ggagagatgt  | ctttgacggt  | 1620 |
| agggcttcac  | cactcagattg | ggttaccgga  | gccttttccg  | atgacaactg  | ctcagaggtt  | 1680 |
| tgggcttgat  | ggtgttagtg  | gcgatgtgtg  | tgggtgggtat | gaagggcaca  | atcgtcagtt  | 1740 |
| tgggagagat  | tttatttggt  | ttagtaataca | tcagtttcta  | catgattttg  | taggttgaga  | 1800 |
| ttattttgtg  | gaaagagaaa  | aaatatgttt  | gacgtttggg  | tatgtataag  | aagatatggg  | 1860 |
| ggaattgaaa  | tgcataatgat | gtgtatatta  | gaatgtttct  | tcttc       |             |      |

(2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 598 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..598  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Cys | Tyr | Ser | Leu | Ser | Leu | Phe | Phe | Phe | Phe | Phe | Cys | Ile |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     | 15  |     |
| Ser | Ser | Thr | Ser | Ser | Phe | Pro | Met | Ala | Asp | Ala | Tyr | Glu | Pro |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |
| Val | Leu | Gln | Gln | Ser | Arg | Arg | Asp | Lys | Leu | Arg | Ile | Pro | Ser |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Ser | His | Phe | His | Phe | His | Pro | Pro | Pro | Pro | Ser | Ser | Gly | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |

Gly<sup>65</sup> Gly Val Phe Pro Leu Ala Asp Ser Asp Phe Leu Ala Ala Gly Gly  
70 75 80  
Phe His Ser Asn Asn Asn Asn His Ile Ser Asn Pro Ser Tyr Ser  
85 90 95  
Asn Phe Met Gly Phe Leu Gly Gly Pro Ser Ser Ser Ser Thr Ala  
100 105 110  
Val Ala Val Ala Gly Asp His Ser Phe Asn Ala Gly Leu Ser Ser Gly  
115 120 125  
Asp Val Leu Val Phe Lys Pro Glu Pro Leu Ser Leu Ser Ser Ser  
130 135 140  
His Pro Arg Leu Ala Tyr Asp Leu Val Val Pro Gly Val Val Asn Ser  
145 150 155 160  
Gly Phe Cys Arg Ser Ala Gly Glu Ala Asn Ala Ala Val Thr Ile  
165 170 175  
Ala Ser Arg Ser Ser Gly Pro Leu Gly Pro Phe Thr Gly Tyr Ala Ser  
180 185 190  
Ile Leu Lys Gly Ser Arg Phe Leu Lys Pro Ala Gln Met Leu Leu Asp  
195 200 205  
Glu Phe Cys Asn Val Gly Arg Gly Ile Tyr Thr Asp Lys Val Ile Asp  
210 215 220  
Asp Asp Asp Ser Ser Leu Phe Asp Pro Thr Val Glu Asn Leu Cys  
225 230 235 240  
Gly Val Ser Asp Gly Gly Gly Asp Asn Gly Lys Lys Lys Ser Lys  
245 250 255  
Leu Ile Ser Met Leu Asp Glu Val Tyr Lys Arg Tyr Lys Gln Tyr Tyr  
260 265 270  
Glu Gln Leu Gln Ala Val Met Gly Ser Phe Glu Cys Val Ala Gly Leu  
275 280 285  
Gly His Ala Ala Pro Tyr Ala Asn Leu Ala Leu Lys Ala Leu Ser Lys  
290 295 300  
His Phe Lys Cys Leu Lys Asn Ala Ile Thr Asp Gln Leu Gln Phe Ser  
305 310 315 320  
His Asn Asn Lys Ile Gln Gln Gln Gln Gln Cys Gly His Pro Met Asn  
325 330 335  
Ser Glu Asn Lys Thr Asp Ser Leu Arg Phe Gly Gly Ser Asp Ser Ser  
340 345 350  
Arg Gly Leu Cys Ser Ala Gly Gln Arg His Gly Phe Pro Asp His His  
355 360 365  
Ala Pro Val Trp Arg Pro His Arg Gly Leu Pro Glu Arg Ala Val Thr  
370 375 380  
Val Leu Arg Ala Trp Leu Phe Asp His Phe Leu His Pro Tyr Pro Thr  
385 390 395 400  
Asp Thr Asp Lys Leu Met Leu Ala Lys Gln Thr Gly Leu Ser Arg Asn  
405 410 415  
Gln Val Ser Asn Trp Phe Ile Asn Ala Arg Val Arg Val Trp Lys Pro  
420 425 430  
Met Val Glu Glu Ile His Met Leu Glu Thr Arg Gln Ser Gln Arg Ser  
435 440 445  
Ser Ser Ser Ser Trp Arg Asp Glu Arg Thr Ser Thr Thr Val Phe Pro  
450 455 460  
Asp Asn Asn Asn Asn Asn Pro Ser Ser Ser Ser Ala Gln Gln Arg Pro  
465 470 475 480  
Asn Asn Ser Ser Pro Pro Arg Arg Ala Arg Asn Asp Asp Val His Gly  
485 490 495  
Thr Asn Asn Asn Asn Ser Tyr Val Asn Ser Gly Ser Gly Gly Gly Ser  
500 505 510  
Ala Val Gly Phe Ser Tyr Gly Ile Gly Ser Ser Asn Val Pro Val Met  
515 520 525  
Asn Ser Ser Thr Asn Gly Gly Val Ser Leu Thr Leu Gly Leu His His  
530 535 540  
Gln Ile Gly Leu Pro Glu Pro Phe Pro Met Thr Thr Ala Gln Arg Phe



(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 575 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..575

(D) OTHER INFORMATION: / Ceres Seq. ID 1498315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Asp | Ala | Tyr | Glu | Pro | Tyr | His | Val | Leu | Gln | Gln | Ser | Arg | Arg |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Asp | Leu | Arg | Ile | Pro | Ser | Leu | Asp | Ser | His | Phe | His | Phe | His | Pro |     |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Pro | Pro | Pro | Ser | Ser | Gly | Gly | Gly | Gly | Val | Phe | His | Pro | Leu | Ala |     |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Asp | Ser | Asp | Phe | Leu | Ala | Ala | Gly | Gly | Phe | His | Ser | Asn | Asn | Asn |     |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Asn | His | Ile | Ser | Asn | Pro | Ser | Tyr | Ser | Asn | Phe | Met | Gly | Phe | Leu | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly | Pro | Ser | Ser | Ser | Ser | Ser | Thr | Ala | Val | Ala | Val | Ala | Gly | Asp | His |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Phe | Asn | Ala | Gly | Leu | Ser | Ser | Gly | Asp | Val | Leu | Val | Phe | Lys | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Pro | Leu | Ser | Leu | Ser | Leu | Ser | Ser | His | Pro | Arg | Leu | Ala | Tyr | Asp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Val | Val | Pro | Gly | Val | Val | Asn | Ser | Gly | Phe | Cys | Arg | Ser | Ala | Gly |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Glu | Ala | Asn | Ala | Ala | Ala | Val | Thr | Ile | Ala | Ser | Arg | Ser | Ser | Gly | Pro |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Gly | Pro | Phe | Thr | Gly | Tyr | Ala | Ser | Ile | Leu | Lys | Gly | Ser | Arg | Phe |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Lys | Pro | Ala | Gln | Met | Leu | Leu | Asp | Glu | Phe | Cys | Asn | Val | Gly | Arg |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Ile | Tyr | Thr | Asp | Lys | Val | Ile | Asp | Asp | Asp | Asp | Ser | Ser | Leu | Leu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Phe | Asp | Pro | Thr | Val | Glu | Asn | Leu | Cys | Gly | Val | Ser | Asp | Gly | Gly | Gly |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Gly | Asp | Asn | Gly | Lys | Lys | Lys | Ser | Lys | Leu | Ile | Ser | Met | Leu | Asp | Glu |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     | 240 |
| Val | Tyr | Lys | Arg | Tyr | Lys | Gln | Tyr | Tyr | Glu | Gln | Leu | Gln | Ala | Val | Met |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gly | Ser | Phe | Glu | Cys | Val | Ala | Gly | Leu | Gly | His | Ala | Ala | Pro | Tyr | Ala |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Asn | Leu | Ala | Leu | Lys | Ala | Leu | Ser | Lys | His | Phe | Lys | Cys | Leu | Lys | Asn |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ala | Ile | Thr | Asp | Gln | Leu | Gln | Phe | Ser | His | Asn | Asn | Lys | Ile | Gln | Gln |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Gln | Gln | Gln | Cys | Gly | His | Pro | Met | Asn | Ser | Glu | Asn | Lys | Thr | Asp | Ser |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     |     | 320 |
| Leu | Arg | Phe | Gly | Gly | Ser | Asp | Ser | Ser | Arg | Gly | Leu | Cys | Ser | Ala | Gly |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |

Gln Arg His Gly Phe Pro Asp His His Ala Pro Val Trp Arg Pro His  
340 345 350  
Arg Gly Leu Pro Glu Arg Ala Val Thr Val Leu Arg Ala Trp Leu Phe  
355 360 365  
Asp His Phe Leu His Pro Tyr Pro Thr Asp Thr Asp Lys Leu Met Leu  
370 375 380  
Ala Lys Gln Thr Gly Leu Ser Arg Asn Gln Val Ser Asn Trp Phe Ile  
385 390 395 400  
Asn Ala Arg Val Arg Val Trp Lys Pro Met Val Glu Glu Ile His Met  
405 410 415  
Leu Glu Thr Arg Gln Ser Gln Arg Ser Ser Ser Ser Trp Arg Asp  
420 425 430  
Glu Arg Thr Ser Thr Thr Val Phe Pro Asp Asn Asn Asn Asn Pro  
435 440 445  
Ser Ser Ser Ser Ala Gln Gln Arg Pro Asn Asn Ser Ser Pro Pro Arg  
450 455 460  
Arg Ala Arg Asn Asp Asp Val His Gly Thr Asn Asn Asn Asn Ser Tyr  
465 470 475 480  
Val Asn Ser Gly Ser Gly Gly Ser Ala Val Gly Phe Ser Tyr Gly  
485 490 495  
Ile Gly Ser Ser Asn Val Pro Val Met Asn Ser Ser Thr Asn Gly Gly  
500 505 510  
Val Ser Leu Thr Leu Gly Leu His His Gln Ile Gly Leu Pro Glu Pro  
515 520 525  
Phe Pro Met Thr Thr Ala Gln Arg Phe Gly Leu Asp Gly Gly Ser Gly  
530 535 540  
Asp Gly Gly Gly Gly Tyr Glu Gly Gln Asn Arg Gln Phe Gly Arg Asp  
545 550 555 560  
Phe Ile Gly Gly Ser Asn His Gln Phe Leu His Asp Phe Val Gly  
565 570 575

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..500
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498316

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

Met Gly Phe Leu Gly Gly Pro Ser Ser Ser Ser Thr Ala Val Ala  
1 5 10 15  
Val Ala Gly Asp His Ser Phe Asn Ala Gly Leu Ser Ser Gly Asp Val  
20 25 30  
Leu Val Phe Lys Pro Glu Pro Leu Ser Leu Ser Leu Ser His Pro  
35 40 45  
Arg Leu Ala Tyr Asp Leu Val Val Pro Gly Val Val Asn Ser Gly Phe  
50 55 60  
Cys Arg Ser Ala Gly Glu Ala Asn Ala Ala Val Thr Ile Ala Ser  
65 70 75 80  
Arg Ser Ser Gly Pro Leu Gly Pro Phe Thr Gly Tyr Ala Ser Ile Leu  
85 90 95  
Lys Gly Ser Arg Phe Leu Lys Pro Ala Gln Met Leu Leu Asp Glu Phe  
100 105 110  
Cys Asn Val Gly Arg Gly Ile Tyr Thr Asp Lys Val Ile Asp Asp Asp  
115 120 125  
Asp Ser Ser Leu Leu Phe Asp Pro Thr Val Glu Asn Leu Cys Gly Val  
130 135 140  
Ser Asp Gly Gly Gly Gly Asp Asn Gly Lys Lys Ser Lys Leu Ile

```

145 150 155 160
Ser Met Leu Asp Glu Val Tyr Lys Arg Tyr Lys Gln Tyr Tyr Glu Gln
165 170 175
Leu Gln Ala Val Met Gly Ser Phe Glu Cys Val Ala Gly Leu Gly His
180 185 190
Ala Ala Pro Tyr Ala Asn Leu Ala Leu Lys Ala Leu Ser Lys His Phe
195 200 205
Lys Cys Leu Lys Asn Ala Ile Thr Asp Gln Leu Gln Phe Ser His Asn
210 215 220
Asn Lys Ile Gln Gln Gln Gln Cys Gly His Pro Met Asn Ser Glu
225 230 235
Asn Lys Thr Asp Ser Leu Arg Phe Gly Gly Ser Asp Ser Ser Arg Gly
245 250 255
Leu Cys Ser Ala Gly Gln Arg His Gly Phe Pro Asp His His Ala Pro
260 265 270
Val Trp Arg Pro His Arg Gly Leu Pro Glu Arg Ala Val Thr Val Leu
275 280 285
Arg Ala Trp Leu Phe Asp His Phe Leu His Pro Tyr Pro Thr Asp Thr
290 295 300
Asp Lys Leu Met Leu Ala Lys Gln Thr Gly Leu Ser Arg Asn Gln Val
305 310 315
Ser Asn Trp Phe Ile Asn Ala Arg Val Arg Val Trp Lys Pro Met Val
325 330 335
Glu Glu Ile His Met Leu Glu Thr Arg Gln Ser Gln Arg Ser Ser Ser
340 345 350
Ser Ser Trp Arg Asp Glu Arg Thr Ser Thr Thr Val Phe Pro Asp Asn
355 360 365
Asn Asn Asn Asn Pro Ser Ser Ser Ala Gln Gln Arg Pro Asn Asn
370 375 380
Ser Ser Pro Pro Arg Arg Ala Arg Asn Asp Asp Val His Gly Thr Asn
385 390 395
Asn Asn Asn Ser Tyr Val Asn Ser Gly Ser Gly Gly Ser Ala Val
405 410 415
Gly Phe Ser Tyr Gly Ile Gly Ser Ser Asn Val Pro Val Met Asn Ser
420 425 430
Ser Thr Asn Gly Gly Val Ser Leu Thr Leu Gly Leu His His Gln Ile
435 440 445
Gly Leu Pro Glu Pro Phe Pro Met Thr Thr Ala Gln Arg Phe Gly Leu
450 455 460
Asp Gly Gly Ser Gly Asp Gly Gly Gly Tyr Glu Gly Gln Asn Arg
465 470 475
Gln Phe Gly Arg Asp Phe Ile Gly Gly Ser Asn His Gln Phe Leu His
485 490 495
Asp Phe Val Gly
500

```

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 755 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..755

(D) OTHER INFORMATION: / Ceres Seq. ID 1498317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

```

aatttcgtca agaaaaaaat tcgatttttt tgcgtctttt gtgggttggt gttgttgaaa 60
atggctggtc gtggaaaaaac tcttgatcc ggtggggcga agaaagctac atctcggagt 120
agcaaaagccg gtcttcaatt cccggtgggt cgtatcgctc gttttctaaa agccggtaaa 180
tacgccgaac gtgtgtgtgc cgtgtctccg gtttatytcg ccgcggttct cgaatatttg 240

```

gcgcgcgagg ttcttgaatt agctggaaac gcagcaagag acaacaagaa gacacgtatt 300  
gttctctctt gctgcgttcc cagctaatcc aagaacctcg gcagccttct atttcttccac 360  
aaagctccag atcactaagc tctctcagc tatgctctac ttggatata tgctcatcgc 420  
ctcttacgcg ttttctgtgc tgaccggaac aatcgggttc tacgcttgct tctggttccac 480  
aagactcact tattcctcgg taaagatcga ttgattcaga aaaacattca agagaagaac 540  
gaaagaaaga aggaaggtaa tatagttaat gatattcaca agtttgtttt tgctcaatat 600  
gggtctcttc ttgtttcgtc ctggttttgg ttacaaagta acaaaagaaa aggttttata 660  
tgtaaacctt tctctttttt agagtgtatt ctgtttgatt tcccacaaatg tcactttgga 720  
ttatcttctt taattgmcaa ttatgtgatt ctttc

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..108
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

Asn Phe Val Lys Lys Lys Ile Arg Phe Phe Cys Ala Leu Cys Gly Leu  
1 5 10 15  
Leu Leu Leu Lys Met Ala Gly Arg Gly Lys Thr Leu Gly Ser Gly Gly  
20 25 30  
Ala Lys Lys Ala Thr Ser Arg Ser Ser Lys Ala Gly Leu Gln Phe Pro  
35 40 45  
Val Gly Arg Ile Ala Arg Phe Leu Lys Ala Gly Lys Tyr Ala Glu Arg  
50 55 60  
Val Gly Ala Gly Ala Pro Val Tyr Xaa Ala Ala Val Leu Glu Tyr Leu  
65 70 75 80  
Ala Ala Glu Val Leu Glu Leu Ala Gly Asn Ala Ala Arg Asp Asn Lys  
85 90 95  
Lys Thr Arg Ile Val Val Ser Cys Cys Val Ser Ser  
100 105

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498319

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

Met Ala Gly Arg Gly Lys Thr Leu Gly Ser Gly Gly Ala Lys Lys Ala  
1 5 10 15  
Thr Ser Arg Ser Ser Lys Ala Gly Leu Gln Phe Pro Val Gly Arg Ile  
20 25 30  
Ala Arg Phe Leu Lys Ala Gly Lys Tyr Ala Glu Arg Val Gly Ala Gly  
35 40 45  
Ala Pro Val Tyr Xaa Ala Ala Val Leu Glu Tyr Leu Ala Ala Glu Val  
50 55 60  
Leu Glu Leu Ala Gly Asn Ala Ala Arg Asp Asn Lys Lys Thr Arg Ile  
65 70 75 80  
Val Val Ser Cys Cys Val Ser Ser  
85

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1233 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1233  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498320  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| atccagaaaa  | aacaaaaaaa  | acaaaaaaat  | aataaaaaca  | aaaaatatct  | tttttttttc  | 60   |
| taataaaaaa  | aaaaaaaata  | aataaatatg  | gaatacacaa  | atgtgtccat  | tttattagcc  | 120  |
| atgttggtga  | tctttgtttc  | accaatgggtg | ttcgcagatg  | atttgacacc  | aatcccagag  | 180  |
| ggcaaacccc  | aagtgggtgca | gtgggttcaat | accacgcttg  | gtccattggt  | tcaacgtaaa  | 240  |
| ggcttagatg  | ctgctctcgt  | agctgtctgag | gctgctccac  | gtatcatcaa  | cgtgaatcca  | 300  |
| aagggagggt  | aattcaaaac  | actaacagac  | gcaataaaga  | gcgttcctgc  | agggaaacaca | 360  |
| aagcgggtga  | tcataaaagt  | ggctcctggt  | gagtacagag  | agaagggtcac | tatcgacagg  | 420  |
| aacaaaccct  | tcattacatt  | gatgggacaa  | cccaatgcc   | tgctgttat   | caoctacgac  | 480  |
| ggtagccg    | ccaagtattg  | aaccgttgat  | agtgcctctc  | tcattatctt  | atccgactat  | 540  |
| ttcatggcgg  | ttaacatcgt  | cgttaaagaac | actgcaccgg  | caccagatgg  | taaaactaag  | 600  |
| ggagcacaag  | ccttatccat  | gagaatctcc  | ggaaactttg  | ctgctttcta  | caactgcaaa  | 660  |
| ttctacgggt  | tcacaagatac | aatctgtgat  | gataccggaa  | accatttctt  | caaggattgt  | 720  |
| tacgtcgaag  | gaacattcga  | tttcatcttc  | ggaagtggaa  | ccctatgta   | cttggaacaa  | 780  |
| caattgcacg  | tgggttgaga  | cgggtattaga | gtgatcgacg  | cgcattgcagg | aaagagcgca  | 840  |
| gaagaaaaata | gtggatactc  | tttgtgtcac  | tgcaagggtga | ctggaactgg  | aggaactaatc | 900  |
| tatttgggaa  | gagcatggat  | gagccaccct  | aagggtgtct  | atgcctacac  | cgagatgacc  | 960  |
| agcgttgtca  | acccaccggt  | atggcaagaa  | aacaagactc  | ccgcacatga  | caagaccggt  | 1020 |
| ttctacggag  | agtaacaagt  | ttcaggacca  | gggtcacaca  | aagccaaagag | aatggccattc | 1080 |
| accaagaagca | tcgacagaca  | agaagctaac  | cgtttcctat  | ccctcggtca  | catccaagga  | 1140 |
| ttcaagtggc  | ttctccacc   | acccgctttg  | taaattcttt  | aatatcaacc  | tattaaat    | 1200 |

aaaaataaaa cgtaaactaa aaatataaac ttc  
(2) INFORMATION FOR SEQ ID NO:343:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 361 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..361  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498321  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Tyr | Thr | Asn | Val | Ser | Ile | Leu | Gly | Met | Leu | Val | Ile | Phe |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Ser | Pro | Met | Val | Phe | Ala | Asp | Asp | Leu | Thr | Pro | Ile | Pro | Glu |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |
| Lys | Pro | Gln | Val | Val | Gln | Trp | Phe | Asn | Thr | His | Val | Gly | Pro | Leu |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |
| Gln | Arg | Lys | Gly | Leu | Asp | Pro | Ala | Leu | Val | Ala | Ala | Glu | Ala | Pro |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |
| Arg | Ile | Ile | Asn | Val | Asn | Pro | Lys | Gly | Gly | Glu | Phe | Lys | Thr | Leu |
|     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Asp | Ala | Ile | Lys | Ser | Val | Pro | Ala | Gly | Asn | Thr | Lys | Arg | Val | Ile |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Met | Ala | Pro | Gly | Glu | Tyr | Arg | Glu | Lys | Val | Thr | Ile | Asp | Arg |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |
| Lys | Pro | Phe | Ile | Thr | Leu | Met | Gly | Gln | Pro | Asn | Ala | Met | Pro | Val |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |
| Thr | Tyr | Asp | Gly | Thr | Ala | Ala | Lys | Tyr | Gly | Thr | Val | Asp | Ser | Ala |
|     |     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |

```

Leu Ile Ile Leu Ser Asp Tyr Phe Met Ala Val Asn Ile Val Val Lys
145 150 155 160
Asn Thr Ala Pro Ala Pro Asp Gly Lys Thr Lys Gly Ala Gln Ala Leu
 165 170 175
Ser Met Arg Ile Ser Gly Asn Phe Ala Ala Phe Tyr Asn Cys Lys Phe
 180 185 190
Tyr Gly Phe Gln Asp Thr Ile Cys Asp Asp Thr Gly Asn His Phe Phe
 195 200 205
Lys Asp Cys Tyr Val Glu Gly Thr Phe Asp Phe Ile Phe Gly Ser Gly
 210 215 220
Thr Ser Met Tyr Leu Gly Thr Gln Leu His Val Val Gly Asp Gly Ile
225 230 235 240
Arg Val Ile Ala Ala His Ala Gly Lys Ser Ala Glu Glu Asn Ser Gly
 245 250 255
Tyr Ser Phe Val His Cys Lys Val Thr Gly Thr Gly Gly Val Ile Tyr
 260 265 270
Leu Gly Arg Ala Trp Met Ser His Pro Lys Val Val Tyr Ala Tyr Thr
 275 280 285
Glu Met Thr Ser Val Val Asn Pro Thr Gly Trp Gln Glu Asn Lys Thr
 290 295 300
Pro Ala His Asp Lys Thr Val Phe Tyr Gly Glu Tyr Lys Cys Ser Gly
305 310 315 320
Pro Gly Ser His Lys Ala Lys Arg Val Pro Phe Thr Gln Asp Ile Asp
 325 330 335
Asp Lys Glu Ala Asn Arg Phe Leu Ser Leu Gly Tyr Ile Gln Gly Ser
 340 345 350
Lys Trp Leu Leu Pro Pro Pro Ala Leu
 355 360

```

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..350
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498322

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

```

Met Leu Val Ile Phe Val Ser Pro Met Val Phe Ala Asp Asp Leu Thr
1 5 10 15
Pro Ile Pro Glu Gly Lys Pro Gln Val Val Gln Trp Phe Asn Thr His
 20 25 30
Val Gly Pro Leu Val Gln Arg Lys Gly Leu Asp Pro Ala Leu Val Ala
 35 40 45
Ala Glu Ala Ala Pro Arg Ile Ile Asn Val Asn Pro Lys Gly Gly Glu
 50 55 60
Phe Lys Thr Leu Thr Asp Ala Ile Lys Ser Val Pro Ala Gly Asn Thr
65 70 75 80
Lys Arg Val Ile Ile Lys Met Ala Pro Gly Glu Tyr Arg Glu Lys Val
 85 90 95
Thr Ile Asp Arg Asn Lys Pro Phe Ile Thr Leu Met Gly Gln Pro Asn
 100 105 110
Ala Met Pro Val Ile Thr Tyr Asp Gly Thr Ala Ala Lys Tyr Gly Thr
 115 120 125
Val Asp Ser Ala Ser Leu Ile Ile Leu Ser Asp Tyr Phe Met Ala Val
 130 135 140
Asn Ile Val Val Lys Asn Thr Ala Pro Ala Pro Asp Gly Lys Thr Lys
145 150 155 160
Gly Ala Gln Ala Leu Ser Met Arg Ile Ser Gly Asn Phe Ala Ala Phe

```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Phe | Ala | Asp | Asp | Leu | Thr | Pro | Ile | Pro | Glu | Gly | Lys | Pro | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Val | Gln | Trp | Phe | Asn | Thr | His | Val | Gly | Pro | Leu | Val | Gln | Arg | Lys |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Leu | Asp | Pro | Ala | Leu | Val | Ala | Ala | Glu | Ala | Ala | Pro | Arg | Ile | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Val | Asn | Pro | Lys | Gly | Gly | Glu | Phe | Lys | Thr | Leu | Thr | Asp | Ala | Ile |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Ser | Val | Pro | Ala | Gly | Asn | Thr | Lys | Arg | Val | Ile | Ile | Lys | Met | Ala |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Pro | Gly | Glu | Tyr | Arg | Glu | Lys | Val | Thr | Ile | Asp | Arg | Asn | Lys | Pro | Phe |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Thr | Leu | Met | Gly | Gln | Pro | Asn | Ala | Met | Pro | Val | Ile | Thr | Tyr | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Thr | Ala | Ala | Lys | Tyr | Gly | Thr | Val | Asp | Ser | Ala | Ser | Leu | Ile | Ile |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Ser | Asp | Tyr | Phe | Met | Ala | Val | Asn | Ile | Val | Val | Lys | Asn | Thr | Ala |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Ala | Pro | Asp | Gly | Lys | Thr | Lys | Gly | Ala | Gln | Ala | Leu | Ser | Met | Arg |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Ile | Ser | Gly | Asn | Phe | Ala | Ala | Phe | Tyr | Asn | Cys | Lys | Phe | Tyr | Gly | Phe |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gln | Asp | Thr | Ile | Cys | Asp | Asp | Thr | Gly | Asn | His | Phe | Phe | Lys | Asp | Cys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Tyr | Val | Glu | Gly | Thr | Phe | Asp | Phe | Ile | Phe | Gly | Ser | Gly | Thr | Ser | Met |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |

Tyr Leu Gly Thr Gln Leu His Val Val Gly Asp Gly Ile Arg Val Ile  
210 215 220  
Ala Ala His Ala Gly Lys Ser Ala Glu Glu Asn Ser Gly Tyr Ser Phe  
225 230 235 240  
Val His Cys Lys Val Thr Gly Thr Gly Gly Val Ile Tyr Leu Gly Arg  
245 250 255  
Ala Trp Met Ser His Pro Lys Val Val Tyr Ala Tyr Thr Glu Met Thr  
260 265 270  
Ser Val Val Asn Pro Thr Gly Trp Gln Glu Asn Lys Thr Pro Ala His  
275 280 285  
Asp Lys Thr Val Phe Tyr Gly Glu Tyr Lys Cys Ser Gly Pro Gly Ser  
290 295 300  
His Lys Ala Lys Arg Val Pro Phe Thr Gln Asp Ile Asp Asp Lys Glu  
305 310 315 320  
Ala Asn Arg Phe Leu Ser Leu Gly Tyr Ile Gln Gly Ser Lys Trp Leu  
325 330 335  
Leu Pro Pro Pro Ala Leu  
340

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1415 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1415  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

ctttttacc catttcgtct ctttcatttt gacgtttttc ttagatctgt taataatcca 60  
tccatggctt ggtctagtca ctagtgggtg tatctctctg tgtggaagaa aaagcaagggt 120  
ttttttagca ctgtgattgt tttaagatat ggcaactttg aacccttttg atttgttgga 180  
tgatgatgct gaggatccaa gccagctcgc tgtttccatc gagaagatgt ataagtccaa 240  
gaaatctgga ccggttttga gottgcctgc taagtcagct cctaagcttc cctctaagcc 300  
acttctctct gctcaagccg tgagagagggc caggagtgat gctccacgtg gtggtggagg 360  
ccgtggagga tttaatcgtg gtcgtgggtg ttacaaccgt gatgatggta caaatggata 420  
tttaggggga tacactaagc cctcagatga aggagatggt tcaaagtctt cttacgagag 480  
gcgtggcggt ggtgaagggg agcgtcctcg aagggccttt gagcgtcgta gtggaactgg 540  
cagaggaggat gacttcaagc gtgacggatc tggctcgtgg aattggggaa ctccaggggga 600  
agagatagct gctgagactg aagcagtatg tgggtgtgag actgagaagg atgttgaggga 660  
gaagccagct gttgatgatg tagctgtcga tgctaacaag gagaatactg ttgttgaggga 720  
gaaagagcct gaggataaag aaatgactct tgatgagtat gaaaaatac ttgaggagaa 780  
gaaaaaggca cttaaatcat taaccacctc tgagaggaaa gttgatacga aagtgtttga 840  
atcaatgcga caactgtcaa acaagaagtc taatgatgaa atcttcacga agctgggttc 900  
tgataaggac aaacgcgaag atgacaaaaga agagaaggct aagaaggctg tgagcatcaa 960  
tgagtttctg aagccagcag aggggtggaa ctactaccga ggaggccgtg gtggccgttg 1020  
acgtggtgtg cgtggccgtg gaggtgtttc tagtgccgaa tctggtggtt accgtaagt 1080  
agctgcacca gctattggag atgctgtcca gttcccatct cttgggggga agtaagatac 1140  
atccatgata acgtccatc acgtgcaccc tcccttagga ttttgtcgga ggtttactgt 1200  
tttactggct tctcgtgtgc agatgtaaat aattagtggt cgtcgtcagt ttttagattt 1260  
tatgctaaac tttaacctg ttggtgttct ttaactttga aacactacac tcttcttagt 1320  
tttaccattt tactcgtttt gtgtttgttg ttttcttatt gggatatgaa acatgttttg 1380  
agacgacat atctaattgt atcgggggtg agtct

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide



(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..328

(D) OTHER INFORMATION: / Ceres Seq. ID 1498325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

Met Ala Thr Leu Asn Pro Phe Asp Leu Leu Asp Asp Ala Glu Asp  
1 5 10 15  
Pro Ser Gln Leu Ala Val Ser Ile Glu Lys Ile Asp Lys Ser Lys Lys  
20 25 30  
Ser Gly Pro Val Ser Ser Leu Pro Ala Lys Ser Ala Pro Lys Leu Pro  
35 40 45  
Ser Lys Pro Leu Pro Pro Ala Gln Ala Val Arg Glu Ala Arg Ser Asp  
50 55 60  
Ala Pro Arg Gly Gly Gly Gly Arg Gly Gly Phe Asn Arg Gly Arg Gly  
65 70 75 80  
Gly Tyr Asn Arg Asp Asp Gly Asn Asn Gly Tyr Leu Gly Gly Tyr Thr  
85 90 95  
Lys Pro Ser Asp Glu Gly Asp Val Ser Lys Ser Ser Tyr Glu Arg Arg  
100 105 110  
Gly Gly Gly Glu Gly Glu Arg Pro Arg Arg Ala Phe Glu Arg Arg Ser  
115 120 125  
Gly Thr Gly Arg Gly Ser Asp Phe Lys Arg Asp Gly Ser Gly Arg Gly  
130 135 140  
Asn Trp Gly Thr Pro Gly Glu Glu Ile Ala Ala Glu Thr Glu Ala Val  
145 150 155 160  
Ala Gly Val Glu Thr Glu Lys Asp Val Gly Glu Lys Pro Ala Val Asp  
165 170 175  
Asp Val Ala Ala Asp Ala Asn Lys Glu Asn Thr Val Val Glu Glu Lys  
180 185 190  
Glu Pro Glu Asp Lys Glu Met Thr Leu Asp Glu Tyr Glu Lys Ile Leu  
195 200 205  
Glu Glu Lys Lys Lys Ala Leu Gln Ser Leu Thr Thr Ser Glu Arg Lys  
210 215 220  
Val Asp Thr Lys Val Phe Glu Ser Met Gln Gln Leu Ser Asn Lys Lys  
225 230 235 240  
Ser Asn Asp Glu Ile Phe Ile Lys Leu Gly Ser Asp Lys Asp Lys Arg  
245 250 255  
Lys Asp Asp Lys Glu Glu Lys Ala Lys Lys Ala Val Ser Ile Asn Glu  
260 265 270  
Phe Leu Lys Pro Ala Glu Gly Gly Asn Tyr Tyr Arg Gly Gly Arg Gly  
275 280 285  
Gly Arg Gly Arg Gly Gly Arg Gly Arg Gly Gly Val Ser Ser Gly Glu  
290 295 300  
Ser Gly Gly Tyr Arg Asn Glu Ala Ala Pro Ala Ile Gly Asp Ala Ala  
305 310 315 320  
Gln Phe Pro Ser Leu Gly Gly Lys  
325

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 525 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..525

(D) OTHER INFORMATION: / Ceres Seq. ID 1498326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

acaaacatta ctcatcaca aaaccatctt aaagcaacta cacaaatctt gaaatcttct  
catatcttct attactata taaactttta atcaaatcaa gattaactat ggctgaggag

60  
120

tacaagaaca acgttccccg gcacgagaca ccaacgggtcg caacagagga atcaccagcg 180  
acgacaacag aggttacgga tcgtcgattg ttgtatttct tggggaagaa ggaagaggaa 240  
gtgaaacccT aagagacaac gacgctcgag tctgagttcg atcataaggc tcagatctct 300  
gaaccggagt tagctcggsa sacgaggaag tgaaggagaa caagattact ctgctagagg 360  
agcttcaaga aaagaccgag gaagatgagg agaacaagcc tagtgtcatc gaaaagcttc 420  
accgatccaa cagctcttct tctcttcga gcgatgaaga aggtgaggaa aagaaggaga 480  
agaagaagaa gatcgttgaa ggagaggaag ataaagaagg actag

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498327

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Asn | Ile | Thr | His | Ser | Gln | Asn | His | Leu | Lys | Ala | Thr | Thr | Gln | Ile |
| 1   |     | 5   |     |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Lys | Phe | Ser | His | Ile | Phe | Tyr | Leu | Leu | Tyr | Lys | Leu | Ile | Lys |     |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Ser | Arg | Leu | Thr | Met | Ala | Glu | Glu | Tyr | Lys | Asn | Asn | Val | Pro | Glu | His |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Glu | Thr | Pro | Thr | Val | Ala | Thr | Glu | Glu | Ser | Pro | Ala | Thr | Thr | Thr | Glu |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Thr | Asp | Arg | Arg | Leu | Phe | Asp | Phe | Leu | Gly | Lys | Lys | Glu | Glu | Glu |
|     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |     |
| Val | Lys | Pro | Gln | Glu | Thr | Thr | Thr | Leu | Glu | Ser | Glu | Phe | Asp | His | Lys |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Ala | Gln | Ile | Ser | Glu | Pro | Glu | Leu | Ala | Ala | Xaa | Thr | Arg | Lys |     |     |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498328

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Glu | Glu | Tyr | Lys | Asn | Asn | Val | Pro | Glu | His | Glu | Thr | Pro | Thr |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Val | Ala | Thr | Glu | Glu | Ser | Pro | Ala | Thr | Thr | Thr | Glu | Val | Thr | Asp | Arg |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Leu | Phe | Asp | Phe | Leu | Gly | Lys | Lys | Glu | Glu | Glu | Val | Lys | Pro | Gln |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Glu | Thr | Thr | Thr | Leu | Glu | Ser | Glu | Phe | Asp | His | Lys | Ala | Gln | Ile | Ser |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Pro | Glu | Leu | Ala | Ala | Xaa | Thr | Arg | Lys |     |     |     |     |     |     |
|     |     |     | 70  |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1354

(D) OTHER INFORMATION: / Ceres Seq. ID 1498329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

```
atctctttct cacaattaga ttctgtgctt cttctgcgat caactaagat cgcgtccgcg 60
agcgttttcag attctgatca gatccgatta agagaagcaa atcgggtcgg gtagtactcg 120
tcgatgttct cactgcaatc acaatggcca caactctcgg acttgtccca atcggcgcgct 180
gaagctcttt ggtgttcgcg tcaccgaagg ttcgatccgg aaaagtgcga gtaggggtaa 240
tcttagccat tacacgggtt ctgcatcggg tgggcatgga accgggttcca acactccggg 300
ttctccgggt gatgtccctc accatgtcgc tggtagtggg tacgcttcgt aggatttcgt 360
tgctggctct toctctagcc gcgagagaaa gaaaggaaact ccatggacag aggaagaaca 420
caggatgttc ttattagggt tacagaagct gggtaaaagg gattggagag gtagtccaag 480
aaactatgtg accactmagg cacctacaca agttgttagc catgtctcaga agtatttcct 540
cagacaatcc aatgtctctc gtcgcaaaag acgttctagt ctctttgata tggttcctga 600
tgagggttgg gatattccca tggatttgca agaaccagag gaagataata ttctgtgga 660
aactgaaatg caagggtgctg actctattca tcagacactt gctcttagct cacttcacgc 720
accgtcaact ttggaaatcg aagaatgtga atcaatggac tccacaaact ctaccacgcg 780
ggaaccaatc gcaactgccg ctgctgcttc ttctttctcc agactagaag aaaccacaca 840
actgcaatca caactgcaac cgcagcgcca actacctggc tcattcccca tactatatcc 900
gacctacttt tcaccatatt acccgtttcc attcccaata tggcctgctg gttattgtcc 960
tgaaccaccc aagaaaagagg aaactcatga aattctcaga ccaactgctg tgcactcgaa 1020
agctctctat aatgttgacg agctcttttg tatgtctaag ctacagccttg cagagtccaa 1080
caaacatgga gaatccgatc agtctctttc attgaagcta ggtggcgggg catcttcaa 1140
acaatcagca ttccaccga atcctagctc tgaattgtca gacatcaaaa gcgtgataca 1200
cgctttataa aagacctgag gaagtgatgg tctaaaatgg gatctggttt ggggtttaca 1260
ggttagttgt tggctcacgt aacttaataa agtttttctt tgtaggttg ttaacttgg 1320
gtaggatgtt ttagttcagc ttgatcatt aggg
```

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 365 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..365

(D) OTHER INFORMATION: / Ceres Seq. ID 1498330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

```
Met Thr Arg Arg Cys Ser His Cys Asn His Asn Gly His Asn Ser Arg
1 5 10 15
Thr Cys Pro Asn Arg Gly Val Lys Leu Phe Gly Val Arg Leu Thr Glu
20 25 30
Gly Ser Ile Arg Lys Ser Ala Ser Met Gly Asn Leu Ser His Tyr Thr
35 40 45
Gly Ser Gly Ser Gly Gly His Gly Thr Gly Ser Asn Thr Pro Gly Ser
50 55 60
Pro Gly Asp Val Pro Asp His Val Ala Gly Asp Gly Tyr Ala Ser Glu
65 70 75 80
Asp Phe Val Ala Gly Ser Ser Ser Ser Arg Glu Arg Lys Lys Gly Thr
85 90 95
Pro Trp Thr Glu Glu Glu His Arg Met Phe Leu Leu Gly Leu Glu Lys
100 105 110
Leu Gly Lys Gly Asp Trp Arg Gly Ile Ser Arg Asn Tyr Val Thr Thr
115 120 125
Xaa Thr Pro Thr Gln Val Ala Ser His Ala Gln Lys Tyr Phe Ile Arg
130 135 140
Gln Ser Asn Val Ser Arg Arg Lys Arg Arg Ser Ser Leu Phe Asp Met
145 150 155 160
```

Val Pro Asp Glu Val Gly Asp Ile Pro Met Asp Leu Gln Glu Pro Glu  
165 170 175  
Glu Asp Asn Ile Pro Val Glu Thr Glu Met Gln Gly Ala Asp Ser Ile  
180 185 190  
His Gln Thr Leu Ala Pro Ser Ser Leu His Ala Pro Ser Ile Leu Glu  
195 200 205  
Ile Glu Glu Cys Glu Ser Met Asp Ser Thr Asn Ser Thr Thr Gly Glu  
210 215 220  
Pro Thr Ala Thr Ala Ala Ala Ser Ser Ser Ser Arg Leu Glu Glu  
225 230 235 240  
Thr Thr Gln Leu Gln Ser Gln Leu Gln Pro Gln Pro Gln Leu Pro Gly  
245 250 255  
Ser Phe Pro Ile Leu Tyr Pro Thr Tyr Phe Ser Pro Tyr Tyr Pro Phe  
260 265 270  
Pro Phe Pro Ile Trp Pro Ala Gly Tyr Val Pro Glu Pro Pro Lys Lys  
275 280 285  
Glu Glu Thr His Glu Ile Leu Arg Pro Thr Ala Val His Ser Lys Ala  
290 295 300  
Pro Ile Asn Val Asp Glu Leu Leu Gly Met Ser Lys Leu Ser Leu Ala  
305 310 315 320  
Glu Ser Asn Lys His Gly Glu Ser Asp Gln Ser Leu Ser Leu Lys Leu  
325 330 335  
Gly Gly Gly Ser Ser Ser Arg Gln Ser Ala Phe His Pro Asn Pro Ser  
340 345 350  
Ser Asp Ser Ser Asp Ile Lys Ser Val Ile His Ala Leu  
355 360 365

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..325
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

Met Gly Asn Leu Ser His Tyr Thr Gly Ser Gly Ser Gly His Gly  
1 5 10 15  
Thr Gly Ser Asn Thr Pro Gly Ser Pro Gly Asp Val Pro Asp His Val  
20 25 30  
Ala Gly Asp Gly Tyr Ala Ser Glu Asp Phe Val Ala Gly Ser Ser Ser  
35 40 45  
Ser Arg Glu Arg Lys Lys Gly Thr Pro Trp Thr Glu Glu His Arg  
50 55 60  
Met Phe Leu Leu Gly Leu Gln Lys Leu Gly Lys Gly Asp Trp Arg Gly  
65 70 75 80  
Ile Ser Arg Asn Tyr Val Thr Thr Xaa Thr Pro Thr Gln Val Ala Ser  
85 90 95  
His Ala Gln Lys Tyr Phe Ile Arg Gln Ser Asn Val Ser Arg Arg Lys  
100 105 110  
Arg Arg Ser Ser Leu Phe Asp Met Val Pro Asp Glu Val Gly Asp Ile  
115 120 125  
Pro Met Asp Leu Gln Glu Pro Glu Glu Asp Asn Ile Pro Val Glu Thr  
130 135 140  
Glu Met Gln Gly Ala Asp Ser Ile His Gln Thr Leu Ala Pro Ser Ser  
145 150 155 160  
Leu His Ala Pro Ser Ile Leu Glu Ile Glu Glu Cys Glu Ser Met Asp  
165 170 175  
Ser Thr Asn Ser Thr Thr Gly Glu Pro Thr Ala Thr Ala Ala Ala

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Phe | Leu | Leu | Gly | Leu | Gln | Lys | Leu | Gly | Lys | Gly | Asp | Trp | Arg | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Ser | Arg | Asn | Tyr | Val | Thr | Thr | Xaa | Thr | Pro | Thr | Gln | Val | Ala | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Ala | Gln | Lys | Tyr | Phe | Ile | Arg | Gln | Ser | Asn | Val | Ser | Arg | Arg | Lys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Arg | Ser | Ser | Leu | Phe | Asp | Met | Val | Pro | Asp | Glu | Val | Gly | Asp | Ile |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Met | Asp | Leu | Gln | Glu | Pro | Glu | Glu | Asp | Asn | Ile | Pro | Val | Glu | Thr |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Glu | Met | Gln | Gly | Ala | Asp | Ser | Ile | His | Gln | Thr | Leu | Ala | Pro | Ser | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | His | Ala | Pro | Ser | Ile | Leu | Glu | Ile | Glu | Glu | Cys | Glu | Ser | Met | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Thr | Asn | Ser | Thr | Thr | Gly | Glu | Pro | Thr | Ala | Thr | Ala | Ala | Ala | Ala |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Ser | Ser | Ser | Ser | Arg | Leu | Glu | Glu | Thr | Thr | Gln | Leu | Gln | Ser | Gln | Leu |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gln | Pro | Gln | Pro | Gln | Leu | Pro | Gly | Ser | Phe | Pro | Ile | Leu | Tyr | Pro | Thr |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Tyr | Phe | Ser | Pro | Tyr | Tyr | Pro | Phe | Pro | Phe | Pro | Ile | Trp | Pro | Ala | Gly |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Tyr | Val | Pro | Glu | Pro | Pro | Lys | Lys | Glu | Glu | Thr | His | Glu | Ile | Leu | Arg |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Pro | Thr | Ala | Val | His | Ser | Lys | Ala | Pro | Ile | Asn | Val | Asp | Glu | Leu | Leu |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gly | Met | Ser | Ser | Lys | Leu | Ser | Leu | Ala | Glu | Ser | Asn | Lys | His | Gly | Gln |
|     |     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Asp | Gln | Ser | Leu | Ser | Leu | Lys | Leu | Gly | Gly | Gly | Ser | Ser | Ser | Arg | Gln |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |     |

(2) INFORMATION FOR SEQ ID NO:355:

(A) LENGTH: 553 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..553

(D) OTHER INFORMATION: / Ceres Seq. ID 1498333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

|              |             |             |             |             |             |     |
|--------------|-------------|-------------|-------------|-------------|-------------|-----|
| acgttttagttt | ttttccacat  | cgacaaatat  | cgccgcgcgtt | ggacgaagaag | agaaagagatg | 60  |
| ggagttttttt  | catctgtgtg  | cagaagacaaa | ggcgggagaat | tgagccgcgaa | gcacacacgaa | 120 |
| ggagatatttg  | aaagcttaacg | tttcttcacc  | tacgatattcc | agccgaacgt  | tggttcagact | 180 |
| gcctctctcgc  | cgagtttaac  | tggcggcggc  | cagttctctt  | tctctcttgt  | ctctcttacc  | 240 |
| ctccgcgctct  | tcgtgtgtgtt | catctgtgtgt | ggtggtgtgt  | gaggtatttg  | tgccggaggga | 300 |
| ggttcagctgt  | cttgaggtgtg | tgtgtgtgtg  | gaagcttcgcg | cagccacaaa  | ggagggaagag | 360 |
| aaagaaagaag  | aaagaattcga | agaggaagaag | ggagaaatttg | gatttgattc  | ctttgtgttaa | 420 |
| gagaccataac  | acaaactttgt | tagtgtttctg | aggtttttct  | atctcaattt  | ctctctcttta | 480 |
| tgaaattatc   | tgtttttttt  | tcggagaaaag | agtaagatac  | atgatgaaaa  | tctgttttgg  | 540 |
| ggcactttttg  | gct         |             |             |             |             |     |

(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1498334

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Leu | Val | Phe | Phe | Thr | Val | Glu | Lys | Ser | Arg | Arg | Arg | Leu | Lys | Lys |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Glu | Glu | Glu | Met | Gly | Val | Phe | Ser | Phe | Val | Cys | Lys | Ser | Lys | Gly | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Trp | Thr | Ala | Lys | Gln | His | Glu | Gly | Asp | Leu | Glu | Ala | Ser | Ala | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Thr | Tyr | Asp | Leu | Gln | Arg | Lys | Leu | Val | Gln | Thr | Ala | Leu | Ser | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Asp | Ser | Ser | Gly | Gly | Val | Gln | Ser | Phe | Ser | Leu | Val | Ser | Pro | Thr |     |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Ala | Val | Phe | Val | Val | Ile | Gly | Gly | Gly | Gly | Gly | Gly | Gly | Phe |     |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ala | Ala | Gly | Gly | Gly | Ala | Ala | Ala | Gly | Gly | Gly | Gly | Gly | Gly | Glu | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Ala | Ala | Thr | Lys | Glu | Glu | Glu | Lys | Lys | Lys | Glu | Glu | Ser | Glu | Glu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Glu | Gly | Asp | Phe | Gly | Phe | Asp | Leu | Phe | Gly |     |     |     |     |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..120  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498335  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:  
Met Gly Val Phe Ser Phe Val Cys Lys Ser Lys Gly Gly Glu Trp Thr  
1 5 10 15  
Ala Lys Gln His Glu Gly Asp Leu Glu Ala Ser Ala Ser Ser Thr Tyr  
20 25 30  
Asp Leu Gln Arg Lys Leu Val Gln Thr Ala Leu Ser Ala Asp Ser Ser  
35 40 45  
Gly Gly Val Gln Ser Ser Phe Ser Leu Val Ser Pro Thr Ser Ala Val  
50 55 60  
Phe Val Val Val Ile Gly Gly Gly Gly Gly Phe Ala Ala Gly  
65 70 75 80  
Gly Gly Ala Ala Ala Gly Gly Gly Gly Gly Glu Ala Ala Ala  
85 90 95  
Thr Lys Glu Glu Glu Lys Lys Lys Glu Glu Ser Glu Glu Glu Gly  
100 105 110  
Asp Phe Gly Phe Asp Leu Phe Gly  
115 120

(2) INFORMATION FOR SEQ ID NO:358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 623 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..623

(D) OTHER INFORMATION: / Ceres Seq. ID 1498336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

aatctctctc aacacaaaaga agaacaaaaga agttatgagc tcaatgatgg agactctcca 60  
gattcgtaaa ccactttccc tcccggttcc tcaacgccct aatgcagcag ccamcgcgca 120  
cgatgcagcct ggtctcatcc gccctcgtct ctcttctcta tcaactcaasc tctcaaacca 180  
accagygagcg atmgmagcta gattcscgag atccaaatct gtttccgcga tgggagaaca 240  
agcaggaagc tctgtgaaag aatggtggga atgggggttg tcatggatcc tttaagaaaa 300  
acctatattc atcagagatc ttgagcttta caaagacgaa gctaatacga ttggttcaca 360  
aaacagagga agtataatgc acgttttctt caaactccgr tctcagatcc gtaattcat 420  
gggaccttct tcagaagatt ctcttcctct ttcttgcaaa tacaagcgctc aacgataaaa 480  
tgattcataa aaggttgaga ttttgtgatt tgtctgttct ttttttactt ttgtgcaatg 540  
gagttataat aagtataaat tcgtcttttt tttttaaact tgatgttgta ttttgctata 600  
attaatttgc ctgattatt att

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..158  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

Ile Ser Leu Asn Thr Lys Lys Asn Lys Glu Val Met Ser Ser Met Met  
1 5 10 15  
Glu Thr Leu Gln Ile Arg Lys Pro Thr Ser Leu Pro Val Ser Gln Arg

(2) INFORMATION FOR SEQ ID NO:360:

(A) LENGTH: 147 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(ix) FEATURE:

(IX) FEATURE:  
(A) NAME

(B) LOCATION: 1..147

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:360:

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:300:  
Ser Ser Met Met Gln Thr Leu Gln Ile Arg I

[illegible]

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

```
(ix) FEATURE:
```

(A) NAME/KEY: peptide

(B) LOCATION: 1..144

(D) OTHER INFORMATION: / Ceres Seq. ID 1498339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:



```

Met Met Glu Thr Leu Gln Ile Arg Lys Pro Thr Ser Leu Pro Val Ser
1 5 10 15
Gln Arg Pro Asn Ala Ala Ala Xaa Ala Asp Glu Pro Gly Leu Ile
20 25 30
Arg Arg Arg Leu Ser Ser Leu Ser Leu Xaa Leu Ser Asn Gln Pro Xaa
35 40 45
Ala Xaa Xaa Ala Arg Phe Xaa Arg Ser Lys Ser Val Ser Ala Met Gly
50 55 60
Glu Gln Ala Gly Ser Ser Val Lys Glu Trp Trp Glu Trp Gly Trp Ser
65 70 75 80
Trp Ile Leu Ser Arg Lys Pro Ile Phe Ile Arg Asp Leu Glu Leu Asn
85 90 95
Lys Asp Glu Ala Lys Ser Ile Gly Ser Gln Asn Arg Gly Ser Ile Met
100 105 110
His Val Phe Phe Lys Leu Xaa Ser Gln Ile Arg Asn Phe Met Gly Pro
115 120 125
Ser Ser Glu Asp Ser Leu Pro Leu Ser Cys Lys Tyr Lys Arg Gln Arg
130 135 140

```

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1152
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

```

accacatgga gaggatccta gggttactac taatctcgaa atcaatcaaa tcaaaagcatc 60
catttttggat tcagacttca gagagacaaa gaaggaagaa aagaagaaaa 120
aactatggag aatgagaggg aaaagcaggt ttacttggct aagctctccg agcaaacccga 180
aagatacgat gaaatgggtgg aggcgatgaa gaaagttgct cagcttgatg tggagctaac 240
tgtggaagag aggaatcttg tatctgtagg gtacaagaat gtgattgggt caaaggagagc 300
atcatggaga atactatctt ccattgagca gaaggaagag tccaagggaat atgatgaaaa 360
tgtcaagagg cttaagaatt atcgttaagag agttgaagat gagcttgcta aagttgttaa 420
tgacatcttg tctgtcattg ataagcatct cattccatct tctaaccgctg tggagtcacac 480
tgtctttttc tacaaaaatga aaggagatta ctatcgctat ctgcgaggat tcagttctggt 540
tgtctaacgc aaggaagctg cagatcagtc tcttgaagca tataaaggctg ctgttctgctg 600
tgcagagaat ggtttggcac ccacacatcc agttagactt ggcttggcgt tgaacttttc 660
agttttctac tatgagatct tgaactctcc cgaaaacgca tgccaattgg ctaagcaagc 720
attogatgat gcaattgctg aacttgacag cctcaacgag gaatcataca aagacagcac 780
tcttattatg cagctactta gagacaatct cacttgtgg acttoagacc ttaatgagga 840
aggagatgag agaaccaaaag gtgctgatga gcctcaagat gagaactaaa tcctctgtga 900
gaagagaaag gactcttgct gcatcctgaa tcttgaagtg aagacagcaa gtgtcgttgt 960
ttgttactgc aatgtgtaat ttttaactca tgtctttctt gatgatgttt tccagatttt 1020
tgaacttttc acaacacacac actgcgttgc gtactttcaa atgtgtgtga 1080
attctgtttt acgcttagtt tgctcttttt gttgttgaat tgagccagca ggcgatgatt 1140
gggtttttgt tt

```

(2) INFORMATION FOR SEQ ID NO:363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..254

(D) OTHER INFORMATION: / Ceres Seq. ID 1498349

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

Met Glu Asn Glu Arg Glu Lys Gln Val Tyr Leu Ala Lys Leu Ser Glu  
1 5 10 15  
Gln Thr Glu Arg Tyr Asp Glu Met Val Glu Ala Met Lys Lys Val Ala  
20 25 30  
Gln Leu Asp Val Glu Leu Thr Val Glu Arg Asn Leu Val Ser Val  
35 40 45  
Gly Tyr Lys Asn Val Ile Gly Ala Arg Arg Ala Ser Trp Arg Ile Leu  
50 55 60  
Ser Ser Ile Glu Gln Lys Lys Glu Glu Ser Lys Gly Asn Asp Glu Asn Val  
65 70 75 80  
Lys Arg Leu Lys Asn Tyr Arg Lys Arg Val Glu Asp Glu Leu Ala Lys  
85 90 95  
Val Cys Asn Asp Ile Leu Ser Val Ile Asp Lys His Leu Ile Pro Ser  
100 105 110  
Ser Asn Ala Val Glu Ser Thr Val Phe Phe Tyr Lys Met Lys Gly Asp  
115 120 125  
Tyr Tyr Arg Tyr Leu Ala Glu Phe Ser Ser Gly Ala Glu Arg Lys Glu  
130 135 140  
Ala Ala Asp Gln Ser Leu Glu Ala Tyr Lys Ala Ala Val Ala Ala Ala  
145 150 155 160  
Glu Asn Gly Leu Ala Pro Thr His Pro Val Arg Leu Gly Leu Ala Leu  
165 170 175  
Asn Phe Ser Val Phe Tyr Tyr Glu Ile Leu Asn Ser Pro Glu Ser Ala  
180 185 190  
Cys Gln Leu Ala Lys Gln Ala Phe Asp Asp Ala Ile Ala Glu Leu Asp  
195 200 205  
Ser Leu Asn Glu Glu Ser Tyr Lys Asp Ser Thr Leu Ile Met Gln Leu  
210 215 220  
Leu Arg Asp Asn Leu Thr Leu Trp Thr Ser Asp Leu Asn Glu Glu Gly  
225 230 235 240  
Asp Glu Arg Thr Lys Gly Ala Asp Glu Pro Gln Asp Glu Asn  
245 250

(2) INFORMATION FOR SEQ ID NO:364:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..231

(D) OTHER INFORMATION: / Ceres Seq. ID 1498350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

Met Val Glu Ala Met Lys Lys Val Ala Gln Leu Asp Val Glu Leu Thr  
1 5 10 15  
Val Glu Glu Arg Asn Leu Val Ser Val Gly Tyr Lys Asn Val Ile Gly  
20 25 30  
Ala Arg Arg Ala Ser Trp Arg Ile Leu Ser Ser Ile Glu Gln Lys Glu  
35 40 45  
Glu Ser Lys Gly Asn Asp Glu Asn Val Lys Arg Leu Lys Asn Tyr Arg  
50 55 60  
Lys Arg Val Glu Asp Glu Leu Ala Lys Val Cys Asn Asp Ile Leu Ser  
65 70 75 80  
Val Ile Asp Lys His Leu Ile Pro Ser Ser Asn Ala Val Glu Ser Thr  
85 90 95  
Val Phe Phe Tyr Lys Met Lys Gly Asp Tyr Tyr Arg Tyr Leu Ala Glu  
100 105 110

Phe Ser Ser Gly Ala Glu Arg Lys Glu Ala Ala Asp Gln Ser Leu Glu  
115 120 125  
Ala Tyr Lys Ala Ala Val Ala Ala Glu Asn Gly Leu Ala Pro Thr  
130 135 140  
His Pro Val Arg Leu Gly Leu Ala Leu Asn Phe Ser Val Phe Tyr Tyr  
145 150 155 160  
Glu Ile Leu Asn Ser Pro Glu Ser Ala Cys Gln Leu Ala Lys Gln Ala  
165 170 175  
Phe Asp Asp Ala Ile Ala Glu Leu Asp Ser Leu Asn Glu Glu Ser Tyr  
180 185 190  
Lys Asp Ser Thr Leu Ile Met Gln Leu Leu Arg Asp Asn Leu Thr Leu  
195 200 205  
Trp Thr Ser Asp Leu Asn Glu Glu Gly Asp Glu Arg Thr Lys Gly Ala  
210 215 220  
Asp Glu Pro Gln Asp Glu Asn  
225 230

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..227
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

Met Lys Lys Val Ala Gln Leu Asp Val Glu Leu Thr Val Glu Glu Arg  
1 5 10 15  
Asn Leu Val Ser Val Gly Tyr Lys Asn Val Ile Gly Ala Arg Arg Ala  
20 25 30  
Ser Trp Arg Ile Leu Ser Ser Ile Glu Gln Lys Glu Glu Ser Lys Gly  
35 40 45  
Asn Asp Glu Asn Val Lys Arg Leu Lys Asn Tyr Arg Lys Arg Val Glu  
50 55 60  
Asp Glu Leu Ala Lys Val Cys Asn Asp Ile Leu Ser Val Ile Asp Lys  
65 70 75 80  
His Leu Ile Pro Ser Ser Asn Ala Val Glu Ser Thr Val Phe Phe Tyr  
85 90 95  
Lys Met Lys Gly Asp Tyr Tyr Arg Tyr Leu Ala Glu Phe Ser Ser Gly  
100 105 110  
Ala Glu Arg Lys Glu Ala Ala Asp Gln Ser Leu Glu Ala Tyr Lys Ala  
115 120 125  
Ala Val Ala Ala Ala Glu Asn Gly Leu Ala Pro Thr His Pro Val Arg  
130 135 140  
Leu Gly Leu Ala Leu Asn Phe Ser Val Phe Tyr Tyr Glu Ile Leu Asn  
145 150 155 160  
Ser Pro Glu Ser Ala Cys Gln Leu Ala Lys Gln Ala Phe Asp Asp Ala  
165 170 175  
Ile Ala Glu Leu Asp Ser Leu Asn Glu Glu Ser Tyr Lys Asp Ser Thr  
180 185 190  
Leu Ile Met Gln Leu Leu Arg Asp Asn Leu Thr Leu Trp Thr Ser Asp  
195 200 205  
Leu Asn Glu Glu Gly Asp Glu Arg Thr Lys Gly Ala Asp Glu Pro Gln  
210 215 220  
Asp Glu Asn  
225

(2) INFORMATION FOR SEQ ID NO:366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1396 base pairs

(ix) FEATURE:

(B) LOCATION: 1..1396

(D) OTHER INFORMATION: / Ceres Seq. ID 1498352

SEQUENCE DESCRIPTION: SEQ ID NO:366:

| (X1)      | SEQUENCE    | DSS         | KLIF100    | Seq        |             |      |
|-----------|-------------|-------------|------------|------------|-------------|------|
| ctgtgaaa  | agtaataacc  | tctctctctt  | gcaccttttg | ctgggtctgg | tgaacaatag  | 60   |
| agctttct  | cttctccaag  | ttaatgataa  | aagggttggt | taggtattgt | tgtctctggct | 120  |
| ctgttgta  | ctctatgaaa  | tcaaacccata | ctgtgattag | actgcaacat | ggatctctct  | 180  |
| ctgctgag  | attgggagca  | tttgtatctt  | tccaactcgt | caaggactga | agatgacagc  | 240  |
| caagtcgt  | ctactgagtg  | ggaaatttgaa | aaagggtgaa | gaattgaatc | tatagttcca  | 300  |
| ctctctac  | gccttgagag  | agtcagtagg  | tggctctgcc | accagctctt | ggcaactcgt  | 360  |
| ctctcgaaa | agctcacagt  | gcacctctat  | caactcatca | tctcccgaa  | ccaaacagtc  | 420  |
| ctgtctga  | tcagaaagt   | ccccctggga  | ttcttcagc  | aacatagact | ttgtccaggt  | 480  |
| ggctccc   | acagctcgt   | aggtatccgt  | tgcctcagc  | gaatcagatc | tttctgttaa  | 540  |
| ctgggaag  | cggagctact  | ctcaagaata  | ctggggtaga | aaacataaat | aaatttgcga  | 600  |
| ctctctat  | agagttgtta  | ctctgatctt  | tgtctcgtgg | aaaaccaaat | tgtgtggcta  | 660  |
| ctcatgcca | gtcccgcgtt  | gccaaatttg  | tggctgtgaa | ctgtgatctc | catctgtcaa  | 720  |
| ttctatcat | gaagtcgaca  | aagctctgca  | aaagcatcca | atggtgccaa | agtgtaacgt  | 780  |
| ggctccctg | cgaactcgtg  | tgtgccaaac  | gtgtgacagg | tctcatgtct | tctctgaatt  | 840  |
| ctgagaa   | aaacccaagt  | gcgaaaaacg  | tctttctcat | cataaatgca | ggcgtgttaa  | 900  |
| caacagga  | gtatttttca  | ttaaaatccg  | gaggggtgat | gatcgaagac | agcatacaaa  | 960  |
| ctgttggtg | aatgggggtg  | cccttaaacg  | gagacttgaa | gaaattgtat | aatggggtaa  | 1020 |
| ctacttat  | gatacaaacg  | ctatgacaac  | ggaaaaaagc | tttactctat | gcttcagagc  | 1080 |
| taattgcg  | ctctgaggacc | agctggttgc  | gtatgcagc  | cgtatgttcc | tctacatctc  | 1140 |
| ctctcagg  | tgggttccca  | gcaggaaga   | ccaagtttca | actctcagtc | gaagatgtgg  | 1200 |
| taatactc  | aggagctctc  | catgaattct  | aagatatacc | ctgtgtctct | tctctctgat  | 1260 |
| ctactctc  | ggagtcctgc  | gcccaaccac  | atgtgcagcc | attttctcta | ctctgttcat  | 1320 |
| ctatttgtt | accaaaatag  | atgtagta    | aatgtgta   | ttgtaaacct | gttactcagt  | 1380 |
| ctatgata  | tttttcc     |             |            |            |             |      |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids

(C) STRANDEDNESS:

(D) TOPOLOGY: linear  
MOLECULE TYPE: pentid

FEATURE:

(B) LOCATION: 1..121

(D) OTHER INFORMATION: / Ceres Seq. ID 1498353

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Cys | Asn | Met | Val | Ser | Ser | Ser | Gln | Trp | Asp | Trp | Glu | His | Leu |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Met | Ser | Asn | Pro | Ser | Arg | Thr | Glu | Asp | Asp | Ser | Lys | Gln | Leu | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Glu | Trp | Glu | Ile | Glu | Lys | Gly | Glu | Gly | Ile | Glu | Ser | Ile | Val | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| His | Phe | Ser | Gly | Leu | Glu | Arg | Val | Ser | Arg | Trp | Leu | Cys | His | Gln | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Ala | His | Cys | Cys | Ile | Glu | Lys | Leu | Thr | Val | Asp | Leu | Tyr | Gln | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ile | Ile | Ser | Arg | Ser | Gln | Thr | Met | Gln | Ala | Cys | Ile | Arg | Lys | Phe | Pro |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Trp | Arg | Phe | Leu | Gln | Gln | His | Arg | Leu | Cys | Pro | Gly | Glu | Gly | Ser | His |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Ser | Arg | Gly | Ile | Arg | Cys | Leu | Ser |     |     |     |     |     |     |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..205
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

Met Lys Leu Leu Thr Pro Ser Val Val Ala Gly Lys Ser Lys Leu Cys  
1 5 10 15  
Gly Gln Ser Met Pro Val Pro Arg Cys Gln Ile Asp Gly Cys Glu Leu  
20 25 30  
Asp Leu Ser Ser Ala Lys Gly Tyr His Arg Lys His Lys Val Cys Glu  
35 40 45  
Lys His Ser Lys Cys Pro Lys Val Ser Val Ser Gly Leu Glu Arg Arg  
50 55 60  
Phe Cys Gln Gln Cys Ser Arg Phe His Ala Val Ser Glu Phe Asp Glu  
65 70 75 80  
Lys Lys Arg Ser Cys Arg Lys Arg Leu Ser His His Asn Ala Arg Arg  
85 90 95  
Arg Lys Pro Gln Gly Val Phe Ser Met Asn Pro Glu Arg Val Tyr Asp  
100 105 110  
Arg Arg Gln His Thr Asn Met Leu Trp Asn Gly Val Ser Leu Asn Ala  
115 120 125  
Arg Ser Glu Glu Met Tyr Glu Trp Gly Asn Asn Thr Tyr Asp Thr Lys  
130 135 140  
Pro Arg Gln Thr Glu Lys Ser Phe Thr Leu Ser Phe Gln Arg Gly Asn  
145 150 155 160  
Gly Ser Glu Asp Gln Leu Val Ala Ser Ser Ser Arg Met Phe Leu Tyr  
165 170 175  
Ile Ser Asn Leu Arg Trp Val Pro Ser Arg Lys Val Gln Val Ser Thr  
180 185 190  
Ser Trp Arg Arg Cys Gly Arg Ile Leu Arg Ser Pro Pro  
195 200 205

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..186
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498355

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

Met Pro Val Pro Arg Cys Gln Ile Asp Gly Cys Glu Leu Asp Leu Ser  
1 5 10 15  
Ser Ala Lys Gly Tyr His Arg Lys His Lys Val Cys Glu Lys His Ser  
20 25 30  
Lys Cys Pro Lys Val Ser Val Ser Gly Leu Glu Arg Arg Phe Cys Gln  
35 40 45  
Gln Cys Ser Arg Phe His Ala Val Ser Glu Phe Asp Glu Lys Lys Arg  
50 55 60  
Ser Cys Arg Lys Arg Leu Ser His His Asn Ala Arg Arg Arg Lys Pro  
65 70 75 80  
Gln Gly Val Phe Ser Met Asn Pro Glu Arg Val Tyr Asp Arg Arg Gln

[illegible]

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Phe | His | Leu | Gln | Phe | Cys | Phe | Tyr | Phe | Ser | Arg | Ser | Phe | Ser | Ser |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Lys | Tyr | Cys | Phe | Arg | Ser | Ile | Asn | Gln | Ser | Ile | Met | Ala | Ser | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Gly | Asn | Lys | Asn | Ile | Asn | Ala | Lys | Leu | Val | Leu | Gly | Asp | Val | Gly |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Ala | Gly | Lys | Ser | Ser | Leu | Val | Leu | Arg | Phe | Val | Lys | Asp | Gln | Phe | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Phe | Gln | Glu | Ser | Thr | Ile | Gly | Ala | Ala | Phe | Phe | Ser | Gln | Thr | Leu |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Ala | Val | Asn | Asp | Ala | Thr | Val | Lys | Phe | Glu | Ile | Trp | Asp | Thr | Ala | Gly |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gln | Glu | Arg | Tyr | His | Ser | Leu | Ala | Pro | Met | Tyr | Tyr | Arg | Gly | Ala | Ala |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Ala | Ala | Ile | Ile | Val | Phe | Asp | Ile | Thr | Asn | Gln | Ala | Ser | Phe | Glu | Arg |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ala | Xaa | Lys | Trp | Val | Gln | Glu | Leu | Gln | Ala | Gln | Gly | Asn | Pro | Asn | Met |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Val | Met | Ala | Leu | Ala | Gly | Asn | Lys | Ala | Asp | Leu | Leu | Asp | Ala | Arg | Lys |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Val | Ser | Ala | Glu | Glu | Ala | Glu | Ile | Tyr | Ala | Gln | Glu | Asn | Ser | Leu | Phe |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Phe | Met | Glu | Thr | Ser | Ala | Lys | Thr | Ala | Thr | Asn | Val | Lys | Asp | Ile | Phe |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Tyr | Glu | Ile | Ala | Lys | Arg | Leu | Pro | Arg | Ile | Gln | Pro | Ala | Glu | Asn | Pro |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     | 255 |     |     |
| Thr | Gly | Met | Val | Leu | Pro | Asn | Gly | Pro | Gly | Ala | Thr | Ala | Val | Ser | Ser |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Ser | Cys | Cys | Ala |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     | 275 |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:372:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..200

(D) OTHER INFORMATION: / Ceres Seq. ID 1498358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Ser | Gly | Asn | Lys | Asn | Ile | Asn | Ala | Lys | Leu | Val | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     | 15  |     |     |     |
| Gly | Asp | Val | Gly | Ala | Gly | Lys | Ser | Ser | Leu | Val | Leu | Arg | Phe | Val | Lys |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Asp | Gln | Phe | Val | Glu | Phe | Gln | Glu | Ser | Thr | Ile | Gly | Ala | Ala | Phe | Phe |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Ser | Gln | Thr | Leu | Ala | Val | Asn | Asp | Ala | Thr | Val | Lys | Phe | Glu | Ile | Trp |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Thr | Ala | Gly | Gln | Glu | Arg | Tyr | His | Ser | Leu | Ala | Pro | Met | Tyr | Tyr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Arg | Gly | Ala | Ala | Ala | Ala | Ile | Ile | Val | Phe | Asp | Ile | Thr | Asn | Gln | Ala |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ser | Phe | Glu | Arg | Ala | Xaa | Lys | Trp | Val | Gln | Glu | Leu | Gln | Ala | Gln | Gly |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Pro | Asn | Met | Val | Met | Ala | Leu | Ala | Gly | Asn | Lys | Ala | Asp | Leu | Leu |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Asp | Ala | Arg | Lys | Val | Ser | Ala | Glu | Glu | Ala | Glu | Ile | Tyr | Ala | Gln | Glu |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asn | Ser | Leu | Phe | Phe | Met | Glu | Thr | Ser | Ala | Lys | Thr | Ala | Thr | Asn | Val |

145 150 155 160  
Lys Asp Ile Phe Tyr Glu Ile Ala Lys Arg Leu Pro Arg Ile Gln Pro  
165 170 175  
Ala Glu Asn Pro Thr Gly Met Val Leu Pro Asn Gly Pro Gly Ala Thr  
180 185 190  
Ala Val Ser Ser Ser Cys Cys Ala  
195 200

(2) INFORMATION FOR SEQ ID NO:373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 644 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..644
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

aaaaaagagt cgcccatattt ctctcattt ttttttgctc ttgacgaaga aacccaaaaa 60  
aaaaaaaaatg agagagatcc ttcatatcca aggcgggtcaa tgtggaaacc agatcggagc 120  
aaagtctctgg gaagtgatctt gcgacgaaca cgccattgat cacaccggctc aatcgcgtgg 180  
cgattctccg ttacagcttg aacgtatoga tgtctatttc aacgaagcta gcggtggaaa 240  
gtacgttctc cgcgctgttc ttatggatct ggagcctgggt accatggatt ctctcagatc 300  
tggtccgcttc ggtcagattt tccgtcctga taacttgcgt tttgttcaat ctggtgcggg 360  
aaataaactgg gcgaaaggtc attacaccga agtctntnag ttgattgatt ctgttctcga 420  
tgttgtgagg aaggaagctg agaacacgca ttgtcttcaa ggtttccaag tgtgtcattc 480  
attgggaggga ggaactggat ctggaatggg aactctattg atttctaaga taagagaaga 540  
gtatccagat cgtatgatga tgactttctc agtgtttctt ctccataagt ctctgacact 600  
gttggtgagc atacantgca ctctctctgt gcatcagctt gtcg

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..214
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

Lys Lys Ser Arg Pro Phe Ser Ser His Phe Leu Leu Thr Lys  
1 5 10 15  
Lys Pro Lys Lys Lys Met Arg Glu Ile Leu His Ile Gln Gly Lys  
20 25 30  
Gln Cys Gly Asn Gln Ile Gly Ala Lys Phe Trp Glu Val Ile Cys Asp  
35 40 45  
Glu His Gly Ile Asp His Thr Gly Gln Tyr Val Gly Asp Ser Pro Leu  
50 55 60  
Gln Leu Glu Arg Ile Asp Val Tyr Phe Asn Glu Ala Ser Gly Gly Lys  
65 70 75 80  
Tyr Val Pro Arg Ala Val Leu Met Asp Leu Glu Pro Gly Thr Met Asp  
85 90 95  
Ser Leu Arg Ser Gly Pro Phe Gly Gln Ile Phe Arg Pro Asp Asn Phe  
100 105 110  
Val Phe Gly Gln Ser Gly Ala Gly Asn Asn Trp Ala Lys Gly His Tyr  
115 120 125  
Thr Glu Val Xaa Glu Leu Ile Asp Ser Val Leu Asp Val Val Arg Lys  
130 135 140  
Glu Ala Glu Asn Ser Asp Cys Leu Gln Gly Phe Gln Val Cys His Ser



145 150 155 160  
Leu Gly Gly Gly Thr Gly Ser Gly Met Gly Thr Leu Leu Ile Ser Lys  
165 170 175  
Ile Arg Glu Glu Tyr Pro Asp Arg Met Met Thr Phe Ser Val Phe  
180 185 190  
Leu Leu Leu Arg Ser Leu Thr Leu Leu Leu Ser Ile Xaa Cys Thr Leu  
195 200 205  
Ser Val His Gln Leu Val  
210

(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..192

(D) OTHER INFORMATION: / Ceres Seq. ID 1498364

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

Met Arg Glu Ile Leu His Ile Gln Gly Gly Gln Cys Gly Asn Gln Ile  
1 5 10 15  
Gly Ala Lys Phe Trp Glu Val Ile Cys Asp Glu His Gly Ile Asp His  
20 25 30  
Thr Gly Gln Tyr Val Gly Asp Ser Pro Leu Gln Leu Glu Arg Ile Asp  
35 40 45  
Val Tyr Phe Asn Glu Ala Ser Gly Gly Lys Tyr Val Pro Arg Ala Val  
50 55 60  
Leu Met Asp Leu Glu Pro Gly Thr Met Asp Ser Leu Arg Ser Gly Pro  
65 70 75 80  
Phe Gly Gln Ile Phe Arg Pro Asp Asn Phe Val Phe Gly Gln Ser Gly  
85 90 95  
Ala Gly Asn Asn Trp Ala Lys Gly His Tyr Thr Glu Val Xaa Glu Leu  
100 105 110  
Ile Asp Ser Val Leu Asp Val Val Arg Lys Glu Ala Glu Asn Ser Asp  
115 120 125  
Cys Leu Gln Gly Phe Gln Val Cys His Ser Leu Gly Gly Thr Gly  
130 135 140  
Ser Gly Met Gly Thr Leu Leu Ile Ser Lys Ile Arg Glu Glu Tyr Pro  
145 150 155 160  
Asp Arg Met Met Met Thr Phe Ser Val Phe Leu Leu Leu Arg Ser Leu  
165 170 175  
Thr Leu Leu Leu Ser Ile Xaa Cys Thr Leu Ser Val His Gln Leu Val  
180 185 190

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1498365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

Met Asp Leu Glu Pro Gly Thr Met Asp Ser Leu Arg Ser Gly Pro Phe  
1 5 10 15

Gly Gln Ile Phe Arg Pro Asp Asn Phe Val Phe Gly Gln Ser Gly Ala  
20 25 30  
Gly Asn Asn Trp Ala Lys Gly His Tyr Thr Glu Val Xaa Glu Leu Ile  
35 40 45  
Asp Ser Val Leu Asp Val Val Arg Lys Glu Ala Glu Asn Ser Asp Cys  
50 55 60  
Leu Gln Gly Phe Gln Val Cys His Ser Leu Gly Gly Thr Gly Ser  
65 70 75 80  
Gly Met Gly Thr Leu Leu Ile Ser Lys Ile Arg Glu Glu Tyr Pro Asp  
85 90 95  
Arg Met Met Met Thr Phe Ser Val Phe Leu Leu Leu Arg Ser Leu Thr  
100 105 110  
Leu Leu Leu Ser Ile Xaa Cys Thr Leu Ser Val His Gln Leu Val  
115 120 125

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 667 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..667

(D) OTHER INFORMATION: / Ceres Seq. ID 1498366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

|            |             |            |            |             |             |     |
|------------|-------------|------------|------------|-------------|-------------|-----|
| ctgaaagacc | ctaggctcaa  | ctgggctcag | gctggggctg | gagagaaacg  | attccagact  | 60  |
| gaaggggctg | accataccat  | tttcgtaggt | gaacttggc  | ctgaggtgac  | tgactatatg  | 120 |
| ctctcgga   | cattcaagaa  | tgtgtatggg | tctgtcaaa  | gggctaaagt  | tgtgcttgac  | 180 |
| aggaccactg | gaaggtccaa  | ggggatggg  | tttgttaggt | ttgcggatga  | aaatgagcag  | 240 |
| atgcgtgcc  | tgactgaaat  | gaatggtcaa | tactgtcga  | caagggcctat | gcgtattgggt | 300 |
| ccgggtgcc  | ataagaatgc  | tcttcgatg  | caaccagcta | tgatatcaaaa | cactcaagga  | 360 |
| gcaaatgctg | gagataatga  | tcttaataac | acaacaattt | ttgttgagg   | tctggatgct  | 420 |
| aattgttacg | acgatgaatt  | aaagtcaatt | tttggccaat | tttgtgaact  | tcttcgatg   | 480 |
| aaaatacctc | caggaaaaacg | ttgtggatc  | gttcaaatg  | ccaacaaggc  | gtctgcagag  | 540 |
| catgcacttt | cggtgctgaa  | tggaaacaca | ttaggtggac | aaagcatccg  | tctttcgtgg  | 600 |
| ggacgtagtc | caacaacagca | gtctgatcaa | gcgcaatgga | acgggtggtg  | atataatgga  | 660 |
| taccctc    |             |            |            |             |             |     |

(2) INFORMATION FOR SEQ ID NO:378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..222

(D) OTHER INFORMATION: / Ceres Seq. ID 1498367

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

|                                                                     |  |
|---------------------------------------------------------------------|--|
| Leu Lys Asp Pro Arg Leu Asn Trp Ala Gln Ala Gly Ala Gly Glu Lys     |  |
| 1 5 10 15                                                           |  |
| Arg Phe Gln Thr Glu Gly Pro Asp His Thr Ile Phe Val Gly Asp Leu     |  |
| 20 25 30                                                            |  |
| Ala Pro Glu Val Thr Asp Tyr Met Leu Ser Asp Thr Phe Lys Asn Val     |  |
| 35 40 45 50 55 60                                                   |  |
| Tyr Gly Ser Val Lys Gly Ala Lys Val Val Leu Asp Arg Thr Thr Gly     |  |
| 65 70 75 80                                                         |  |
| Arg Ser Lys Gly Tyr Gly Phe Val Arg Phe Ala Asp Glu Asn Glu Gln     |  |
| Met Arg Ala Met Thr Gly Leu Met Asn Gly Gln Tyr Cys Ser Thr Arg Pro |  |

|                                                                 |     |  |     |  |     |
|-----------------------------------------------------------------|-----|--|-----|--|-----|
|                                                                 | 85  |  | 90  |  | 95  |
| Met Arg Ile Gly Pro Ala Ala Asn Lys Asn Ala Leu Pro Met Gln Pro | 100 |  | 105 |  | 110 |
| Ala Met Tyr Gln Asn Thr Gln Gly Ala Asn Ala Gly Asp Asn Asp Pro | 115 |  | 120 |  | 125 |
| Asn Asn Thr Thr Ile Phe Val Gly Gly Leu Asp Ala Asn Val Thr Asp | 130 |  | 135 |  | 140 |
| Asp Glu Leu Lys Ser Ile Phe Gly Gln Phe Gly Glu Leu Leu His Val | 145 |  | 150 |  | 155 |
| Lys Ile Pro Pro Gly Lys Arg Cys Gly Phe Val Gln Tyr Ala Asn Lys | 165 |  | 170 |  | 175 |
| Ala Ser Ala Glu His Ala Leu Ser Val Leu Asn Gly Thr Gln Leu Gly | 180 |  | 185 |  | 190 |
| Gly Gln Ser Ile Arg Leu Ser Trp Gly Arg Ser Pro Asn Lys Gln Ser | 195 |  | 200 |  | 205 |
| Asp Gln Ala Gln Trp Asn Gly Gly Tyr Tyr Gly Tyr Pro             | 210 |  | 215 |  | 220 |

(2) INFORMATION FOR SEQ ID NO:379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..183

(D) OTHER INFORMATION: / Ceres Seq. ID 1498368

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

|                                                                 |     |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|-----|
| Met Leu Ser Asp Thr Phe Lys Asn Val Tyr Gly Ser Val Lys Gly Ala | 1   | 5   | 10  | 15  |
| Lys Val Val Leu Asp Arg Thr Thr Gly Arg Ser Lys Gly Tyr Gly Phe | 20  | 25  | 30  |     |
| Val Arg Phe Ala Asp Glu Asn Glu Gln Met Arg Ala Met Thr Glu Met | 35  | 40  | 45  |     |
| Asn Gly Gln Tyr Cys Ser Thr Arg Pro Met Arg Ile Gly Pro Ala Ala | 50  | 55  | 60  |     |
| Asn Lys Asn Ala Leu Pro Met Gln Pro Ala Met Tyr Gln Asn Thr Gln | 65  | 70  | 75  | 80  |
| Gly Ala Asn Ala Gly Asp Asn Asp Pro Asn Asn Thr Thr Ile Phe Val | 85  | 90  | 95  |     |
| Gly Gly Leu Asp Ala Asn Val Thr Asp Asp Glu Leu Lys Ser Ile Phe | 100 | 105 | 110 |     |
| Gly Gln Phe Gly Glu Leu Leu His Val Lys Ile Pro Pro Gly Lys Arg | 115 | 120 | 125 |     |
| Cys Gly Phe Val Gln Tyr Ala Asn Lys Ala Ser Ala Glu His Ala Leu | 130 | 135 | 140 |     |
| Ser Val Leu Asn Gly Thr Gln Leu Gly Gly Gln Ser Ile Arg Leu Ser | 145 | 150 | 155 | 160 |
| Trp Gly Arg Ser Pro Asn Lys Gln Ser Asp Gln Ala Gln Trp Asn Gly | 165 | 170 | 175 |     |
| Gly Gly Tyr Tyr Gly Tyr Pro                                     | 180 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..142  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Arg | Ala | Met | Thr | Glu | Met | Asn | Gly | Gln | Tyr | Cys | Ser | Thr | Arg | Pro |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Met | Arg | Ile | Gly | Pro | Ala | Ala | Asn | Lys | Asn | Ala | Leu | Pro | Met | Gln | Pro |  |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |
| Ala | Met | Tyr | Gln | Asn | Thr | Gln | Gly | Ala | Asn | Ala | Gly | Asp | Asn | Asp | Pro |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Asn | Asn | Thr | Thr | Ile | Phe | Val | Gly | Gly | Leu | Asp | Ala | Asn | Val | Thr | Asp |  |
|     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |  |
| Asp | Glu | Leu | Lys | Ser | Ile | Phe | Gly | Gln | Phe | Gly | Glu | Leu | Leu | His | Val |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Lys | Ile | Pro | Pro | Gly | Lys | Arg | Cys | Gly | Phe | Val | Gln | Tyr | Ala | Asn | Lys |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Ala | Ser | Ala | Glu | His | Ala | Leu | Ser | Val | Leu | Asn | Gly | Thr | Gln | Leu | Gly |  |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |  |
| Gly | Gln | Ser | Ile | Arg | Leu | Ser | Trp | Gly | Arg | Ser | Pro | Asn | Lys | Gln | Ser |  |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |  |
| Asp | Gln | Ala | Gln | Trp | Asn | Gly | Gly | Gly | Tyr | Tyr | Gly | Tyr | Pro |     |     |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1125 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1125  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

|             |             |             |            |            |            |      |
|-------------|-------------|-------------|------------|------------|------------|------|
| agttgaaatt  | ccacaagcaa  | ccagtcacgc  | cgtcccatct | cacaagcgac | ctgaagcagt | 60   |
| tactaagcgg  | tgattcagct  | ggacagttac  | tttcatggac | agtaccagat | gagacattaa | 120  |
| gagcttcaat  | gaacacaagct | tcattataaac | aggcttcatt | aaacaggctt | tcactgaaac | 180  |
| aggcttcac   | ggtttagaat  | ccaaagcaga  | gaccagtaaa | tccccttttg | gtttctctga | 240  |
| ctagaaatga  | aagagctggc  | cagggaactt  | aaggacagga | ccacgtagga | ggaagcagac | 300  |
| caaagtctga  | acatagtgtt  | gtctccgaaa  | gagagtata  | cgagccactc | tcaactctgc | 360  |
| ttgttggtg   | agttttcagg  | tttgagaagg  | agaaggagaa | gagggttggt | ttgagaattt | 420  |
| gtgtaaatag  | atgaaaagat  | tacaagcttt  | ttacagggaa | gtgtgtgtac | tgtgtacagt | 480  |
| attgtatttt  | tgccgctctc  | ttttttgtat  | tccttacgta | aaattatttc | ctacacaaaa | 540  |
| ttcccactca  | ccacacacaa  | caaaagaata  | gtgatcgaag | ctcatggcgt | ctcttgtaac | 600  |
| cgtcgccgct  | gtgaaacccat | ccgcgcgcct  | aaaaggactc | ggcggcagct | cactcgccgg | 660  |
| agctaaagctc | tcctatcaagc | cttcgccgct  | gagctttaaa | cccaaatcca | tccgggctaa | 720  |
| tggtgtggtg  | gctaagtatg  | gagacaaaag  | tgctactttt | gacttagaag | atttgggtaa | 780  |
| cacaacaggt  | caatgggaagc | tatacggtc   | tgatgctcct | ttctcttaca | atctctttca | 840  |
| gagcaagtcc  | tttgagacat  | tcgctgcccc  | attcacaaag | agaggattgc | tcctcaagtt | 900  |
| cttgatcctt  | ggaggaggct  | ctttgcttac  | ttatgtcagc | gctacctcta | ccggcggaag | 960  |
| tcttcccatc  | aagagaggtc  | ctcaggagcc  | gcctaagctc | ggctcctcgc | gcaagctctg | 1020 |
| atctatattc  | atgtttacctt | tcctcttctc  | cttctaaaa  | tcataaacat | ttctcaatac | 1080 |
| tgcaaacctt  | tttaagtaat  | tttatgtata  | ttatgtttat | ctgttt     |            |      |

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..145  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498371

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

Met Ala Ser Leu Ala Thr Val Ala Ala Val Lys Pro Ser Ala Ala Ile  
1 5 10 15  
Lys Gly Leu Gly Gly Ser Ser Leu Ala Gly Ala Lys Leu Ser Ile Lys  
20 25 30  
Pro Ser Arg Leu Ser Phe Lys Pro Lys Ser Ile Arg Ala Asn Gly Val  
35 40 45  
Val Ala Lys Tyr Gly Asp Lys Ser Val Tyr Phe Asp Leu Glu Asp Leu  
50 55 60  
Gly Asn Thr Thr Gly Gln Trp Asp Val Tyr Gly Ser Asp Ala Pro Ser  
65 70 75 80  
Pro Tyr Asn Pro Leu Gln Ser Lys Phe Phe Glu Thr Phe Ala Ala Pro  
85 90 95  
Phe Thr Lys Arg Gly Leu Leu Leu Lys Phe Leu Ile Leu Gly Gly Gly  
100 105 110  
Ser Leu Leu Thr Tyr Val Ser Ala Thr Ser Thr Gly Glu Val Leu Pro  
115 120 125  
Ile Lys Arg Gly Pro Gln Glu Pro Pro Lys Leu Gly Pro Arg Gly Lys  
130 135 140

Leu  
145

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1112 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1112  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

aagggtatgac tcaatcttca cttagttggt gaatttagtt ctgactctta ttagattgta 60  
gtctctggcct ttgtagatat gctatagtta ctggaggaggaa tagaggaatt ggatttgaga 120  
tatgcagaca attagcaaac aaaggggatta gggttatttt gacatctaga gatgagaaac 180  
aaaggccttga agctgttgag acattgaaga aaagagcttga gatttctgat caaagcattg 240  
tcctttcatca gcttgatgtc tctgatcctt ctagtgtcac ttctcttgct aagtttgtga 300  
aaacccattt cgggaaactc gatattcttga tcaataatgc tgggggttgg ggtgtaatca 360  
ctgatgttga tgctctttaga gctgggacag ggaagaaggg ttccaagtgg gaggaacta 420  
tcaactgagac ttaatgagta gctgaagaat gcataaagat taactattat ggaccaaaaga 480  
gaatgtgtga ggcttttatt catcttctgc agttatctaa ttctccaaga atcgttaatg 540  
tatcatcctt catgggtcaa gtaaagaatt tactaaaacga atgggcaaaa gggactccta 600  
gtgacgcaga gaactcaacg gaggttaagaa ttgaccaagt gatcaaccaa ctctctcaatg 660  
atctgaagaa agatacggct aagacaaaag attgggctaa agtcatgtcg gttacgttg 720  
tttcgaagcg cggtttgaat gcttacacga ggatcttagc gaagaaacat cccgagattc 780  
gcgtttaact gggtttgctc gatgttgtag agactgatat gaatyttaaa atctggaatt 840  
tatctgttga agaagagagca tcaagtctcg tgaggttagc ttgtctcca catcaagaat 900  
ctcctctcgg ttgtttcttt gatgcgcaaac aagtttcaga gttctgaaat ctttgtgtgg 960  
agatagataa gccaaagttt tattcatgta atgagaatta ttgtttgaaa gctaaacaga 1020  
aagtatcgac tattcaataa acagaaacat tattaagcct taaaaaaaaa aaaaaaaaaa 1080  
aaaaaaaaa aaaaaaaaaa attkttcccc cc

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1498380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

```
Met Cys Glu Ala Phe Ile His Leu Leu Gln Leu Ser Asn Ser Pro Arg
1 5 10 15
Ile Val Asn Val Ser Ser Phe Met Gly Gln Val Lys Asn Leu Asn
20 25 30
Glu Trp Ala Lys Gly Ile Leu Ser Asp Ala Glu Asn Leu Thr Glu Val
35 40 45
Arg Ile Asp Gln Val Ile Asn Gln Leu Leu Asn Asp Leu Lys Glu Asp
50 55 60
Thr Ala Lys Thr Lys Asp Trp Ala Lys Val Met Ser Ala Tyr Val Val
65 70 75 80
Ser Lys Ala Gly Leu Asn Ala Tyr Thr Arg Ile Leu Ala Lys Lys His
85 90 95
Pro Glu Ile Arg Val Asn Ser Val Cys Pro Gly Phe Val Lys Thr Asp
100 105 110
Met Asn Xaa Lys Thr Gly Ile Leu Ser Val Glu Gly Ala Ser Ser
115 120 125
Pro Val Arg Leu Ala Leu Leu Pro His Gln Glu Ser Pro Ser Gly Cys
130 135 140
Phe Phe Asp Arg Lys Gln Val Ser Glu Phe
145 150
```

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..131

(D) OTHER INFORMATION: / Ceres Seq. ID 1498381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

```
Met Gly Gln Val Lys Asn Leu Leu Asn Glu Trp Ala Lys Gly Ile Leu
1 5 10 15
Ser Asp Ala Glu Asn Leu Thr Glu Val Arg Ile Asp Gln Val Ile Asn
20 25 30
Gln Leu Leu Asn Asp Leu Lys Glu Asp Thr Ala Lys Thr Lys Asp Trp
35 40 45
Ala Lys Val Met Ser Ala Tyr Val Val Ser Lys Ala Gly Leu Asn Ala
50 55 60
Tyr Thr Arg Ile Leu Ala Lys Lys His Pro Glu Ile Arg Val Asn Ser
65 70 75 80
Val Cys Pro Gly Phe Val Lys Thr Asp Met Asn Xaa Lys Thr Gly Ile
85 90 95
Leu Ser Val Glu Glu Gly Ala Ser Ser Pro Val Arg Leu Ala Leu Leu
100 105 110
Pro His Gln Glu Ser Pro Ser Gly Cys Phe Phe Asp Arg Lys Gln Val
115 120 125
Ser Glu Phe
130
```

(2) INFORMATION FOR SEQ ID NO:386:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..80  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1498382  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:  
Met Ser Ala Tyr Val Val Ser Lys Ala Gly Leu Asn Ala Tyr Thr Arg  
1                    5                    10                    15  
Ile Leu Ala Lys Lys His Pro Glu Ile Arg Val Asn Ser Val Cys Pro  
                    20                    25                    30  
Gly Phe Val Lys Thr Asp Met Asn Xaa Lys Thr Gly Ile Leu Ser Val  
                    35                    40                    45  
Glu Glu Gly Ala Ser Ser Pro Val Arg Leu Ala Leu Pro His Gln  
                    50                    55                    60  
Glu Ser Pro Ser Gly Cys Phe Phe Asp Arg Lys Gln Val Ser Glu Phe  
65                    70                    75                    80

(2) INFORMATION FOR SEQ ID NO:387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1211 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1211

(D) OTHER INFORMATION: / Ceres Seq. ID 1498383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

|             |             |            |             |             |             |      |
|-------------|-------------|------------|-------------|-------------|-------------|------|
| cttttgccct  | cactcaattg  | tctttttcaa | tttcgcccac  | gacgaatccg  | acgtcagtaa  | 60   |
| cttccgaccg  | cagtttccga  | aactcgtgat | cgcttttctc  | ttcgaataatg | ttggcgctcg  | 120  |
| tacgggtgaa  | tcagctgcaa  | agacttcttc | tctotgctcg  | tcgattatct  | tcttacccaa  | 180  |
| taaatcctcc  | gtcgcgttta  | cttcaccagc | ggctatttct  | gaactcagac  | actgatgctt  | 240  |
| cggtgcctac  | tttttttctc  | tcgcatccga | aaatacaaac  | gcttgaaggc  | aaagcttcta  | 300  |
| ataaaagccg  | aagcacatcg  | tcaacaacat | ctttgaatga  | agatgaactt  | gccaaattct  | 360  |
| ctgcatttgc  | tcataacctg  | tggcattctg | aaggaccctt  | taaaccgttg  | catcaaatga  | 420  |
| atccaaactc  | gttggctttc  | atccgcctga | ccttatgcag  | gcacttcagt  | aaggatccga  | 480  |
| gtttctgtaa  | gccttttygam | ggactgaaat | ttatcgatat  | aggttgccgt  | ggcggactac  | 540  |
| tttctgagcc  | tctagcacg   | atgggagcaa | ctgtcacagg  | agttgatgct  | gttgataaga  | 600  |
| atgtcaaaat  | tgcctgcttt  | cacgctgata | tggatccagt  | gacttcaacg  | attgaatact  | 660  |
| tatgtactac  | acgagaaaag  | ctagcggatg | aaggcaggaa  | gtttgatgct  | gtcttttctt  | 720  |
| tagaggtgat  | cgagcatgta  | gcaaaacctg | cagagttctg  | taagtcgttg  | tcagcatgta  | 780  |
| ctatccccaa  | cggggctaca  | gtactttcta | caatcaatcg  | cactatgcga  | gcataatgat  | 840  |
| caaccattgt  | tggagcagag  | tacattctca | gttggcttcc  | taaaggcaca  | caccagtggt  | 900  |
| caagttttgt  | aactcctgaa  | gaatgatgta | tgatattaca  | acgtgcttca  | gtcgtatgta  | 960  |
| aagagatagc  | tggatttgtg  | tacaacccaa | taacaggagag | atgggtattg  | tcagatgata  | 1020 |
| ttagtgtcaa  | ctatattgct  | tatgggacga | aaaggaagga  | tcttgagagc  | atataatacaa | 1080 |
| ctgtttccaa  | tcgtgtttct  | ctgcataatc | gcttctgagt  | tataactcta  | gttcatgctt  | 1140 |
| gaaaaaactag | gtactctgga  | agttgcttag | gacgaggaca  | gtagttgttt  | tgcaataaagt | 1200 |

gagaaacatt c

(2) INFORMATION FOR SEQ ID NO:388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..322

(D) OTHER INFORMATION: / Ceres Seq. ID 1498384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

```
Met Leu Ala Ser Val Arg Val Asn Gln Leu Gln Arg Leu Leu Leu Ser
1 5 10 15
Ala Arg Arg Leu Ser Ser Ser Pro Ile Ile Pro Pro Ser Arg Leu Leu
20 25 30
His Gln Arg Leu Phe Ser Thr Ser Asp Thr Asp Ala Ser Ala Ala Ser
35 40 45
Phe Ser Ser Ser His Pro Lys Ile Gln Thr Leu Glu Gly Lys Ala Ser
50 55 60
Asn Lys Ser Arg Ser Thr Ser Ser Thr Thr Ser Leu Asn Glu Asp Glu
65 70 75 80
Leu Ala Lys Phe Ser Ala Ile Ala His Thr Trp Trp His Ser Glu Gly
85 90 95
Pro Phe Lys Pro Leu His Gln Met Asn Pro Thr Arg Leu Ala Phe Ile
100 105 110
Arg Ser Thr Leu Cys Arg His Phe Ser Lys Asp Pro Ser Ser Ala Lys
115 120 125
Pro Xaa Xaa Gly Leu Lys Phe Ile Asp Ile Gly Cys Gly Gly Gly Leu
130 135 140
Leu Ser Glu Pro Leu Ala Arg Met Gly Ala Thr Val Thr Gly Val Asp
145 150 155 160
Ala Val Asp Lys Asn Val Lys Ile Ala Arg Leu His Ala Asp Met Asp
165 170 175
Pro Val Thr Ser Thr Ile Glu Tyr Leu Cys Thr Thr Ala Glu Lys Leu
180 185 190
Ala Asp Glu Gly Arg Lys Phe Asp Ala Val Leu Ser Leu Glu Val Ile
195 200 205
Glu His Val Ala Asn Pro Ala Glu Phe Cys Lys Ser Leu Ser Ala Leu
210 215 220
Thr Ile Pro Asn Gly Ala Thr Val Leu Ser Thr Ile Asn Arg Thr Met
225 230 235 240
Arg Ala Tyr Ala Ser Thr Ile Val Gly Ala Glu Tyr Ile Leu Arg Trp
245 250 255
Leu Pro Lys Gly Thr His Gln Trp Ser Ser Phe Val Thr Pro Glu Glu
260 265 270
Met Ser Met Ile Leu Gln Arg Ala Ser Val Asp Val Lys Glu Ile Ala
275 280 285
Gly Phe Val Tyr Asn Pro Ile Thr Gly Arg Trp Leu Leu Ser Asp Asp
290 295 300
Ile Ser Val Asn Tyr Ile Ala Tyr Gly Thr Lys Arg Lys Asp Leu Gly
305 310 315 320
Asp Ile
```

(2) INFORMATION FOR SEQ ID NO:389:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..219

(D) OTHER INFORMATION: / Ceres Seq. ID 1498385

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

```
Met Asn Pro Thr Arg Leu Ala Phe Ile Arg Ser Thr Leu Cys Arg His
1 5 10 15
Phe Ser Lys Asp Pro Ser Ser Ala Lys Pro Xaa Xaa Gly Leu Lys Phe
20 25 30
```



```

Ile Asp Ile Gly Cys Gly Gly Gly Leu Leu Ser Glu Pro Leu Ala Arg
 35 40 45
Met Gly Ala Thr Val Thr Gly Val Asp Ala Val Asp Lys Asn Val Lys
 50 55 60
Ile Ala Arg Leu His Ala Asp Met Asp Pro Val Thr Ser Thr Ile Glu
 65 70 75 80
Tyr Leu Cys Thr Thr Ala Glu Lys Leu Ala Asp Glu Gly Arg Lys Phe
 85 90 95
Asp Ala Val Leu Ser Leu Glu Val Ile Glu His Val Ala Asn Pro Ala
 100 105 110
Glu Phe Cys Lys Ser Leu Ser Ala Leu Thr Ile Pro Asn Gly Ala Thr
 115 120 125
Val Leu Ser Thr Ile Asn Arg Thr Met Arg Ala Tyr Ala Ser Thr Ile
 130 135 140
Val Gly Ala Glu Tyr Ile Leu Arg Trp Leu Pro Lys Gly Thr His Gln
 145 150 155 160
Trp Ser Ser Phe Val Thr Pro Glu Glu Met Ser Met Ile Leu Gln Arg
 165 170 175
Ala Ser Val Asp Val Lys Glu Ile Ala Gly Phe Val Tyr Asn Pro Ile
 180 185 190
Thr Gly Arg Trp Leu Leu Ser Asp Asp Ile Ser Val Asn Tyr Ile Ala
 195 200 205
Tyr Gly Thr Lys Arg Lys Asp Leu Gly Asp Ile
 210 215

```

(2) INFORMATION FOR SEQ ID NO:390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..171
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498386

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

```

Met Gly Ala Thr Val Thr Gly Val Asp Ala Val Asp Lys Asn Val Lys
 1 5 10 15
Ile Ala Arg Leu His Ala Asp Met Asp Pro Val Thr Ser Thr Ile Glu
 20 25 30
Tyr Leu Cys Thr Thr Ala Glu Lys Leu Ala Asp Glu Gly Arg Lys Phe
 35 40 45
Asp Ala Val Leu Ser Leu Glu Val Ile Glu His Val Ala Asn Pro Ala
 50 55 60
Glu Phe Cys Lys Ser Leu Ser Ala Leu Thr Ile Pro Asn Gly Ala Thr
 65 70 75 80
Val Leu Ser Thr Ile Asn Arg Thr Met Arg Ala Tyr Ala Ser Thr Ile
 85 90 95
Val Gly Ala Glu Tyr Ile Leu Arg Trp Leu Pro Lys Gly Thr His Gln
 100 105 110
Trp Ser Ser Phe Val Thr Pro Glu Glu Met Ser Met Ile Leu Gln Arg
 115 120 125
Ala Ser Val Asp Val Lys Glu Ile Ala Gly Phe Val Tyr Asn Pro Ile
 130 135 140
Thr Gly Arg Trp Leu Leu Ser Asp Asp Ile Ser Val Asn Tyr Ile Ala
 145 150 155 160
Tyr Gly Thr Lys Arg Lys Asp Leu Gly Asp Ile
 165 170

```

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1397 base pairs

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1397

(D) OTHER INFORMATION: / Ceres Seq. ID 1498387

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| aaaaaatatt  | tatgttgggt  | caggcttaaa  | ccagagagag  | actgtgtgtg  | gtcgagccat  | 60   |
| ttgaccacaa  | gcacaaactt  | aaaactgggt  | tcagatctga  | agtaaaaggg  | ttttgtctcg  | 120  |
| gattctccgg  | cgctgcttaa  | atgatctctg  | accatctctc  | cttggctctaa | taattctgtg  | 180  |
| ccctcctttt  | atctcttttt  | actgttgatt  | tatctgaata  | tgccacgctc  | ttctctccac  | 240  |
| atgtttatct  | tcctcttcct  | tcttcaacac  | aagcgtctgg  | actaagaaaa  | gcacacacaa  | 300  |
| aaatctgggt  | tcaagcaggt  | tggcaggagt  | ttgtcaaccg  | ttctccatt   | cggattgggt  | 360  |
| tcagatacaa  | agttacagtc  | tacattttca  | atttatctct  | cacactctga  | gatcaaccac  | 420  |
| cattctagta  | gtgaagctct  | tatgcacagt  | gattccgcac  | agaatcagtt  | caacaaacgt  | 480  |
| gctcgattgt  | ttgaagatcc  | tgaactcaaa  | gatgctaagg  | tcatttatcc  | atcgaaacct  | 540  |
| gaatctactg  | aaccagtgaa  | taaaggttat  | ggcggttcta  | cagccatcca  | aagctttttc  | 600  |
| aaagaatacta | aagctgaaga  | aacgcccaag  | gtacttaaga  | agagagggaag | gaagaagaag  | 660  |
| aatctctaact | ccgagggaagt | aaactcttca  | actcccggtg  | gagatgactc  | agagaaaccgc | 720  |
| tcaaaagtctc | acgagagtgc  | ttctgctaga  | aagagaactg  | taactgcaga  | ggaagagagag | 780  |
| agagccgctga | atgcagccaa  | aacattcgaa  | ccaacaaatc  | ctttacttta  | gagttgttct  | 840  |
| gcgaccatca  | tatctataca  | gaggttgcat  | catgtactgt  | ccatctgggt  | ttgtgagaaa  | 900  |
| atactctaa   | gggatatctg  | gtttcatcaa  | gcctccagctc | ggtagagaac  | aatggccagt  | 960  |
| gaggtgcctc  | tacaaagcag  | ggagagctaa  | gtttagccaa  | ggatggatag  | agttcacact  | 1020 |
| cgagaacaat  | ataggcgaag  | gagatgtatg  | tgtgtttgag  | ctactcagaa  | ctcgggattt  | 1080 |
| cgttctcgaa  | gtcaaccgct  | ttcgtgtcaa  | tgagtatgtg  | tgacaaaaaa  | agatttccct  | 1140 |
| ttcatcagcg  | atcttgcagg  | tagctttcca  | aagttaaaat  | ttatgtaggg  | ggtctcttaa  | 1200 |
| ccattctctc  | ttctgcattg  | gttgctctctg | ttctagtagt  | gttttgagtg  | aaatttcagg  | 1260 |
| ttctatgttt  | tggatgtgga  | taagtatttg  | acgattataa  | taacctctga  | gtgaaaacct  | 1320 |
| ttgtttgag   | tgttagctag  | gttcaaaagt  | agagttgtat  | atacttttat  | cttcatcagg  | 1380 |
| ataattatgt  | ttatttgg    |             |             |             |             |      |

- (2) INFORMATION FOR SEQ ID NO:392:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..129

(D) OTHER INFORMATION: / Ceres Seq. ID 1498388

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Gln | Met | Asp | Ser | Ala | Gln | Asn | Gln | Phe | Asn | Lys | Arg | Ala | Arg | Leu |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |  |
| Phe | Glu | Asp | Pro | Glu | Leu | Lys | Asp | Ala | Lys | Val | Ile | Tyr | Pro | Ser | Asn |  |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |  |
| Pro | Glu | Ser | Thr | Glu | Pro | Val | Asn | Lys | Gly | Tyr | Gly | Gly | Ser | Thr | Ala |  |
|     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |  |
| Ile | Gln | Ser | Phe | Phe | Lys | Glu | Ser | Lys | Ala | Glu | Glu | Thr | Pro | Lys | Val |  |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     |     | 60  |  |
| Leu | Lys | Lys | Arg | Gly | Arg | Lys | Lys | Lys | Asn | Pro | Asn | Pro | Glu | Glu | Val |  |
|     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     |     | 75  |  |
| Asn | Ser | Ser | Thr | Pro | Gly | Gly | Asp | Asp | Ser | Glu | Asn | Arg | Ser | Lys | Phe |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |  |
| Tyr | Glu | Ser | Ala | Ser | Ala | Arg | Lys | Arg | Thr | Val | Thr | Ala | Glu | Glu | Arg |  |
|     |     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |  |
| Glu | Arg | Ala | Val | Asn | Ala | Ala | Lys | Thr | Phe | Glu | Pro | Thr | Asn | Pro | Leu |  |
|     |     |     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |  |

Leu

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..127
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Ser | Ala | Gln | Asn | Gln | Phe | Asn | Lys | Arg | Ala | Arg | Leu | Phe | Glu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Asp | Pro | Glu | Leu | Lys | Asp | Ala | Lys | Val | Ile | Tyr | Pro | Ser | Asn | Pro | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Thr | Glu | Pro | Val | Asn | Lys | Gly | Tyr | Gly | Gly | Ser | Thr | Ala | Ile | Gln |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Phe | Phe | Lys | Glu | Ser | Lys | Ala | Glu | Glu | Thr | Pro | Lys | Val | Leu | Lys |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Arg | Gly | Arg | Lys | Lys | Lys | Asn | Pro | Asn | Pro | Glu | Glu | Val | Asn | Ser |
|     |     |     | 65  |     |     | 70  |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Thr | Pro | Gly | Gly | Asp | Asp | Ser | Glu | Asn | Arg | Ser | Lys | Phe | Tyr | Glu |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ser | Ala | Ser | Ala | Arg | Lys | Arg | Thr | Val | Thr | Ala | Glu | Glu | Arg | Glu | Arg |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Ala | Val | Asn | Ala | Ala | Lys | Thr | Phe | Glu | Pro | Thr | Asn | Pro | Leu | Leu |     |
|     |     |     | 115 |     |     | 120 |     |     |     |     |     |     | 125 |     |     |

(2) INFORMATION FOR SEQ ID NO:394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1498390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Pro | Lys | His | Ser | Asn | Gln | Gln | Ile | Leu | Tyr | Phe | Arg | Val | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Arg | Pro | Ser | Tyr | Leu | Tyr | Arg | Gly | Cys | Ile | Met | Tyr | Leu | Pro | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Phe | Ala | Glu | Lys | Tyr | Leu | Ser | Gly | Ile | Ser | Gly | Phe | Ile | Lys | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Leu | Gly | Glu | Lys | Gln | Trp | Pro | Val | Arg | Cys | Leu | Tyr | Lys | Ala | Gly |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Ala | Lys | Phe | Ser | Gln | Gly | Trp | Tyr | Glu | Phe | Thr | Leu | Glu | Asn | Asn |
|     |     |     | 65  |     |     | 70  |     |     | 75  |     |     |     |     | 80  |     |
| Ile | Gly | Glu | Gly | Asp | Val | Cys | Val | Phe | Glu | Leu | Leu | Arg | Thr | Arg | Asp |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Phe | Val | Leu | Glu | Val | Thr | Ala | Phe | Arg | Val | Asn | Glu | Tyr | Val |     |     |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |

(2) INFORMATION FOR SEQ ID NO:395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1267

(D) OTHER INFORMATION: / Ceres Seq. ID 1498391

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

|             |            |             |             |            |            |      |
|-------------|------------|-------------|-------------|------------|------------|------|
| atctatcttt  | aaaaacatac | ttgaaaatgc  | aaggaacgat  | ttcttgtgca | agaaattata | 60   |
| acatgacgac  | aaccgtcggg | gaatctctgc  | ggccgctatc  | gcttaaaacg | cagggaaacg | 120  |
| gcgagagagt  | tcggatgggt | gtggaggaga  | acgcggtgat  | tgtgattgga | cggagaggat | 180  |
| gttgcatgtg  | tcatgtgggt | aggagcgctc  | ttcttggaat  | tggagtgaat | ccggcggtcc | 240  |
| ttgagattga  | tgaggagagg | gaagatgaag  | ttttgagtga  | gttggagatt | attggagttc | 300  |
| aaggcgccgg  | aggtacgggt | aagttaccgg  | cggtttatgt  | aggaggaggg | aaaaaaaaaa | 360  |
| actcagagag  | acaaatctaa | atggcgatga  | ttacgcgcaa  | caccgccacg | cgctccctcc | 420  |
| tcctcctcca  | atctcaacgc | gcgctgcgcg  | ctgcctcggt  | ctctcacctc | cacacatccc | 480  |
| ttcccgctct  | ctctcctctc | acatcaccca  | cttccataac  | cagacctggg | ctctctcgca | 540  |
| ctccctctcc  | tcctctcggt | ctctctaaag  | cgcccggaat  | tgtgatctcc | aaggtatgat | 600  |
| ctcatgaact  | gggctcgtag | cggatcgatc  | tggccataga  | cctttgggtc | cgcttggctc | 660  |
| gccgtcgaaa  | tgatgcatac | cggtgctgct  | cgctacgata  | tcgatcgatt | cggtatcctc | 720  |
| ttcaggcgca  | gtcctcgcca | gtctgattgt  | atgattgtcg  | ccggtactct | taccaataag | 780  |
| atggctccgg  | ctcttcgcaa | ggtttatgac  | cagatgcctg  | agccaaagtg | ggtgatttca | 840  |
| atgggaagtt  | gtgccaatgg | atgtggatac  | tatcaactact | cctactcggt | ggttcgagga | 900  |
| tgtgacagaa  | tgtctcccat | cgacataatac | gtcccggggt  | gccaccaaac | cgctgagggt | 960  |
| ttgctctatg  | gactactcca | gcttcagaag  | aaaatacaaca | ggcgaagaa  | tttcttgcat | 1020 |
| tgttggaaca  | agtgagcttc | gaaccgcgtc  | tccaatcgtg  | aaagggaact | ttttcagaca | 1080 |
| gttttaccaca | agttttgggg | ataataaatc  | gtggacgttt  | catgtcatat | ttctttgtgg | 1140 |
| tggagatgcc  | atgtaaaagg | gtgtgtttct  | aagtttgttg  | tggaaactta | ataaacttaa | 1200 |
| gatgtttgtt  | gtctgagttc | ttttatgggc  | ttctttatta  | tatatctctc | tctaccagtt | 1260 |
| ttcagcc     |            |             |             |            |            |      |

- (2) INFORMATION FOR SEQ ID NO:396:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1498392

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ser | Leu | Lys | Thr | Thr | Leu | Lys | Met | Gln | Gly | Thr | Ile | Ser | Cys | Ala |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Arg | Asn | Tyr | Asn | Met | Thr | Thr | Thr | Val | Gly | Glu | Ser | Leu | Arg | Pro | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Ser | Leu | Lys | Thr | Gln | Gly | Asn | Gly | Glu | Arg | Val | Arg | Met | Val | Val | Glu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Asn | Ala | Val | Ile | Val | Ile | Gly | Arg | Arg | Gly | Cys | Cys | Met | Cys | His |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Val | Val | Arg | Arg | Leu | Leu | Gly | Gly | Val | Asn | Pro | Ala | Val | Leu |     |     |
|     |     |     | 65  |     |     | 70  |     | 75  |     |     |     |     | 80  |     |     |
| Glu | Ile | Asp | Glu | Glu | Arg | Glu | Asp | Glu | Val | Leu | Ser | Glu | Leu | Glu | Asn |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ile | Gly | Val | Gln | Gly | Gly | Gly | Gly | Thr | Val | Lys | Leu | Pro | Ala | Val | Thr |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Val | Gly | Gly | Arg | Lys | Lys | Lys | Asn | Ser | Glu | Arg | Gln | Ile |     |     |     |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

- (2) INFORMATION FOR SEQ ID NO:397:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..143  
(D) OTHER INFORMATION: / Ceres Seq. ID 1498393  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:  
Met Asn Trp Ala Arg Thr Gly Ser Ile Trp Pro Met Thr Phe Gly Leu  
1 5 10 15  
Ala Cys Cys Ala Val Glu Met Met His Thr Gly Ala Ala Arg Tyr Asp  
20 25 30  
Leu Asp Arg Phe Gly Ile Ile Phe Arg Pro Ser Pro Arg Gln Ser Asp  
35 40 45  
Cys Met Ile Val Ala Gly Thr Leu Thr Asn Lys Met Ala Pro Ala Leu  
50 55 60  
Arg Lys Val Tyr Asp Gln Met Pro Glu Pro Arg Trp Val Ile Ser Met  
65 70 75 80  
Gly Ser Cys Ala Asn Gly Cys Gly Tyr Tyr His Tyr Ser Tyr Ser Val  
85 90 95  
Val Arg Gly Cys Asp Arg Ile Val Pro Val Asp Ile Tyr Val Pro Gly  
100 105 110  
Cys Pro Pro Thr Ala Glu Ala Leu Leu Tyr Gly Leu Leu Gln Leu Gln  
115 120 125  
Lys Lys Ile Asn Arg Arg Lys Asp Phe Leu His Trp Trp Asn Lys  
130 135 140

(2) INFORMATION FOR SEQ ID NO:398:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1498394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

Met Thr Phe Gly Leu Ala Cys Cys Ala Val Glu Met Met His Thr Gly  
1 5 10 15  
Ala Ala Arg Tyr Asp Leu Asp Arg Phe Gly Ile Ile Phe Arg Pro Ser  
20 25 30  
Pro Arg Gln Ser Asp Cys Met Ile Val Ala Gly Thr Leu Thr Asn Lys  
35 40 45  
Met Ala Pro Ala Leu Arg Lys Val Tyr Asp Gln Met Pro Glu Pro Arg  
50 55 60  
Trp Val Ile Ser Met Gly Ser Cys Ala Asn Gly Cys Gly Tyr Tyr His  
65 70 75 80  
Tyr Ser Tyr Ser Val Val Arg Gly Cys Asp Arg Ile Val Pro Val Asp  
85 90 95  
Ile Tyr Val Pro Gly Cys Pro Pro Thr Ala Glu Ala Leu Leu Tyr Gly  
100 105 110  
Leu Leu Gln Leu Gln Lys Lys Ile Asn Arg Arg Lys Asp Phe Leu His  
115 120 125  
Trp Trp Asn Lys  
130

(2) INFORMATION FOR SEQ ID NO:399:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2084 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..2084

(D) OTHER INFORMATION: / Ceres Seq. ID 1498395

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| aagcaactctt | ctctccgctt  | cgtaaagtcc  | gccgaaaaa   | acccaaatcct | tcactactct  | 60   |
| gtctcagctgt | tcgacctctc  | tcttctcatt  | cctttgcaac  | ttctcacttc  | tcgaattctct | 120  |
| ttctcttcaa  | atcagaaaatg | gtctcaagtgg | ttgctaccag  | gtcaattcaa  | ggctcgtagt  | 180  |
| tattctcccaa | cggtggatct  | gtgtctacaa  | gatccgagaa  | gctattgaaa  | ccagcgagtt  | 240  |
| ttgcagttaa  | gggtttgtga  | aacgaagcaa  | agagaagtgt  | aagagctctc  | tgtaagaagc  | 300  |
| agaagaggtg  | gttgatactc  | ctgtgagatc  | cgctcagatt  | gagactgaag  | tcattctctg  | 360  |
| ttctcttgaa  | gatgtgccta  | acagagagga  | gcagcgtgag  | aggtgtgtgg  | aaatcgacga  | 420  |
| gtttggtgat  | acatcggtag  | ggatgtggtc  | gaagccgaca  | gtgaggagga  | agacaaagat  | 480  |
| tgtttgcacc  | gtttggtcgt  | cgaccaacac  | acgagaaaatg | atatggaaaat | tggctgaagc  | 540  |
| tgggattgaa  | gttgctagga  | tgaatatgtc  | tcattggagat | catgcttcac  | ataagaaggt  | 600  |
| tattgatttg  | gttaaagaat  | acaatgcaca  | aactaaagac  | aacactattg  | ctatcatgct  | 660  |
| tgacaccaa   | ggctccgaag  | ttaggagttg  | agattttacct | cagccaatta  | tgtagatcc   | 720  |
| tggtcaagag  | tttaccctta  | caattgagag  | aggagtcagc  | acaccaagtt  | gtgtcagttg  | 780  |
| taactatgat  | gatttcgtta  | atgacgtgga  | agcgggtgac  | atgcttcttg  | ttgatgtgtg  | 840  |
| tatgatgtcg  | tttatgtgtg  | agtcaaaagc  | caaagactct  | gtcaaatgtg  | aagttgttga  | 900  |
| tggtgtgaaa  | cttgatctca  | ggagacacct  | gaatgtccga  | ggaaaagagt  | caacttaacc  | 960  |
| ttcaatcact  | gagaaggatt  | gggaggatat  | taaatttggg  | gtggagaaaca | aagttgactt  | 1020 |
| ttatgcagtt  | tcctttgtca  | aagatgctca  | agttgtacac  | gagttgaaga  | ataaccttca  | 1080 |
| aaatagttgt  | gctgatatac  | acgtgatagt  | gaaaaattgag | agtgcgagact | ccatacctaa  | 1140 |
| cttgcaactcc | attatcacag  | catcagatgg  | ggcaatggtt  | gcaagaggtg  | atcttgggtc  | 1200 |
| agagcttcca  | attgaagaag  | ttcccatctc  | tcaggaggag  | atcattaaac  | ttgtccgttag | 1260 |
| tttggtgaaa  | gctgtttatt  | ttgcgactaa  | catgcttgag  | agtatgatag  | ttcatccaac  | 1320 |
| ttcaacccgg  | gcagaggtct  | cagacattgc  | tatcgctgtt  | agagaaggtg  | ctgatcggtg  | 1380 |
| aatgctttcca | ggagaaaactg | ctcaccgaaa  | gttcccatgt  | aaagctgctg  | gagtgatgca  | 1440 |
| cactgtttgca | ttgtcgaacag | aagcaacocat | tactagcggt  | gaaaatgccac | ctaatctgtg  | 1500 |
| tcaagccttc  | aagaaccata  | tgagtgtgat  | gtttgcatac  | catgcaacca  | tgatgtcaaa  | 1560 |
| cacaacttga  | aactcaactg  | ttgtcttcac  | cagaaccggt  | ttcatggcca  | tattgttaag  | 1620 |
| tcactactgt  | cttcccgcca  | caatctatgc  | cttcacaaat  | gagaaaaaaa  | tacaacaaag  | 1680 |
| attagctttg  | tatcaaggtg  | tatgccccat  | atatatggag  | ttcacagatg  | atgcagaaga  | 1740 |
| aactttttgt  | aatgcttttg  | ctacattact  | gaacaaagga  | atggtgaaga  | agggagagga  | 1800 |
| aatagcaatc  | gtacagagcg  | gtacacagcc  | aatctggcga  | ttctcaatga  | catataaact  | 1860 |
| ccaagtccgc  | aaggtttttaa | gcttctttta  | agatgggatg  | ttcttaatat  | gtagaacctc  | 1920 |
| gtttttgtgt  | ataattttgc  | ttgcatgtct  | ctcttctctc  | gtactattca  | cacttgtgtg  | 1980 |
| ttgtgtatcc  | ttctcttcca  | gtttgctttg  | ctacgattgt  | ggtttttga   | gacattatag  | 2040 |
| ctcattaaact | gtttgtgaga  | ccaaatgtgt  | cagaatccgc  | tatt        |             |      |

- (2) INFORMATION FOR SEQ ID NO:400:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 488 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..488

(D) OTHER INFORMATION: / Ceres Seq. ID 1498396

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Gln | Phe | Gly | Asp | Thr | Ser | Val | Gly | Met | Trp | Ser | Lys | Pro | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Arg | Arg | Lys | Thr | Lys | Ile | Val | Cys | Thr | Val | Gly | Pro | Ser | Thr | Asn |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |
| Thr | Arg | Glu | Met | Ile | Trp | Lys | Leu | Ala | Glu | Ala | Gly | Met | Asn | Val | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Met | Asn | Met | Ser | His | Gly | Asp | His | Ala | Ser | His | Lys | Lys | Val | Ile |

|         |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|---------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| 50      |     |     |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |  |  |
| Asp 65  | Leu | Val | Lys | Glu | Tyr | Asn | Ala | Gln | Thr | Lys | Asp | Asn | Thr | Ile | Ala |  |  |
| 70      |     |     |     |     |     | 75  |     |     |     |     |     | 80  |     |     |     |  |  |
| Ile 85  | Met | Leu | Asp | Thr | Lys | Gly | Pro | Glu | Val | Arg | Ser | Gly | Asp | Leu | Pro |  |  |
| 90      |     |     |     |     |     | 95  |     |     |     |     |     | 100 |     |     |     |  |  |
| Gln 105 | Pro | Ile | Met | Leu | Asp | Pro | Gly | Gln | Glu | Phe | Thr | Phe | Thr | Ile | Glu |  |  |
| 110     |     |     |     |     |     | 115 |     |     |     |     |     | 120 |     |     |     |  |  |
| Arg 125 | Gly | Val | Ser | Thr | Pro | Ser | Cys | Val | Ser | Val | Asn | Tyr | Asp | Asp | Phe |  |  |
| 130     |     |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |  |  |
| Val 145 | Asn | Asp | Val | Glu | Ala | Gly | Asp | Met | Leu | Leu | Val | Asp | Gly | Gly | Met |  |  |
| 150     |     |     |     |     |     | 155 |     |     |     |     |     | 160 |     |     |     |  |  |
| Met 165 | Ser | Phe | Met | Val | Lys | Ser | Lys | Thr | Lys | Asp | Ser | Val | Lys | Cys | Glu |  |  |
| 170     |     |     |     |     |     | 175 |     |     |     |     |     | 180 |     |     |     |  |  |
| Val 185 | Val | Val | Asp | Gly | Gly | Glu | Leu | Lys | Ser | Arg | Arg | His | Leu | Asn | Val |  |  |
| 190     |     |     |     |     |     | 195 |     |     |     |     |     | 200 |     |     |     |  |  |
| Gly 205 | Lys | Ser | Ala | Thr | Leu | Pro | Ser | Ile | Thr | Glu | Lys | Asp | Trp | Glu | Asp |  |  |
| 210     |     |     |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |  |  |
| Ile 225 | Lys | Phe | Gly | Val | Glu | Asn | Lys | Val | Asp | Phe | Tyr | Ala | Val | Ser | Phe |  |  |
| 230     |     |     |     |     |     | 235 |     |     |     |     |     | 240 |     |     |     |  |  |
| Val 245 | Lys | Asp | Ala | Gln | Val | Val | His | Glu | Leu | Lys | Lys | Tyr | Leu | Gln | Asn |  |  |
| 250     |     |     |     |     |     | 255 |     |     |     |     |     | 260 |     |     |     |  |  |
| Ser 265 | Gly | Ala | Asp | Ile | His | Val | Ile | Val | Lys | Ile | Glu | Ser | Ala | Asp | Ser |  |  |
| 270     |     |     |     |     |     | 275 |     |     |     |     |     | 280 |     |     |     |  |  |
| Ile 285 | Pro | Asn | Leu | His | Ser | Ile | Ile | Thr | Ala | Ser | Asp | Gly | Ala | Met | Val |  |  |
| 290     |     |     |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |  |  |
| Ala 305 | Arg | Gly | Asp | Leu | Gly | Ala | Glu | Leu | Pro | Ile | Glu | Glu | Val | Pro | Ile |  |  |
| 310     |     |     |     |     |     | 315 |     |     |     |     |     | 320 |     |     |     |  |  |
| Leu 325 | Gln | Glu | Glu | Ile | Ile | Asn | Leu | Cys | Arg | Ser | Met | Gly | Lys | Ala | Val |  |  |
| 330     |     |     |     |     |     | 335 |     |     |     |     |     | 340 |     |     |     |  |  |
| Ile 345 | Val | Ala | Thr | Asn | Met | Leu | Glu | Ser | Met | Ile | Val | His | Pro | Thr | Pro |  |  |
| 350     |     |     |     |     |     | 355 |     |     |     |     |     | 360 |     |     |     |  |  |
| Thr 365 | Arg | Ala | Val | Val | Ser | Asp | Ile | Ala | Ile | Ala | Val | Arg | Glu | Gly | Ala |  |  |
| 370     |     |     |     |     |     | 375 |     |     |     |     |     | 380 |     |     |     |  |  |
| Asp 385 | Ala | Val | Met | Leu | Ser | Gly | Glu | Thr | Ala | His | Gly | Lys | Phe | Pro | Leu |  |  |
| 390     |     |     |     |     |     | 395 |     |     |     |     |     | 400 |     |     |     |  |  |
| Lys 405 | Ala | Ala | Gly | Val | Met | His | Thr | Val | Ala | Leu | Arg | Thr | Glu | Ala | Thr |  |  |
| 410     |     |     |     |     |     | 415 |     |     |     |     |     | 420 |     |     |     |  |  |
| Ile 425 | Thr | Ser | Gly | Glu | Met | Pro | Pro | Asn | Leu | Gly | Gln | Ala | Phe | Lys | Asn |  |  |
| 430     |     |     |     |     |     | 435 |     |     |     |     |     | 440 |     |     |     |  |  |
| His 445 | Met | Ser | Glu | Met | Phe | Ala | Tyr | His | Ala | Thr | Met | Met | Ser | Asn | Thr |  |  |
| 450     |     |     |     |     |     | 455 |     |     |     |     |     | 460 |     |     |     |  |  |
| Leu 465 | Gly | Thr | Ser | Thr | Val | Val | Phe | Thr | Arg | Thr | Gly | Phe | Met | Ala | Ile |  |  |
| 470     |     |     |     |     |     | 475 |     |     |     |     |     | 480 |     |     |     |  |  |
| Leu 485 | Leu | Ser | His | Tyr | Arg | Pro | Ser | Gly | Thr | Ile | Tyr | Ala | Phe | Thr | Asn |  |  |
| 490     |     |     |     |     |     | 495 |     |     |     |     |     | 500 |     |     |     |  |  |
| Glu 505 | Lys | Lys | Ile | Gln | Gln | Arg | Leu | Ala | Leu | Tyr | Gln | Gly | Val | Cys | Pro |  |  |
| 510     |     |     |     |     |     | 515 |     |     |     |     |     | 520 |     |     |     |  |  |
| Ile 525 | Tyr | Met | Glu | Phe | Thr | Asp | Asp | Ala | Glu | Glu | Thr | Phe | Ala | Asn | Ala |  |  |
| 530     |     |     |     |     |     | 535 |     |     |     |     |     | 540 |     |     |     |  |  |
| Leu 545 | Ala | Thr | Leu | Leu | Lys | Gln | Gly | Met | Val | Lys | Lys | Gly | Glu | Glu | Ile |  |  |
| 550     |     |     |     |     |     | 555 |     |     |     |     |     | 560 |     |     |     |  |  |
| Ala 565 | Ile | Val | Gln | Ser | Gly | Thr | Gln | Pro | Ile | Trp | Arg | Ser | Gln | Ser | Thr |  |  |
| 570     |     |     |     |     |     | 57  |     |     |     |     |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..478

(D) OTHER INFORMATION: / Ceres Seq. ID 1498397

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Trp | Ser | Lys | Pro | Thr | Val | Arg | Arg | Lys | Thr | Lys | Ile | Val | Cys | Thr |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Val | Gly | Pro | Ser | Thr | Asn | Thr | Arg | Glu | Met | Ile | Trp | Lys | Leu | Ala | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Gly | Met | Asn | Val | Ala | Arg | Met | Asn | Met | Ser | His | Gly | Asp | His | Ala |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Ser | His | Lys | Lys | Val | Ile | Asp | Leu | Val | Lys | Glu | Tyr | Asn | Ala | Gln | Thr |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Asp | Asn | Thr | Ile | Ala | Ile | Met | Leu | Asp | Thr | Lys | Gly | Pro | Glu | Val |
|     |     |     | 65  |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Arg | Ser | Gly | Asp | Leu | Pro | Gln | Pro | Ile | Met | Leu | Asp | Pro | Gly | Gln | Glu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Phe | Thr | Phe | Thr | Ile | Glu | Arg | Gly | Val | Ser | Thr | Pro | Ser | Cys | Val | Ser |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Val | Asn | Tyr | Asp | Asp | Phe | Val | Asn | Asp | Val | Glu | Ala | Gly | Asp | Met | Leu |
|     |     |     | 115 |     |     |     | 120 |     |     |     | 125 |     |     |     |     |
| Leu | Val | Asp | Gly | Gly | Met | Met | Ser | Phe | Met | Val | Lys | Ser | Lys | Thr | Lys |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asp | Ser | Val | Lys | Cys | Glu | Val | Val | Asp | Gly | Gly | Glu | Leu | Lys | Ser | Arg |
|     |     |     | 145 |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Arg | His | Leu | Asn | Val | Arg | Gly | Lys | Ser | Ala | Thr | Leu | Pro | Ser | Ile | Thr |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Glu | Lys | Asp | Trp | Glu | Asp | Ile | Lys | Phe | Gly | Val | Glu | Asn | Lys | Val | Asp |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Phe | Tyr | Ala | Val | Ser | Phe | Val | Lys | Asp | Ala | Gln | Val | Val | His | Glu | Leu |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |
| Lys | Lys | Tyr | Leu | Gln | Asn | Ser | Gly | Ala | Asp | Ile | His | Val | Ile | Val | Lys |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ile | Glu | Ser | Ala | Asp | Ser | Ile | Pro | Asn | Leu | His | Ser | Ile | Ile | Thr | Ala |
|     |     |     | 225 |     | 230 |     |     |     | 235 |     |     |     |     | 240 |     |
| Ser | Asp | Gly | Ala | Met | Val | Ala | Arg | Gly | Asp | Leu | Gly | Ala | Glu | Leu | Pro |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Ile | Glu | Glu | Val | Pro | Ile | Leu | Gln | Glu | Gly | Ile | Ile | Asn | Leu | Cys | Arg |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ser | Met | Gly | Lys | Ala | Val | Ile | Val | Ala | Thr | Asn | Met | Leu | Glu | Ser | Met |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ile | Val | His | Pro | Thr | Pro | Thr | Arg | Ala | Glu | Val | Ser | Asp | Ile | Ala | Ile |
|     |     |     | 290 |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Ala | Val | Arg | Glu | Gly | Ala | Asp | Ala | Val | Met | Leu | Ser | Gly | Glu | Thr | Ala |
|     |     |     | 305 |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| His | Gly | Lys | Phe | Pro | Leu | Lys | Ala | Ala | Gly | Val | Met | His | Thr | Val | Ala |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |     |
| Leu | Arg | Thr | Glu | Ala | Thr | Ile | Thr | Ser | Gly | Glu | Met | Pro | Pro | Asn | Leu |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Gly | Gln | Ala | Phe | Lys | Asn | His | Met | Ser | Glu | Met | Phe | Ala | Tyr | His | Ala |
|     |     |     | 355 |     |     |     | 360 |     |     |     | 365 |     |     |     |     |
| Thr | Met | Met | Ser | Asn | Thr | Leu | Gly | Thr | Ser | Thr | Val | Phe | Thr | Arg |     |
|     |     |     | 370 |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Thr | Gly | Phe | Met | Ala | Ile | Leu | Leu | Ser | His | Tyr | Arg | Pro | Ser | Gly | Thr |
|     |     |     | 385 |     | 390 |     |     |     |     | 395 |     |     |     | 400 |     |
| Ile | Tyr | Ala | Phe | Thr | Asn | Glu | Lys | Lys | Ile | Gln | Gln | Arg | Leu | Ala | Leu |
|     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |     |
| Tyr | Gln | Gly | Val | Cys | Pro | Ile | Tyr | Met | Glu | Phe | Thr | Asp | Asp | Ala | Glu |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     | 430 |     |     |     |
| Glu | Thr | Phe | Ala | Asn | Ala | Leu | Ala | Thr | Leu | Leu | Lys | Gln | Gly | Met | Val |



435 440 445  
Lys Lys Gly Glu Glu Ile Ala Ile Val Gln Ser Gly Thr Gln Pro Ile  
450 455 460  
Trp Arg Ser Gln Ser Thr His Asn Ile Gln Val Arg Lys Val  
465 470 475

(2) INFORMATION FOR SEQ ID NO:402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..453

(D) OTHER INFORMATION: / Ceres Seq. ID 1498398

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

Met Ile Trp Lys Leu Ala Glu Ala Gly Met Asn Val Ala Arg Met Asn  
1 5 10 15  
Met Ser His Gly Asp His Ala Ser His Lys Lys Val Ile Asp Leu Val  
20 25 30  
Lys Glu Tyr Asn Ala Gln Thr Lys Asp Asn Thr Ile Ala Ile Met Leu  
35 40 45  
Asp Thr Lys Gly Pro Glu Val Arg Ser Gly Asp Leu Pro Gln Pro Ile  
50 55 60  
Met Leu Asp Pro Gly Gln Glu Phe Thr Phe Thr Ile Glu Arg Gly Val  
65 70 75 80  
Ser Thr Pro Ser Cys Val Ser Val Asn Tyr Asp Asp Phe Val Asn Asp  
85 90 95  
Val Glu Ala Gly Asp Met Leu Leu Val Asp Gly Gly Met Met Ser Phe  
100 105 110  
Met Val Lys Ser Lys Thr Lys Asp Ser Val Lys Cys Glu Val Val Asp  
115 120 125  
Gly Gly Glu Leu Lys Ser Arg Arg His Leu Asn Val Arg Gly Lys Ser  
130 135 140  
Ala Thr Leu Pro Ser Ile Thr Glu Lys Asp Trp Glu Asp Ile Lys Phe  
145 150 155 160  
Gly Val Glu Asn Lys Val Asp Phe Tyr Ala Val Ser Phe Val Lys Asp  
165 170 175  
Ala Gln Val Val His Glu Leu Lys Lys Tyr Leu Gln Asn Ser Gly Ala  
180 185 190  
Asp Ile His Val Ile Val Lys Ile Glu Ser Ala Asp Ser Ile Pro Asn  
195 200 205  
Leu His Ser Ile Ile Thr Ala Ser Asp Gly Ala Met Val Ala Arg Gly  
210 215 220  
Asp Leu Gly Ala Glu Leu Pro Ile Glu Glu Val Pro Ile Leu Gln Glu  
225 230 235 240  
Glu Ile Ile Asn Leu Cys Arg Ser Met Gly Lys Ala Val Ile Val Ala  
245 250 255  
Thr Asn Met Leu Glu Ser Met Ile Val His Pro Thr Pro Thr Arg Ala  
260 265 270  
Glu Val Ser Asp Ile Ala Ile Ala Val Arg Glu Gly Ala Asp Ala Val  
275 280 285  
Met Leu Ser Gly Glu Thr Ala His Gly Lys Phe Pro Leu Lys Ala Ala  
290 295 300  
Gly Val Met His Thr Val Ala Leu Arg Thr Glu Ala Thr Ile Thr Ser  
305 310 315 320  
Gly Glu Met Pro Pro Asn Leu Gly Gln Ala Phe Lys Asn His Met Ser  
325 330 335  
Glu Met Phe Ala Tyr His Ala Thr Met Met Ser Asn Thr Leu Gly Thr  
340 345 350

```

Ser Thr Val Val Phe Thr Arg Thr Gly Phe Met Ala Ile Leu Leu Ser
 355 360 365
His Tyr Arg Pro Ser Gly Thr Ile Tyr Ala Phe Thr Asn Glu Lys Lys
 370 375 380
Ile Gln Gln Arg Leu Ala Leu Tyr Gln Gly Val Cys Pro Ile Tyr Met
 385 390 395 400
Glu Phe Thr Asp Asp Ala Glu Glu Thr Phe Ala Asn Ala Leu Ala Thr
 405 410 415
Leu Leu Lys Gln Gly Met Val Lys Lys Gly Glu Glu Ile Ala Ile Val
 420 425 430
Gln Ser Gly Thr Gln Pro Ile Trp Arg Ser Gln Ser Thr His Asn Ile
 435 440 445
Gln Val Arg Lys Val
 450

```

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..692

(D) OTHER INFORMATION: / Ceres Seq. ID 1498399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

```

atcacttact taacatacta agagagttat tagatcttga aaaacatggc ttccaaggct 60
ttgattctgt tgggtctctt cgcaattctt ctggtggtct ccgaagtttc tgccgcaagg 120
atnccggcat ggtgaagcca gagagtgagg aaactgtgca acctgaaggt tatcacggag 180
gacatggtgg tcacggaggg ggaggccact acggaggagg aggccacggg catggaggac 240
acaacggagg agggggccac ggacttgacg gatacggagg aggcacatga ggacatacag 300
gaggaggagg ccacggactt gacggatacg gaggaggtgg aggacactat ggaggaggtg 360
gaggacacta cggaggaggt ggaggacact acggaggagg tggaggagac tacggaggag 420
gtggtggagg acacggaggt ggaggacact acggaggtgg tggaggagga tacggaggtg 480
gaggaggaca ccacggagga ggaggccacg ggctaaacga acctgttcag actaagccgg 540
gtgttttaaa ctatataata tcttctactac catgcatgat tgcataata tatatacgct 600
tatgtattat ctatatgcct ataaataaac catggtgagt ttgtaacgca gtgccttcag 660
aatgttcgg aataaatttc cataatatta gt

```

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..181

(D) OTHER INFORMATION: / Ceres Seq. ID 1498400

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

```

His Leu Leu Asn Ile Leu Arg Glu Leu Leu Asp Leu Glu Lys His Gly
1 5 10 15
Phe Gln Gly Phe Asp Ser Val Gly Ser Leu Arg Asn Ser Ser Gly Gly
 20 25 30
Leu Arg Ser Phe Cys Arg Lys Asp Xaa Gly Met Val Lys Pro Glu Ser
 35 40 45
Glu Glu Thr Val Gln Pro Glu Gly Tyr His Gly Gly His Gly Gly His
 50 55 60
Gly Gly Gly Gly His Tyr Gly Gly Gly His Gly His Gly Gly His
65 70 75 80
Asn Gly Gly Gly Gly His Gly Leu Asp Gly Tyr Gly Gly Gly His Gly

```

85 90 95  
Gly His Tyr Gly Gly Gly Gly His Gly Leu Asp Gly Tyr Gly Gly Gly  
100 105 110  
Gly Gly His Tyr Gly Gly Gly Gly Gly His Tyr Gly Gly Gly Gly Gly  
115 120 125  
His Tyr Gly Gly Gly Gly Gly His Tyr Gly Gly Gly Gly Gly Gly His  
130 135 140  
Gly Gly Gly Gly His Tyr Gly Gly Gly Gly Gly Tyr Gly Gly Gly  
145 150 155 160  
Gly Gly His His Gly Gly Gly Gly His Gly Leu Asn Glu Pro Val Gln  
165 170 175  
Thr Lys Pro Gly Val  
180

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..139

- (D) OTHER INFORMATION: / Ceres Seq. ID 1498401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

Met Val Lys Pro Glu Ser Glu Glu Thr Val Gln Pro Glu Gly Tyr His  
1 5 10 15  
Gly Gly His Gly Gly His Gly Gly Gly Gly His Tyr Gly Gly Gly Gly  
20 25 30  
His Gly His Gly Gly His Asn Gly Gly Gly His Gly Leu Asp Gly  
35 40 45  
Tyr Gly Gly Gly His Gly Gly His Tyr Gly Gly Gly His Gly Leu  
50 55 60  
Asp Gly Tyr Gly Gly Gly Gly His Tyr Gly Gly Gly Gly His  
65 70 75 80  
Tyr Gly Gly Gly Gly Gly His Tyr Gly Gly Gly Gly Tyr Gly  
85 90 95  
Gly Gly Gly Gly Gly His Gly Gly Gly His Tyr Gly Gly Gly  
100 105 110  
Gly Gly Tyr Gly Gly Gly Gly Gly His His Gly Gly Gly Gly His Gly  
115 120 125  
Leu Asn Glu Pro Val Gln Thr Lys Pro Gly Val  
130 135

(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..110

- (D) OTHER INFORMATION: / Ceres Seq. ID 1498402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

Met Val Val Thr Glu Gly Glu Ala Thr Thr Glu Glu Glu Ala Thr Gly  
1 5 10 15  
Met Glu Asp Thr Thr Glu Glu Gly Ala Thr Asp Leu Thr Asp Thr Gly  
20 25 30  
Glu Asp Met Glu Asp Thr Thr Glu Glu Glu Ala Thr Asp Leu Thr Asp  
35 40 45

Thr Glu Glu Val Glu Asp Thr Met Glu Glu Val Glu Asp Thr Thr Glu  
50 55 60  
Glu Val Glu Asp Thr Thr Glu Glu Val Glu Asp Thr Thr Glu Glu Val  
65 70 75 80  
Val Glu Asp Thr Glu Val Glu Asp Thr Thr Glu Val Val Glu Glu Asp  
85 90 95  
Thr Glu Val Glu Glu Asp Thr Thr Glu Glu Ala Thr Gly  
100 105 110

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1451
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

accagaagaa gagccacaca ctcacaaatt aaaaagagag agagagagag agagacagag 60  
agagagagag attctgcgga gagagcttctt cttcgtaggg tgttcacgtg tattaacgtt 120  
atgcgcccta cgtcagctcc atctccagaa acatgggtgc aggtggaaga agtccgggttc 180  
ctactttctc caagaatctg gaaaccgaca ccacaaagcg tgtgcgctg gagaaaaccgc 240  
ctttctcggt gggagatctg aagaagacaa tcccgcgcga ttgtttcaaa cgctcaatcc 300  
ctgcctcttt ctccctaccct ctcaagtaca tcattatagc ctcatgcttc tactacgttg 360  
ccaccaatla ctctctctct ctccctcagc ctctctctta cttggcttgg ccactctatt 420  
gggcctgtca aggctgtgtc ctaactggta tctgggtcat agcccaagaa tgcggtcacc 480  
acgcattcag cgactaccaa tggctggatg acacagttgg tcttatcttc cattctctcc 540  
tctctgtccc ttaacttccc tggaaagata gtcactgcgc tcaccattcc aacactggat 600  
ccctcgaaag agatgaagta tttgtcccaa agcagaatcc agcaatcaag tggtagcgga 660  
aatacctcaa caaccctctt ggacgcatca tgatgttaac cgtccagttt gtccctcggt 720  
ggcccttgta cttagccttt aacgtctctg gcagacgcta tgacgggttc gcttgccatt 780  
tcttcccaaa cgtcccaatc tacaatgacc gagaacgcct ccagatatac ctctctgatg 840  
cggttattct agccgtctgt tttggtcttt accgttacgc tgcgtcacaa gggatggcct 900  
cgatgatctc cctctacgga gtaccgcttc tgatagttaa tgcgttcttc gtcttgatca 960  
cttacttgca gcacactcat cctcgttgcc ctcactacga ttcacacag tgggactggc 1020  
tcaggggagc ttgggtacc gttagacagag actacngaat cttgaacaag gtgttccaca 1080  
acattacaga cacacacgtg gtcacaccc ttgtctcgac aatgccgcac tataacgcac 1140  
tggaaagctac aaaggcgata aaagcaatcc tgggagacta ttaccagttc gatggaacac 1200  
cgtgtatgtg ggcgatgtat agggaggcaa agcagtgatc ctatgtagaa ccggacaggg 1260  
aaggtgacaa gaaaggtgtg tactggtaca acaataagtt atgaggatga tggtagaaga 1320  
attgtcgact ttctctctgt ctgtttgtct tttgttaaag aagctatgct tcgttttaat 1380  
aatcttattg tccattttgt tgtgttatga cattttggct gctcattatg ttatgtggga 1440  
agttagtgc c

(2) INFORMATION FOR SEQ ID NO:408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..383
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

Met Gly Ala Gly Gly Arg Met Pro Val Pro Thr Ser Ser Lys Ser  
1 5 10 15  
Glu Thr Asp Thr Thr Lys Arg Val Pro Cys Glu Lys Pro Pro Phe Ser  
20 25 30

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gly | Asp | Leu | Lys | Lys | Ala | Ile | Pro | Pro | His | Cys | Phe | Lys | Arg | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Ile | Pro | Arg | Ser | Phe | Ser | Tyr | Ile | Ser | Asp | Ile | Ile | Ile | Ala | Ser |     |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Cys | Phe | Tyr | Tyr | Val | Ala | Thr | Asn | Tyr | Phe | Ser | Leu | Leu | Pro | Gln | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Leu | Ser | Tyr | Leu | Ala | Trp | Pro | Leu | Tyr | Trp | Ala | Cys | Gln | Gly | Cys | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Thr | Gly | Ile | Trp | Val | Ile | Ala | His | Glu | Cys | Gly | His | His | Ala | Phe |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Asp | Tyr | Gln | Trp | Leu | Asp | Asp | Thr | Val | Gly | Leu | Ile | Phe | His | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Phe | Leu | Leu | Val | Pro | Tyr | Phe | Ser | Trp | Lys | Tyr | Ser | His | Arg | Arg | His |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| His | Ser | Asn | Thr | Gly | Ser | Leu | Glu | Arg | Asp | Glu | Val | Phe | Val | Pro | Lys |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gln | Lys | Ser | Ala | Ile | Lys | Trp | Tyr | Gly | Lys | Tyr | Leu | Asn | Asn | Pro | Leu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gly | Arg | Ile | Met | Met | Leu | Thr | Val | Gln | Phe | Val | Leu | Gly | Trp | Pro | Leu |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Tyr | Leu | Ala | Phe | Asn | Val | Ser | Gly | Arg | Pro | Tyr | Asp | Gly | Phe | Ala | Cys |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| His | Phe | Phe | Pro | Asn | Ala | Pro | Ile | Tyr | Asn | Asp | Arg | Glu | Arg | Leu | Gln |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ile | Tyr | Leu | Ser | Asp | Ala | Gly | Ile | Leu | Ala | Val | Cys | Phe | Gly | Leu | Tyr |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Arg | Tyr | Ala | Ala | Ala | Gln | Gly | Met | Ala | Ser | Met | Ile | Cys | Leu | Tyr | Gly |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Val | Pro | Leu | Leu | Ile | Val | Asn | Ala | Phe | Leu | Val | Leu | Ile | Thr | Tyr | Leu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Gln | His | Thr | His | Pro | Ser | Leu | Pro | His | Tyr | Asp | Ser | Ser | Glu | Trp | Asp |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Trp | Leu | Arg | Gly | Ala | Leu | Ala | Thr | Val | Asp | Arg | Asp | Tyr | Xaa | Ile | Leu |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Asn | Lys | Val | Phe | His | Asn | Ile | Thr | Asp | Thr | His | Val | Ala | His | His | Leu |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Phe | Ser | Thr | Met | Pro | His | Tyr | Asn | Ala | Met | Glu | Ala | Thr | Lys | Ala | Ile |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Lys | Pro | Ile | Leu | Gly | Asp | Tyr | Tyr | Gln | Phe | Asp | Gly | Thr | Pro | Trp | Tyr |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Val | Ala | Met | Tyr | Arg | Glu | Ala | Lys | Glu | Cys | Ile | Tyr | Val | Glu | Pro | Asp |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Arg | Glu | Gly | Asp | Lys | Lys | Gly | Val | Tyr | Trp | Tyr | Asn | Asn | Lys | Leu |     |
|     |     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- ```
(A) NAME/KEY: peptide
(B) LOCATION: 1..377
(D) OTHER INFORMATION: / Ceres Seq. ID 1498409
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

(xi) SEQUENCE DESCRIPTION															
Met	Val	Pro	Val	Thr	Ser	Ser	Lys	Lys	Ser	Glu	Thr	Asp	Thr	Thr	Lys
1				5					10					15	
Arg	Val	Pro	Cys	Glu	Lys	Pro	Pro	Phe	Ser	Val	Gly	Asp	Leu	Lys	Lys
			20					25					30		
Ala	Ile	Pro	Pro	His	Cys	Phe	Lys	Arg	Ser	Ile	Pro	Arg	Ser	Phe	Ser

Met	Met	Leu	Thr	Val	Gln	Phe	Val	Leu	Gly	Trp	Pro	Leu	Tyr	Leu	Ala
1				5					10					15	
Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	Gly	Phe	Ala	Cys	His	Phe	Phe
			20					25					30		
Pro	Asn	Ala	Pro	Ile	Tyr	Asn	Asp	Arg	Glu	Arg	Leu	Gln	Ile	Tyr	Leu
		35					40					45			

Ser	Asp	Ala	Gly	Ile	Leu	Ala	Val	Cys	Phe	Gly	Leu	Tyr	Arg	Tyr	Ala
50						55					60				
Ala	Ala	Gln	Gly	Met	Ala	Ser	Met	Ile	Cys	Leu	Tyr	Gly	Val	Pro	Leu
65					70				75					80	
Leu	Ile	Val	Asn	Ala	Phe	Leu	Val	Leu	Ile	Thr	Tyr	Leu	Gln	His	Thr
			85						90					95	
His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Ser	Glu	Trp	Asp	Trp	Leu	Arg
			100					105						110	
Gly	Ala	Leu	Ala	Thr	Val	Asp	Arg	Asp	Tyr	Xaa	Ile	Leu	Asn	Lys	Val
		115					120					125			
Phe	His	Asn	Ile	Thr	Asp	Thr	His	Val	Ala	His	His	Leu	Phe	Ser	Thr
	130					135					140				
Met	Pro	His	Tyr	Asn	Ala	Met	Glu	Ala	Thr	Lys	Ala	Ile	Lys	Pro	Ile
145					150					155				160	
Leu	Gly	Asp	Tyr	Tyr	Gln	Phe	Asp	Gly	Thr	Pro	Trp	Tyr	Val	Ala	Met
			165						170					175	
Tyr	Arg	Glu	Ala	Lys	Glu	Cys	Ile	Tyr	Val	Glu	Pro	Asp	Arg	Glu	Gly
			180					185						190	
Asp	Lys	Lys	Gly	Val	Tyr	Trp	Tyr	Asn	Asn	Lys	Leu				
		195					200								

(2) INFORMATION FOR SEQ ID NO:411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1877 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1877
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498411

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

aaacccaaac	amcaattaag	ctaaaaaaa	aaccaaagga	tgtctcagaa	acctatgttc	60
ttgttcaacc	ttgctgcct	ctcctcgtaa	ccatctcctt	ttatctccgc	ccaaataccg	120
gccattggaa	atgccacttc	accgtcaaat	atatgtagat	tcgcgcgcga	tccatcttat	180
tgtagatcgg	ttcttcacaa	ccagcccgga	gatatatat	cctacggacg	ttgtctctta	240
cgaagatccc	tctccagccc	gccggttcat	ttcgatgac	gaecgtgaac	ttgaccggaa	300
aggcaaatgt	gctgtataat	ccacagtagg	ggctctcgaa	gactgcaaat	tcctagccaa	360
ctgactatg	gactacctcc	ttagttagct	acagacggct	gattccacca	aaacactgtc	420
gttatctagg	gccgaggatg	ttcatatcatt	ctctgagtgc	gccatcacca	atgagcagac	480
ttgtcttgaa	ggaacttaaat	caacggcgct	cgaaaaatggt	ctttccgggt	atcttttcaa	540
cgatacaaaa	ctctatgggg	ttgtctcttc	ccctttctcc	aaaggttggt	tgccaagaag	600
gaaagatcgc	agaccgattt	ggcaaccaca	agccaggttc	aaaaagtttt	ttggtttccg	660
taacggtaaa	ttacctgtaa	agatgacgga	aaggcgacgt	gcggtttaca	acaccgtgac	720
tagaagaagg	ctcttccaat	cggatgcaga	cgccgttcag	gtgagcgaca	ttgtgacggc	780
gatccagaac	gggacgggaa	acttcaacgac	cataaacgcc	gccattgcag	ctgcaccaaa	840
taaaactgac	ggtagttaacg	gttacttctt	gatctacgta	acggcgggat	gttacggagg	900
atacgtggaa	gttcccaaga	acaagagata	tgtgatgatg	atcgggtgac	gcatacaaca	960
gaccgttatc	accggaacaa	ggagtgtcgt	tgtatggatg	acaaactttc	attacgccac	1020
atttatctta	tcaggttccca	actttattgg	tgtaaacata	acaaatccga	atacgcagg	1080
accaaccaaa	ggccaaagct	tggtcattgag	gagtggtggg	gacttgtctg	ttttctacag	1140
ttgtagtttt	gaagctctac	atacacacat	ttctctcagc	gtctctcagc	ttttattatc	1200
tgaatgtgat	gtctatggta	ctgttgattt	tatatattgt	aacgctgcag	ttgtattaca	1260
aaactctaat	ttgtatccac	gtcaacctcg	caaaagtgca	tcgaagtgct	ttacggtcca	1320
aggctgtaac	gatccgaacc	aaaacactgg	gacggcaatt	catggttgta	ctataagacc	1380
ggcagatgat	ttggcttgac	gaaactatac	agtgaaagct	tatcttggta	gaccatggaa	1440
ggaaattatt	agaacccgtg	tcatgcaaac	ttacatagac	gggttttcag	aacccagtggt	1500
ttgggaatga	ttgtcttggt	attttgcatt	gagcacactt	tactacgcgg	aataataata	1560
taccggacct	ggttctgaca	cgacaaacgc	agtcacttgg	cctgggttat	acgtcatcaa	1620
cgcaactgat	gcttccaaat	tcacggtcac	caatttctct	gttggtgaag	gttggattgg	1680
ataacccgga	gtgccttttc	ttgggtggact	gatcgcataa	tcacacacaa	ttatacata	1740

tatgatattg taattagtta aattatttaa tcattcatgt gttgtttttt taatcaaata 1800
attatttagt ggtgcctgat tcaatacatg ttgtaataac tttaaacttac tattgtacaa 1860
ccgaatgggt ttcttcg

(2) INFORMATION FOR SEQ ID NO:412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..529

(D) OTHER INFORMATION: / Ceres Seq. ID 1498412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

Met	Pro	Leu	His	Arg	Gln	Ile	Tyr	Val	Asp	Ser	Arg	Arg	Ile	His	Leu
1			5					10						15	
Ile	Val	Asp	Arg	Phe	Phe	Gln	Thr	Ser	Pro	Glu	Ile	Tyr	Ile	Pro	Thr
			20				25						30		
Asp	Val	Cys	Leu	Tyr	Glu	Asp	Pro	Ser	Pro	Ala	Arg	Arg	Phe	Ile	Ser
		35				40					45				
Met	Ile	Asp	Ala	Glu	Leu	Asp	Arg	Lys	Gly	Lys	Val	Ala	Ala	Lys	Ser
	50					55					60				
Thr	Val	Gly	Ala	Leu	Glu	Asp	Cys	Lys	Phe	Leu	Ala	Ser	Leu	Thr	Met
	65				70				75					80	
Asp	Tyr	Leu	Leu	Ser	Ser	Ser	Gln	Thr	Ala	Asp	Ser	Thr	Lys	Thr	Leu
			85					90					95		
Ser	Leu	Ser	Arg	Ala	Glu	Asp	Val	His	Thr	Phe	Leu	Ser	Ala	Ala	Ile
			100					105					110		
Thr	Asn	Glu	Gln	Thr	Cys	Leu	Glu	Gly	Leu	Lys	Ser	Thr	Ala	Ser	Glu
		115					120					125			
Asn	Gly	Leu	Ser	Gly	Asp	Leu	Phe	Asn	Asp	Thr	Lys	Leu	Tyr	Gly	Val
	130					135					140				
Ser	Leu	Ala	Leu	Phe	Ser	Lys	Gly	Trp	Val	Pro	Arg	Arg	Gln	Arg	Ser
	145				150					155				160	
Arg	Pro	Ile	Trp	Gln	Pro	Gln	Ala	Arg	Phe	Lys	Lys	Phe	Phe	Gly	Phe
			165					170					175		
Arg	Asn	Gly	Lys	Leu	Pro	Leu	Lys	Met	Thr	Glu	Arg	Ala	Arg	Ala	Val
		180						185					190		
Tyr	Asn	Thr	Val	Thr	Arg	Arg	Lys	Leu	Leu	Gln	Ser	Asp	Ala	Asp	Ala
		195					200					205			
Val	Gln	Val	Ser	Asp	Ile	Val	Thr	Val	Ile	Gln	Asn	Gly	Thr	Gly	Asn
	210					215						220			
Phe	Thr	Thr	Ile	Asn	Ala	Ala	Ile	Ala	Ala	Ala	Pro	Asn	Lys	Thr	Asp
	225			230						235				240	
Gly	Ser	Asn	Gly	Tyr	Phe	Leu	Ile	Tyr	Val	Thr	Ala	Gly	Leu	Tyr	Glu
			245						250					255	
Glu	Tyr	Val	Glu	Val	Pro	Lys	Asn	Lys	Arg	Tyr	Val	Met	Met	Ile	Gly
		260						265					270		
Asp	Gly	Ile	Asn	Gln	Thr	Val	Ile	Thr	Gly	Asn	Arg	Ser	Val	Val	Asp
	275						280					285			
Gly	Trp	Thr	Thr	Phe	Asn	Ser	Ala	Thr	Phe	Ile	Leu	Ser	Gly	Pro	Asn
	290				295						300				
Phe	Ile	Gly	Val	Asn	Ile	Thr	Ile	Arg	Asn	Thr	Ala	Gly	Pro	Thr	Lys
	305			310					315					320	
Gly	Gln	Ala	Val	Ala	Leu	Arg	Ser	Gly	Gly	Asp	Leu	Ser	Val	Phe	Tyr
		325						330						335	
Ser	Cys	Ser	Phe	Glu	Ala	Tyr	Gln	Asp	Thr	Leu	Tyr	Thr	His	Ser	Leu
		340						345					350		
Arg	Gln	Phe	Thr	Arg	Glu	Cys	Asp	Val	Tyr	Gly	Thr	Val	Asp	Phe	Ile
		355				360						365			

Phe Gly Asn Ala Ala Val Val Leu Gln Asn Cys Asn Leu Tyr Pro Arg
370 375 380
Gln Pro Arg Lys Gly Gln Ser Asn Glu Val Thr Ala Gln Gly Arg Thr
385 390 395 400
Asp Pro Asn Gln Asn Thr Gly Thr Ala Ile His Gly Cys Thr Ile Arg
405 410 415
Pro Ala Asp Asp Leu Ala Thr Ser Asn Tyr Thr Val Lys Thr Tyr Leu
420 425 430
Gly Arg Pro Trp Lys Glu Tyr Ser Arg Thr Val Val Met Gln Thr Tyr
435 440 445
Ile Asp Gly Phe Leu Glu Pro Ser Gly Trp Asn Ala Trp Ser Gly Asp
450 455 460
Phe Ala Leu Ser Thr Leu Tyr Tyr Ala Glu Tyr Asn Asn Thr Gly Pro
465 470 475 480
Gly Ser Asp Thr Thr Asn Arg Val Thr Trp Pro Gly Tyr His Val Ile
485 490 495
Asn Ala Thr Asp Ala Ser Asn Phe Thr Val Thr Asn Phe Leu Val Gly
500 505 510
Glu Gly Trp Ile Gly Gln Thr Gly Val Pro Phe Val Gly Gly Leu Ile
515 520 525
Ala

(2) INFORMATION FOR SEQ ID NO:413:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 481 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..481

(D) OTHER INFORMATION: / Ceres Seq. ID 1498413

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

Met Ile Asp Ala Glu Leu Asp Arg Lys Gly Lys Val Ala Ala Lys Ser
1 5 10 15
Thr Val Gly Ala Leu Glu Asp Cys Lys Phe Leu Ala Ser Leu Thr Met
20 25 30
Asp Tyr Leu Leu Ser Ser Ser Gln Thr Ala Asp Ser Thr Lys Thr Leu
35 40 45
Ser Leu Ser Arg Ala Glu Asp Val His Thr Phe Leu Ser Ala Ala Ile
50 55 60
Thr Asn Glu Gln Thr Cys Leu Glu Gly Leu Lys Ser Thr Ala Ser Glu
65 70 75 80
Asn Gly Leu Ser Gly Asp Leu Phe Asn Asp Thr Lys Leu Tyr Gly Val
85 90 95
Ser Leu Ala Leu Phe Ser Lys Gly Trp Val Pro Arg Arg Gln Arg Ser
100 105 110
Arg Pro Ile Trp Gln Pro Gln Ala Arg Phe Lys Lys Phe Phe Gly Phe
115 120 125
Arg Asn Gly Lys Leu Pro Leu Lys Met Thr Glu Arg Ala Arg Ala Val
130 135 140
Tyr Asn Thr Val Thr Arg Arg Lys Leu Leu Gln Ser Asp Ala Asp Ala
145 150 155 160
Val Gln Val Ser Asp Ile Val Thr Val Ile Gln Asn Gly Thr Gly Asn
165 170 175
Phe Thr Thr Ile Asn Ala Ala Ile Ala Ala Pro Asn Lys Thr Asp
180 185 190
Gly Ser Asn Gly Tyr Phe Leu Ile Tyr Val Thr Ala Gly Leu Tyr Glu
195 200 205
Glu Tyr Val Glu Val Pro Lys Asn Lys Arg Tyr Val Met Met Ile Gly

210	215	220
Asp Gly Ile Asn Gln Thr Val Ile Thr Gly Asn Arg Ser Val Val Asp		
225	230	235
Gly Trp Thr Thr Phe Asn Ser Ala Thr Phe Ile Leu Ser Gly Pro Asn		240
	245	250
Phe Ile Gly Val Asn Ile Thr Ile Arg Asn Thr Ala Gly Pro Thr Lys		255
	260	265
Gly Gln Ala Val Ala Leu Arg Ser Gly Asp Leu Ser Val Phe Tyr		270
	275	280
Ser Cys Ser Phe Glu Ala Tyr Gln Asp Thr Leu Tyr Thr His Ser Leu		285
	290	300
Arg Gln Phe Tyr Arg Glu Cys Asp Val Tyr Gly Thr Val Asp Phe Ile		310
305	315	320
Phe Gly Asn Ala Ala Val Val Leu Gln Asn Cys Asn Leu Tyr Pro Arg		330
	335	340
Gln Pro Arg Lys Gly Gln Ser Asn Glu Val Thr Ala Gln Gly Arg Thr		350
	355	360
Asp Pro Asn Gln Asn Thr Gly Thr Ala Ile His Gly Cys Thr Ile Arg		365
	370	375
Pro Ala Asp Asp Leu Ala Thr Ser Asn Tyr Thr Val Lys Thr Tyr Leu		380
	385	390
Gly Arg Pro Trp Lys Glu Tyr Ser Arg Thr Val Val Met Gln Thr Tyr		395
385	400	405
Ile Asp Gly Phe Leu Glu Pro Ser Gly Trp Asn Ala Trp Ser Gly Asp		410
	415	420
Phe Ala Leu Ser Thr Leu Tyr Tyr Ala Glu Tyr Asn Asn Thr Gly Pro		425
	430	435
Gly Ser Asp Thr Thr Asn Arg Val Thr Trp Pro Gly Tyr His Val Ile		440
	445	450
Asn Ala Thr Asp Ala Ser Asn Phe Thr Val Thr Asn Phe Leu Val Gly		455
	460	465
Glu Gly Trp Ile Gly Gln Thr Gly Val Pro Phe Val Gly Gly Leu Ile		470
465	475	480
Ala		

(2) INFORMATION FOR SEQ ID NO:414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..450
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498414

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

Met Asp Tyr Leu Leu Ser Ser Ser Gln Thr Ala Asp Ser Thr Lys Thr	
1	5
Leu Ser Leu Ser Arg Ala Glu Asp Val His Thr Phe Leu Ser Ala Ala	
	20
Ile Thr Asn Glu Gln Thr Cys Leu Glu Gly Leu Lys Ser Thr Ala Ser	
	35
Glu Asn Gly Leu Ser Gly Asp Leu Phe Asn Asp Thr Lys Leu Tyr Gly	
	50
Val Ser Leu Ala Leu Phe Ser Lys Gly Trp Val Pro Arg Arg Gln Arg	
65	70
Ser Arg Pro Ile Trp Gln Pro Gln Ala Arg Phe Lys Lys Phe Gly	
	85
Phe Arg Asn Gly Lys Leu Pro Leu Lys Met Thr Glu Arg Ala Arg Ala	
	100
	105
	110

Val Tyr Asn Thr Val Thr Arg Arg Lys Leu Leu Gln Ser Asp Ala Asp
115 120 125
Ala Val Gln Val Ser Asp Ile Val Thr Val Ile Gln Asn Gly Thr Gly
130 135 140
Asn Phe Thr Thr Ile Asn Ala Ala Ile Ala Ala Pro Asn Lys Thr
145 150 155 160
Asp Gly Ser Asn Gly Tyr Phe Leu Ile Tyr Val Thr Ala Gly Leu Tyr
165 170 175
Glu Glu Tyr Val Glu Val Pro Lys Asn Lys Arg Tyr Val Met Met Ile
180 185 190
Gly Asp Gly Ile Asn Gln Thr Val Ile Thr Gly Asn Arg Ser Val Val
195 200 205
Asp Gly Trp Thr Thr Phe Asn Ser Ala Thr Phe Ile Leu Ser Gly Pro
210 215 220
Asn Phe Ile Gly Val Asn Ile Thr Ile Arg Asn Thr Ala Gly Pro Thr
225 230 235 240
Lys Gly Gln Ala Val Ala Leu Arg Ser Gly Gly Asp Leu Ser Val Phe
245 250 255
Tyr Ser Cys Ser Phe Glu Ala Tyr Gln Asp Thr Leu Tyr Thr His Ser
260 265 270
Leu Arg Gln Phe Tyr Arg Glu Cys Asp Val Tyr Gly Thr Val Asp Phe
275 280 285
Ile Phe Gly Asn Ala Ala Val Val Leu Gln Asn Cys Asn Leu Tyr Pro
290 295 300
Arg Gln Pro Arg Lys Gly Gln Ser Asn Glu Val Thr Ala Gln Gly Arg
305 310 315 320
Thr Asp Pro Asn Gln Asn Thr Gly Thr Ala Ile His Gly Cys Thr Ile
325 330 335
Arg Pro Ala Asp Asp Leu Ala Thr Ser Asn Tyr Thr Val Lys Thr Tyr
340 345 350
Leu Gly Arg Pro Trp Lys Glu Tyr Ser Arg Thr Val Val Met Gln Thr
355 360 365
Tyr Ile Asp Gly Phe Leu Glu Pro Ser Gly Trp Asn Ala Trp Ser Gly
370 375 380
Asp Phe Ala Leu Ser Thr Leu Tyr Tyr Ala Glu Tyr Asn Asn Thr Gly
385 390 395 400
Pro Gly Ser Asp Thr Thr Asn Arg Val Thr Trp Pro Gly Tyr His Val
405 410 415
Ile Asn Ala Thr Asp Ala Ser Asn Phe Thr Val Thr Asn Phe Leu Val
420 425 430
Gly Glu Gly Trp Ile Gly Gln Thr Gly Val Pro Phe Val Gly Leu Leu
435 440 445
Ile Ala
450

(2) INFORMATION FOR SEQ ID NO:415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1877 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1877
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

atcttttgcc	ccctgaaaga	aagtcaaat	actcaacagc	gtcgtttctt	cttgttttatc	60
gccaatcgcc	attattatcg	cggtgctctt	tctcacctct	cgccgtctct	ttgaaccgga	120
gggttctctc	accoccttgaa	aattccatca	tcgattgacc	tatagctccg	agatctgctc	180
ttcaatttga	tgctctttcca	ttagttagaa	aagttgcttt	tgatcgagc	aactatgggg	240
tcgtcttttg	agaccatcga	tatcggtacc	agtgcctcga	gaattggcgt	agataatcgt	300

attttctctca	aatttttactt	caggatcgct	gataatatcc	tcaaacaggc	caacatat	360
cgggcagaga	agaatgttat	tgatttatat	gtcatgcttc	tgcggttttc	aagcttggtc	420
ctcgagacta	tacggtccca	tcgagattac	agaacatctc	tataaagcaa	taaagagtat	480
ttggaatga	gactactaga	tgctttgacg	gagctggaga	agttgaaacc	agttgtacag	540
caaaagattg	atgaactgta	tcccaagctc	aaacctcgat	ataacgttca	agctcatcat	600
gcaaatgggt	ccctaggctg	gtctttctgc	gtgaaaccgt	cattttaata	ctatgatcat	660
gcaaaagtaa	gaaatctctc	tgacataaat	tctggctaca	tggtgtccag	gggtcagcaa	720
tttttgaacg	ctgcaccact	tgaagagcgt	tcccgaaaga	tgctcggtga	cttcgcacca	780
aatgaagaaa	ccctttccaa	gcattcttat	ttgggtccag	gtggactctc	tgccacagt	840
cagccaccaa	agtatgatac	aaagggttcaa	tatccaaagca	atatagattt	ttgcctgttt	900
gtaatcccaa	gcttccaaca	actgtgtggc	agcaaaccaa	tgataacgaa	tgccagtaac	960
gatgaacctg	aaaagccaat	tgtggaaccc	agtggttcag	ctaattgaaa	aatccagaaa	1020
aattacactg	aaagactctt	ttccatgatt	tctttcgaag	agccagaaa	cgttaatgag	1080
aacaactctca	ttaggtcaacc	ttcaaccact	ccagtgtctg	cagaagtcca	agacttggtt	1140
ccctgcttat	gtcctgaagt	tagaagaacc	gaatgtatga	tagaaaaact	tctgccggtg	1200
gaagtctctac	ggtcggagtc	tctctctgaa	cttcatattg	cgacttcaat	gatggatacc	1260
tttatgaggg	ttgccaagtc	aaacactaaa	aagaatttag	agacgtgtgg	tattcttgcc	1320
gggttcaacta	aaaacagaaa	attttacatt	acagctctca	tcataccaaa	gcaggaatcg	1380
acatctgact	cgtgtcaggc	cacgaacgaa	gaagagatat	ttgaagtaca	ggacaagcaa	1440
tcctttttcc	cactcggagt	gattcatcac	catccgacac	agtcttggtt	catgtcatcc	1500
attgatgttc	acacacacta	ttcataccag	attatgttac	cagaagctgt	ggcaatcgtt	1560
atggcgccac	agaactcttc	aaggaatcac	ggaatatctc	ggctgacgac	gccgggagga	1620
atgacggtga	taaggaaatt	tgaccggcgt	gggtttcatg	cgcacagctt	accggaggac	1680
ggaggaccaa	tttacaatac	ctgtaaggaa	gtttacatga	acccaatact	caagtttgat	1740
gtcattgac	tcagatagca	ctacttcgcg	gtttgaaagt	gaaactatgt	tctcaaggcc	1800
atcttttctc	tacgattgta	acaattatgt	atctgtttat	atccccgatt	taatatgac	1860
tacgtaaagt	ttcgtg					

(2) INFORMATION FOR SEQ ID NO:416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..507
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

Met	Gly	Ser	Ser	Phe	Glu	Thr	Ile	Asp	Ile	Gly	Thr	Ser	Ala	Arg	Arg
1			5					10					15		
Ile	Gly	Val	Asp	Asn	Arg	Ile	Ser	Leu	Lys	Phe	Tyr	Phe	Arg	Ile	Ala
			20					25				30			
Asp	Asn	Ile	Leu	Lys	Gln	Ala	Asn	Ile	Phe	Arg	Ala	Glu	Lys	Asn	Val
		35					40				45				
Ile	Asp	Leu	Tyr	Val	Met	Leu	Leu	Arg	Phe	Ser	Ser	Leu	Ala	Leu	Glu
		50					55				60				
Thr	Ile	Pro	Ser	His	Arg	Asp	Tyr	Arg	Thr	Ser	Leu	Lys	Ser	Asn	Lys
		65			70				75						
Glu	Tyr	Leu	Arg	Met	Arg	Leu	Leu	Asp	Val	Leu	Thr	Glu	Leu	Glu	Lys
			85					90				95			
Leu	Lys	Pro	Val	Val	Gln	Gln	Arg	Ile	Asp	Glu	Leu	Tyr	Pro	Lys	Leu
			100				105					110			
Lys	Pro	Arg	Tyr	Asn	Val	Gln	Ala	His	Pro	Ala	Asn	Gly	Ser	Leu	Gly
			115				120					125			
Trp	Ser	Ser	Ala	Val	Lys	Pro	Ser	Phe	Asn	Ser	Tyr	Asp	His	Ala	Lys
		130				135					140				
Val	Arg	Asn	Pro	Pro	Gly	His	Asn	Ser	Gly	Tyr	Met	Gly	Ser	Arg	Gly
		145			150					155				160	
Gln	Gln	Phe	Leu	Asn	Ala	Ala	Pro	Leu	Glu	Glu	Arg	Phe	Arg	Lys	Met
			165					170						175	

Ser Val Asn Phe Arg Pro Asn Glu Glu Thr Leu Ser Lys His Ser Ile
180 185 190
Leu Gly Pro Gly Gly Leu Ser Ala Gln Trp Gln Pro Pro Lys Tyr Asp
195 200 205
Thr Lys Val Gln Tyr Pro Ser Asn Ile Asp Phe Ser Pro Val Val Ile
210 215 220
Pro Ser Phe Gln Gln Leu Val Asp Ser Lys Pro Met Ile Thr Asn Gly
225 230 235 240
Ser Asn Asp Glu Pro Glu Lys Pro Ile Val Glu Pro Ser Val Ala Ser
245 250 255
Asn Glu Lys Ile Gln Lys Asn Tyr Thr Glu Glu Leu Ser Ser Met Ile
260 265 270
Ser Phe Glu Glu Pro Glu Ser Val Asn Glu Asn Asn Ile Arg Gln
275 280 285
Pro Ser Pro Pro Pro Val Leu Ala Glu Val Gln Asp Leu Val Pro Ala
290 295 300
Leu Cys Pro Glu Val Arg Glu Pro Glu Cys Met Ile Glu Asn Ser Leu
305 310 315 320
Pro Asp Glu Ser Leu Arg Ser Glu Ser Pro Leu Glu Leu His Ile Ala
325 330 335
Thr Ser Met Met Asp Thr Phe Met Arg Leu Ala Lys Ser Asn Thr Lys
340 345 350
Lys Asn Leu Glu Thr Cys Gly Ile Leu Ala Gly Ser Leu Lys Asn Arg
355 360 365
Lys Phe Tyr Ile Thr Ala Leu Ile Ile Pro Lys Gln Glu Ser Thr Ser
370 375 380
Asp Ser Cys Gln Ala Thr Asn Glu Glu Glu Ile Phe Glu Val Gln Asp
385 390 395 400
Lys Gln Ser Leu Phe Pro Leu Gly Trp Ile His Thr His Pro Thr Gln
405 410 415
Ser Cys Phe Met Ser Ser Ile Asp Val His Thr His Tyr Ser Tyr Gln
420 425 430
Ile Met Leu Pro Glu Ala Val Ala Ile Val Met Ala Pro Gln Asp Ser
435 440 445
Ser Arg Asn His Gly Ile Phe Arg Leu Thr Thr Pro Gly Gly Met Thr
450 455 460
Val Ile Arg Asn Cys Asp Arg Arg Gly Phe His Ala His Ser Ser Pro
465 470 475 480
Glu Asp Gly Gly Pro Ile Tyr Asn Thr Cys Lys Glu Val Tyr Met Asn
485 490 495
Pro Asn Leu Lys Phe Asp Val Ile Asp Leu Arg
500 505

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 454 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..454

(D) OTHER INFORMATION: / Ceres Seq. ID 1498425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

Met Leu Leu Arg Phe Ser Ser Leu Ala Leu Glu Thr Ile Pro Ser His
1 5 10 15
Arg Asp Tyr Arg Thr Ser Leu Lys Ser Asn Lys Glu Tyr Leu Arg Met
20 25 30
Arg Leu Leu Asp Val Leu Thr Glu Leu Glu Lys Leu Lys Pro Val Val
35 40 45
Gln Gln Arg Ile Asp Glu Leu Tyr Pro Lys Leu Lys Pro Arg Tyr Asn

(B) LOCATION: 1.423

(D) OTHER INFORMATION: / Ceres Seq. ID 1498426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

Met	Arg	Leu	Leu	Asp	Val	Leu	Thr	Glu	Leu	Glu	Lys	Leu	Lys	Pro	Val	
1				5				10						15		
Val	Gln	Gln	Arg	Ile	Asp	Glu	Leu	Tyr	Pro	Lys	Leu	Lys	Pro	Arg	Tyr	
			20				25						30			
Asn	Val	Gln	Ala	His	Pro	Ala	Asn	Gly	Ser	Leu	Gly	Trp	Ser	Ser	Ala	
			35				40					45				
Val	Lys	Pro	Ser	Phe	Asn	Ser	Tyr	Asp	His	Ala	Lys	Val	Arg	Asn	Pro	
			50				55				60					
Pro	Gly	His	Asn	Ser	Gly	Tyr	Met	Gly	Ser	Arg	Gly	Gln	Gln	Phe	Leu	
65					70				75						80	
Asn	Ala	Ala	Pro	Leu	Glu	Glu	Arg	Phe	Arg	Lys	Met	Ser	Val	Asn	Phe	
				85					90				95			
Arg	Pro	Asn	Glu	Glu	Thr	Leu	Ser	Lys	His	Ser	Ile	Leu	Gly	Pro	Gly	
			100					105					110			
Gly	Leu	Ser	Ala	Gln	Trp	Gln	Pro	Pro	Lys	Tyr	Asp	Thr	Lys	Val	Gln	
			115				120					125				
Tyr	Pro	Ser	Asn	Ile	Asp	Phe	Ser	Pro	Val	Val	Ile	Pro	Ser	Phe	Gln	
			130			135					140					
Gln	Leu	Val	Asp	Ser	Lys	Pro	Met	Ile	Thr	Asn	Gly	Ser	Asn	Asp	Glu	
145					150				155						160	
Pro	Glu	Lys	Pro	Ile	Val	Glu	Pro	Ser	Val	Ala	Ser	Asn	Glu	Lys	Ile	
				165					170					175		
Gln	Lys	Asn	Tyr	Thr	Glu	Glu	Leu	Ser	Met	Ile	Ser	Phe	Glu	Glu		
			180				185					190				
Pro	Glu	Ser	Val	Asn	Glu	Asn	Asn	Leu	Ile	Arg	Gln	Pro	Ser	Pro	Pro	
			195				200					205				
Pro	Val	Leu	Ala	Glu	Val	Gln	Asp	Leu	Val	Pro	Ala	Leu	Cys	Pro	Glu	
			210			215					220					
Val	Arg	Glu	Pro	Glu	Cys	Met	Ile	Glu	Asn	Ser	Leu	Pro	Asp	Glu	Ser	
225					230				235						240	
Leu	Arg	Ser	Glu	Ser	Pro	Leu	Glu	Leu	His	Ile	Ala	Thr	Ser	Met	Met	
				245					250					255		
Asp	Thr	Phe	Met	Arg	Leu	Ala	Lys	Ser	Asn	Thr	Lys	Lys	Asn	Leu	Glu	
			260				265						270			
Thr	Cys	Gly	Ile	Leu	Ala	Gly	Ser	Leu	Lys	Asn	Arg	Lys	Phe	Tyr	Ile	
			275				280					285				
Thr	Ala	Leu	Ile	Ile	Pro	Lys	Gln	Glu	Ser	Thr	Ser	Asp	Ser	Cys	Gln	
			290			295					300					
Ala	Thr	Asn	Glu	Glu	Glu	Ile	Phe	Glu	Val	Gln	Asp	Lys	Gln	Ser	Leu	
305					310				315						320	
Phe	Pro	Leu	Gly	Trp	Ile	His	Thr	His	Pro	Thr	Gln	Ser	Cys	Phe	Met	
				325					330					335		
Ser	Ser	Ile	Asp	Val	His	Thr	His	Tyr	Ser	Tyr	Gln	Ile	Met	Leu	Pro	
			340				345					350				
Glu	Ala	Val	Ala	Ile	Val	Met	Ala	Pro	Gln	Asp	Ser	Ser	Arg	Asn	His	
			355				360					365				
Gly	Ile	Phe	Arg	Leu	Thr	Thr	Pro	Gly	Gly	Met	Thr	Val	Ile	Arg	Asn	
			370			375					380					
Cys	Asp	Arg	Arg	Gly	Phe	His	Ala	His	Ser	Ser	Pro	Glu	Asp	Gly	Gly	
385					390				395						400	
Pro	Ile	Tyr	Asn	Thr	Cys	Lys	Glu	Val	Tyr	Met	Asn	Pro	Asn	Leu	Lys	
				405					410					415		
Phe	Asp	Val	Ile	Asp	Leu	Arg										
				420												

(2) INFORMATION FOR SEQ ID NO:419:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1321 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..1321
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

ttttcatcat	cactctcagtc	tctctcgaag	tttcaagttc	gcgactattg	cagcagcgat	60
gtctctctct	tggttgcgctt	cctcgcgttcg	tttaaatocca	ttcaaacgga	ccttgttttc	120
ttcaatccat	tatccggcca	aaacccttct	tctacgacca	ctaaaaccgt	cggaagttcc	180
ttccttttgc	cggacgatca	tcactttcca	gaaaatttca	accgggattg	tctctccacc	240
atcgctctca	tcactcgcgt	cgagctatgg	agaccttcaa	ccaatcgaag	agcttccacc	300
gaagctacaa	gagatcgtca	agctttttcca	atcggtacaa	gagccaaagg	ctaatacga	360
gcagcttatg	ttctacggga	agaactctgac	accctctgat	tctcaattca	agacgaggga	420
gaataaaagt	gaaggatgtg	tttctcaggt	ttgggttagg	gctttctttg	atgagggaacg	480
taatgtttgt	tatgaagctg	attctgattc	gggtctcact	aaaggsgttg	ctgcttctatt	540
agtcgaagggt	ttatctggaa	gacctgtccc	tgagattttg	aggataaacac	ctgattttgc	600
tgcttctctc	gggtttgcagc	agagttctgtc	tccttctaga	aaacatggat	tacttaatat	660
gcttaagctg	atgcagaaaa	aggctcttca	tttggaagtc	aaaggtgagg	aagattcaag	720
ttctggagag	agttcagaa	ccagctttgt	gtctattcct	gagactaagg	acgaagctaa	780
tgttccggag	gtggatttgg	agctctaaacc	tgactctagtt	gaggattttg	gaacagaaaa	840
gattgatgat	tctgagagtg	ggctcaaatgt	tggtgtctta	gggagtagag	ggatgaggat	900
aaagagagaaa	ttgggaagg	agctagatcc	tgttgagttt	gaagttgaag	atgtttctta	960
ccagcacgca	ggacatgccg	ctgttagagg	tagtgctgtg	gatgatgggg	aaacacattt	1020
caacttgcga	atcgttttcg	atgctttcca	aggtaaaagc	ttggtcaaga	gacataggct	1080
gatataagac	ttgttgcaag	atgagttgaa	gagcgggtta	catgctctct	ctattgtggc	1140
aaagactcct	gtcgaggttt	gagggtgtaa	cattggaaga	agctcaggta	tgattctctt	1200
acttcttttg	gtccatttgc	tttgatatt	gttctctgga	ccttcttcta	atgttcaagg	1260
ctgcgacagg	attgtgttaa	atgagagata	gatattgaag	gatataaata	atgtttctgt	1320

c

(2) INFORMATION FOR SEQ ID NO:420:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 386 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..386
(D) OTHER INFORMATION: / Ceres Seq. ID 1498428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

Phe	His	His	His	Leu	Ser	Leu	Ser	Arg	Ser	Phe	Lys	Phe	Ala	Thr	Met
1				5						10				15	
Ala	Ala	Ala	Met	Ser	Ser	Ser	Cys	Cys	Ala	Ser	Ser	Ser	Leu	Arg	Leu
				20				25						30	Ile
Pro	Phe	Lys	Arg	Thr	Leu	Phe	Ser	Ser	Ile	His	Tyr	Pro	Ala	Lys	Thr
				35				40						45	
Leu	Leu	Leu	Arg	Pro	Leu	Lys	Pro	Ser	Glu	Val	Pro	Ser	Phe	Arg	Arg
				50				55						60	
Thr	Ile	Ile	Thr	Phe	Gln	Lys	Ile	Ser	Thr	Gly	Ile	Val	Pro	Pro	Pro
65					70					75				80	
Ser	Ala	Ser	Ser	Ser	Pro	Ser	Ser	Tyr	Gly	Asp	Leu	Gln	Pro	Ile	Glu
					85				90					95	
Glu	Leu	Pro	Pro	Lys	Leu	Gln	Glu	Ile	Val	Lys	Leu	Phe	Gln	Ser	Val
				100				105						110	
Gln	Glu	Pro	Lys	Ala	Lys	Tyr	Glu	Gln	Leu	Met	Phe	Tyr	Gly	Lys	Asn
				115				120					125		
Leu	Thr	Pro	Leu	Asp	Ser	Gln	Phe	Lys	Thr	Arg	Glu	Asn	Lys	Val	Glu
				130				135						140	
Gly	Cys	Val	Ser	Gln	Val	Trp	Val	Arg	Ala	Phe	Phe	Asp	Glu	Glu	Arg

145		150		155		160
Asn	Val	Val	Tyr	Glu	Ala	Asp
		165		170		175
Ala	Ala	Leu	Leu	Val	Lys	Gly
		180		185		190
Leu	Arg	Ile	Thr	Pro	Asp	Phe
		195		200		205
Leu	Ser	Pro	Ser	Arg	Asn	Asn
		210		215		220
Gln	Lys	Lys	Ala	Leu	His	Leu
		225		230		235
Ser	Gly	Glu	Ser	Ser	Glu	Ser
		245		250		255
Asp	Glu	Ala	Asn	Val	Pro	Glu
		260		265		270
Val	Glu	Asp	Leu	Gly	Thr	Glu
		275		280		285
Asn	Val	Val	Ala	Leu	Gly	Ser
		290		295		300
Glu	Lys	Glu	Leu	Asp	Pro	Val
		305		310		315
Gln	His	Ala	Gly	His	Ala	Ala
		325		330		335
Glu	Thr	His	Phe	Asn	Leu	Arg
		340		345		350
Ser	Leu	Val	Lys	Arg	His	Arg
		355		360		365
Leu	Lys	Ser	Gly	Leu	His	Ala
		370		375		380
Glu	Val					
		385				

(2) INFORMATION FOR SEQ ID NO:421:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 371 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..371

(D) OTHER INFORMATION: / Ceres Seq. ID 1498429

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

Met	Ala	Ala	Ala	Met	Ser	Ser	Ser	Cys	Cys	Ala	Ser	Ser	Leu	Arg	Leu
1				5				10					15		
Ile	Pro	Phe	Lys	Arg	Thr	Leu	Phe	Ser	Ser	Ile	His	Tyr	Pro	Ala	Lys
			20					25					30		
Thr	Leu	Leu	Leu	Arg	Pro	Leu	Lys	Pro	Ser	Glu	Val	Pro	Ser	Phe	Arg
			35				40					45			
Arg	Thr	Ile	Ile	Thr	Phe	Gln	Lys	Ile	Ser	Thr	Gly	Ile	Val	Pro	Pro
			50				55				60				
Pro	Ser	Ala	Ser	Ser	Ser	Pro	Ser	Ser	Tyr	Gly	Asp	Leu	Gln	Pro	Ile
			65			70				75			80		
Glu	Glu	Leu	Pro	Pro	Lys	Leu	Gln	Glu	Ile	Val	Lys	Leu	Phe	Gln	Ser
			85				90						95		
Val	Gln	Glu	Pro	Lys	Ala	Lys	Tyr	Glu	Gln	Leu	Met	Phe	Tyr	Gly	Lys
			100				105					110			
Asn	Leu	Thr	Pro	Leu	Asp	Ser	Gln	Phe	Lys	Thr	Arg	Glu	Asn	Lys	Val
			115				120					125			
Glu	Gly	Cys	Val	Ser	Gln	Val	Trp	Val	Arg	Ala	Phe	Phe	Asp	Glu	Glu
			130				135					140			

Arg Asn Val Val Tyr Glu Ala Asp Ser Asp Ser Val Leu Thr Lys Gly
145 150 155 160
Leu Ala Ala Leu Leu Val Lys Gly Leu Ser Gly Arg Pro Val Pro Glu
165 170 175
Ile Leu Arg Ile Thr Pro Asp Phe Ala Val Leu Leu Gly Leu Gln Gln
180 185 190
Ser Leu Ser Pro Ser Arg Asn Asn Gly Leu Leu Asn Met Leu Lys Leu
195 200 205
Met Gln Lys Lys Ala Leu His Leu Glu Val Lys Gly Glu Glu Asp Ser
210 215 220
Ser Ser Gly Glu Ser Ser Glu Ser Ser Phe Val Ser Ile Pro Glu Thr
225 230 235 240
Lys Asp Glu Ala Asn Val Pro Glu Val Asp Leu Glu Ser Lys Pro Asp
245 250 255
Leu Val Glu Asp Leu Gly Thr Glu Lys Ile Asp Asp Ser Glu Ser Gly
260 265 270
Ser Asn Val Val Ala Leu Gly Ser Arg Gly Met Arg Ile Arg Glu Lys
275 280 285
Leu Glu Lys Glu Leu Asp Pro Val Glu Leu Glu Val Glu Asp Val Ser
290 295 300
Tyr Gln His Ala Gly His Ala Ala Val Arg Gly Ser Ala Gly Asp Asp
305 310 315 320
Gly Glu Thr His Phe Asn Leu Arg Ile Val Ser Asp Ala Phe Gln Gly
325 330 335
Lys Ser Leu Val Lys Arg His Arg Leu Ile Tyr Asp Leu Leu Gln Asp
340 345 350
Glu Leu Lys Ser Gly Leu His Ala Leu Ser Ile Val Ala Lys Thr Pro
355 360 365
Ala Glu Val
370

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..367
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498430

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

Met Ser Ser Ser Cys Cys Ala Ser Ser Leu Arg Leu Ile Pro Phe Lys
1 5 10 15
Arg Thr Leu Phe Ser Ser Ile His Tyr Pro Ala Lys Thr Leu Leu
20 25 30
Arg Pro Leu Lys Pro Ser Glu Val Pro Ser Phe Arg Arg Thr Ile Ile
35 40 45
Thr Phe Gln Lys Ile Ser Thr Gly Ile Val Pro Pro Pro Ser Ala Ser
50 55 60
Ser Ser Pro Ser Ser Tyr Gly Asp Leu Gln Pro Ile Glu Glu Leu Pro
65 70 75 80
Pro Lys Leu Gln Glu Ile Val Lys Leu Phe Gln Ser Val Gln Glu Pro
85 90 95
Lys Ala Lys Tyr Glu Gln Leu Met Phe Tyr Gly Lys Asn Leu Thr Pro
100 105 110
Leu Asp Ser Gln Phe Lys Thr Arg Glu Asn Lys Val Glu Gly Cys Val
115 120 125
Ser Gln Val Trp Val Arg Ala Phe Phe Asp Glu Glu Arg Asn Val Val
130 135 140
Tyr Glu Ala Asp Ser Asp Ser Val Leu Thr Lys Gly Leu Ala Ala Leu

145		150		155		160
Leu Val Lys Gly Leu Ser Gly Arg Pro Val Pro Glu Ile Leu Arg Ile						
	165			170		175
Thr Pro Asp Phe Ala Val Leu Leu Gly Leu Gln Gln Ser Leu Ser Pro						
	180			185		190
Ser Arg Asn Asn Gly Leu Leu Asn Met Leu Lys Leu Met Gln Lys Lys						
	195			200		205
Ala Leu His Leu Glu Val Lys Gly Glu Glu Asp Ser Ser Ser Gly Glu						
	210			215		220
Ser Ser Glu Ser Ser Phe Val Ser Ile Pro Glu Thr Lys Asp Glu Ala						
	225			230		235
Asn Val Pro Glu Val Asp Leu Glu Ser Lys Pro Asp Leu Val Glu Asp						
	245			250		255
Leu Gly Thr Glu Lys Ile Asp Asp Ser Glu Ser Gly Ser Asn Val Val						
	260			265		270
Ala Leu Gly Ser Arg Gly Met Arg Ile Arg Glu Lys Leu Glu Lys Glu						
	275			280		285
Leu Asp Pro Val Glu Leu Glu Val Glu Asp Val Ser Tyr Gln His Ala						
	290			295		300
Gly His Ala Ala Val Arg Gly Ser Ala Gly Asp Asp Gly Glu Thr His						
	305			310		315
Phe Asn Leu Arg Ile Val Ser Asp Ala Phe Gln Gly Lys Ser Leu Val						
	325			330		335
Lys Arg His Arg Leu Ile Tyr Asp Leu Leu Gln Asp Glu Leu Lys Ser						
	340			345		350
Gly Leu His Ala Leu Ser Ile Val Ala Lys Thr Pro Ala Glu Val						
	355			360		365

(2) INFORMATION FOR SEQ ID NO:423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1725 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1725
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

atttttttaa	cattgtttcca	ccaactcctc	ccacattctc	tccgcctctc	tcgtttacaa	60
atcccaactc	aaaggtcgac	tcctttatct	tcttctcacc	aaccacaact	ctccaatggc	120
ttctcagagt	tcagtcgccc	tcatttctct	cgcgcgcgcc	agaggtgaat	cattcccaga	180
ttcaaaagaa	ccaatcggtt	cagttcgggt	ccaacaaccc	ctccgtctct	ccttctcgta	240
ctgtaagtca	gggaatatgt	catctagaat	ctgcgctatg	gccaaaccaa	atgatgctga	300
gactctttca	tcactagtag	atatgtcact	tagccgcgca	gttcagtcct	taaaaccttc	360
caagactagt	gttataaocg	atcttgcagc	cactcttggt	caatccgggt	ttccggttat	420
tagactagct	gcgggagaa	ccgatttcga	cactcccaaa	gtcgtagctg	aggctgggat	480
caacgcgatt	cgagaaggtt	ttactagtag	tacgtttaat	gcaggatatta	cagaaactcag	540
agaagcaata	tgtcgaaagc	taaaagagga	gaatggattg	tcttatgcgc	ctgatcagat	600
cttggttagt	aatggaagct	aacaaagtct	cttacaagca	gtgcttgcag	tttgttctcc	660
tggagatgaa	gttataaatt	ctgcaccgta	ttgggtgagt	tacacagaa	aggcgagatt	720
ggctgatgca	acgcccgtgg	ttattctctc	caagatttct	aacaattttt	tgttgcattc	780
aaaggatctt	gagttctaat	tgaactgaaa	atctagactt	cttattctct	gctctccttc	840
caaccctact	ggatctgttt	accccaagag	tttgctcgaa	gagattgcac	ggatcattgc	900
taagcatcca	agactctctg	tgctttcgga	tgaatatata	gaacacatta	tttatgcacc	960
tgcaacacac	acaagctttg	ctctctttgc	tgacatgtat	gaagaagaat	tgacagttaa	1020
cggtttctca	aggcgttttc	caatgacagg	ttggaggcct	ggatatcttg	ctggtctcaa	1080
acatatgttg	gcagctttga	gtaaaattca	aggccagggt	agttccaggag	ctagtagcat	1140
tgctgatgaa	gcaggtgttg	ctgcgctagg	gttaggcgaa	gcgtgctagg	aaacgggttg	1200
agagatgggt	aaagcttata	gagaaagacg	agatttcttg	gttaaaagct	taggtgatat	1260
caaaggtggt	aagatctctg	accctcaggg	agctttttat	ctctttattg	acttcagtgc	1320

ttactatgga	tcagaagctg	aaggttttgg	tttgatcaat	gattcgtcgt	ctcttgcact	1380
atactttctt	gacaagtttc	aggttgcaat	gggttcctgt	gatgcttttg	gagatcatag	1440
ttgtatccga	atatcttatg	ccacatctct	cgacgttctt	caagcagctg	ttgagaagat	1500
caggaaaagcc	cttgagccac	tcctgtccac	tgctctccgt	taacagtttcg	gacacagaaa	1560
tggtgtttaag	attgtttatg	atatgtttga	acttatttat	cagctttgtc	tccaatccaa	1620
taaaaagctc	ttttctatgc	tttgttcgtt	ccctcaaatt	catatataac	cataaacaat	1680
tatcttaatt	gtaaatcatt	tattagtatt	taaggttgct	tgtagc		

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 475 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..475

(D) OTHER INFORMATION: / Ceres Seq. ID 1498432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

Met	Ala	Ser	Gln	Ser	Ser	Val	Ala	Val	Ile	Ser	Ser	Ala	Ala	Ala	Arg
1			5						10					15	
Gly	Glu	Ser	Phe	Pro	Asp	Ser	Lys	Lys	Pro	Ile	Gly	Ser	Val	Arg	Phe
			20					25					30		
Gln	Gln	Pro	Leu	Arg	Leu	Ser	Phe	Ser	Tyr	Cys	Lys	Ser	Gly	Asn	Met
			35				40					45			
Ser	Ser	Arg	Ile	Cys	Ala	Met	Ala	Lys	Pro	Asn	Asp	Ala	Glu	Thr	Leu
			50				55				60				
Ser	Ser	Ser	Val	Asp	Met	Ser	Leu	Ser	Pro	Arg	Val	Gln	Ser	Leu	Lys
			65			70			75				80		
Pro	Ser	Lys	Thr	Met	Val	Ile	Thr	Asp	Leu	Ala	Ala	Thr	Leu	Val	Gln
			85				90					95			
Ser	Gly	Val	Pro	Val	Ile	Arg	Leu	Ala	Gly	Glu	Pro	Asp	Phe	Asp	
			100				105					110			
Thr	Pro	Lys	Val	Val	Ala	Glu	Ala	Gly	Ile	Asn	Ala	Ile	Arg	Glu	Gly
			115				120					125			
Phe	Thr	Arg	Tyr	Thr	Leu	Asn	Ala	Gly	Ile	Thr	Glu	Leu	Arg	Glu	Ala
			130				135				140				
Ile	Cys	Arg	Lys	Leu	Lys	Glu	Glu	Asn	Gly	Leu	Ser	Tyr	Ala	Pro	Asp
			145			150				155				160	
Gln	Ile	Leu	Val	Ser	Asn	Gly	Ala	Lys	Gln	Ser	Leu	Leu	Gln	Ala	Val
			165					170					175		
Leu	Ala	Val	Cys	Ser	Pro	Gly	Asp	Glu	Val	Ile	Ile	Pro	Ala	Pro	Tyr
			180				185					190			
Trp	Val	Ser	Tyr	Thr	Glu	Gln	Ala	Arg	Leu	Ala	Asp	Ala	Thr	Pro	Val
			195				200					205			
Val	Ile	Pro	Thr	Lys	Ile	Ser	Asn	Asn	Phe	Leu	Leu	Asp	Pro	Lys	Asp
			210				215					220			
Leu	Glu	Ser	Lys	Leu	Thr	Glu	Lys	Ser	Arg	Leu	Leu	Ile	Leu	Cys	Ser
			225			230				235				240	
Pro	Ser	Asn	Pro	Thr	Gly	Ser	Val	Tyr	Pro	Lys	Ser	Leu	Leu	Glu	Glu
			245					250						255	
Ile	Ala	Arg	Ile	Ile	Ala	Lys	His	Pro	Arg	Leu	Leu	Val	Leu	Ser	Asp
			260				265					270			
Glu	Ile	Tyr	Glu	His	Ile	Ile	Tyr	Ala	Pro	Ala	Thr	His	Thr	Ser	Phe
			275				280					285			
Ala	Ser	Leu	Pro	Asp	Met	Tyr	Glu	Arg	Thr	Leu	Thr	Val	Asn	Gly	Phe
			290			295					300				
Ser	Lys	Ala	Phe	Ala	Met	Thr	Gly	Trp	Arg	Leu	Gly	Tyr	Leu	Ala	Gly
			305			310				315				320	
Pro	Lys	His	Ile	Val	Ala	Ala	Cys	Ser	Lys	Leu	Gln	Gly	Gln	Val	Ser
			325						330					335	

Ser Gly Ala Ser Ser Ile Ala Gln Lys Ala Gly Val Ala Ala Leu Gly
340 345 350
Leu Gly Lys Ala Gly Gly Glu Thr Val Ala Glu Met Val Lys Ala Tyr
355 360 365
Arg Glu Arg Arg Asp Phe Leu Val Lys Ser Leu Gly Asp Ile Lys Gly
370 375 380
Val Lys Ile Ser Glu Pro Gln Gly Ala Phe Tyr Leu Phe Ile Asp Phe
385 390 395 400
Ser Ala Tyr Tyr Gly Ser Glu Ala Glu Gly Phe Gly Leu Ile Asn Asp
405 410 415
Ser Ser Ser Leu Ala Leu Tyr Phe Leu Asp Lys Phe Gln Val Ala Met
420 425 430
Val Pro Gly Asp Ala Phe Gly Asp His Ser Cys Ile Arg Ile Ser Tyr
435 440 445
Ala Thr Ser Leu Asp Val Leu Gln Ala Ala Val Glu Lys Ile Arg Lys
450 455 460
Ala Leu Glu Pro Leu Arg Ala Thr Val Ser Val
465 470 475

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 428 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..428

(D) OTHER INFORMATION: / Ceres Seq. ID 1498433

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

Met Ser Ser Arg Ile Cys Ala Met Ala Lys Pro Asn Asp Ala Glu Thr
1 5 10 15
Leu Ser Ser Ser Val Asp Met Ser Leu Ser Pro Arg Val Gln Ser Leu
20 25 30
Lys Pro Ser Lys Thr Met Val Ile Thr Asp Leu Ala Ala Thr Leu Val
35 40 45
Gln Ser Gly Val Pro Val Ile Arg Leu Ala Ala Gly Glu Pro Asp Phe
50 55 60
Asp Thr Pro Lys Val Val Ala Glu Ala Gly Ile Asn Ala Ile Arg Glu
65 70 75 80
Gly Phe Thr Arg Tyr Thr Leu Asn Ala Gly Ile Thr Glu Leu Arg Glu
85 90 95
Ala Ile Cys Arg Lys Leu Lys Glu Glu Asn Gly Leu Ser Tyr Ala Pro
100 105 110
Asp Gln Ile Leu Val Ser Asn Gly Ala Lys Gln Ser Leu Leu Gln Ala
115 120 125
Val Leu Ala Val Cys Ser Pro Gly Asp Glu Val Ile Pro Ala Pro
130 135 140
Tyr Trp Val Ser Tyr Thr Glu Gln Ala Arg Leu Ala Asp Ala Thr Pro
145 150 155 160
Val Val Ile Pro Thr Lys Ile Ser Asn Asn Phe Leu Leu Asp Pro Lys
165 170 175
Asp Leu Glu Ser Lys Leu Thr Glu Lys Ser Arg Leu Leu Ile Leu Cys
180 185 190
Ser Pro Ser Asn Pro Thr Gly Ser Val Tyr Pro Lys Ser Leu Leu Glu
195 200 205
Glu Ile Ala Arg Ile Ile Ala Lys His Pro Arg Leu Leu Val Leu Ser
210 215 220
Asp Glu Ile Tyr Glu His Ile Ile Tyr Ala Pro Ala Thr His Thr Ser
225 230 235 240
Phe Ala Ser Leu Pro Asp Met Tyr Glu Arg Thr Leu Thr Val Asn Gly

Met	Ala	Lys	Pro	Asn	Asp	Ala	Glu	Thr	Leu	Ser	Ser	Ser	Val	Asp	Met
1			5						10					15	
Ser	Leu	Ser	Pro	Arg	Val	Gln	Ser	Leu	Lys	Pro	Ser	Lys	Thr	Met	Val
			20					25					30		
Ile	Thr	Asp	Leu	Ala	Ala	Thr	Leu	Val	Gln	Ser	Gly	Val	Pro	Val	Ile
		35					40					45			
Arg	Leu	Ala	Ala	Gly	Glu	Pro	Asp	Phe	Asp	Thr	Pro	Lys	Val	Val	Ala
	50					55					60				
Glu	Ala	Gly	Ile	Asn	Ala	Ile	Arg	Glu	Gly	Phe	Thr	Arg	Tyr	Thr	Leu
65				70					75					80	
Asn	Ala	Gly	Ile	Thr	Glu	Leu	Arg	Glu	Ala	Ile	Cys	Arg	Lys	Leu	Lys
				85				90						95	
Glu	Glu	Asn	Gly	Leu	Ser	Tyr	Ala	Pro	Asp	Gln	Ile	Leu	Val	Ser	Asn
			100					105					110		
Gly	Ala	Lys	Gln	Ser	Leu	Leu	Gln	Ala	Val	Leu	Ala	Val	Cys	Ser	Pro
		115					120					125			
Gly	Asp	Glu	Val	Ile	Ile	Pro	Ala	Pro	Tyr	Trp	Val	Ser	Tyr	Thr	Glu
		130				135					140				
Gln	Ala	Arg	Leu	Ala	Asp	Ala	Thr	Pro	Val	Val	Ile	Pro	Thr	Lys	Ile
145					150					155				160	
Ser	Asn	Asn	Phe	Leu	Leu	Asp	Pro	Lys	Asp	Leu	Glu	Ser	Lys	Leu	Thr
				165				170						175	
Glu	Lys	Ser	Arg	Leu	Leu	Ile	Leu	Cys	Ser	Pro	Ser	Asn	Pro	Thr	Gly
			180					185					190		
Ser	Val	Tyr	Pro	Lys	Ser	Leu	Leu	Glu	Glu	Ile	Ala	Arg	Ile	Ile	Ala
		195					200					205			

Lys His Pro Arg Leu Leu Val Leu Ser Asp Glu Ile Tyr Glu His Ile
210 215 220
Ile Tyr Ala Pro Ala Thr His Thr Ser Phe Ala Ser Leu Pro Asp Met
225 230 235 240
Tyr Glu Arg Thr Leu Thr Val Asn Gly Phe Ser Lys Ala Phe Ala Met
245 250 255
Thr Gly Trp Arg Leu Gly Tyr Leu Ala Gly Pro Lys His Ile Val Ala
260 265 270
Ala Cys Ser Lys Leu Gln Gly Gln Val Ser Ser Gly Ala Ser Ser Ile
275 280 285
Ala Gln Lys Ala Gly Val Ala Ala Leu Gly Leu Gly Lys Ala Gly Gly
290 295 300
Glu Thr Val Ala Glu Met Val Lys Ala Tyr Arg Glu Arg Arg Asp Phe
305 310 315 320
Leu Val Lys Ser Leu Gly Asp Ile Lys Gly Val Lys Ile Ser Glu Pro
325 330 335
Gln Gly Ala Phe Tyr Leu Phe Ile Asp Phe Ser Ala Tyr Tyr Gly Ser
340 345 350
Glu Ala Glu Gly Phe Gly Leu Ile Asn Asp Ser Ser Ser Leu Ala Leu
355 360 365
Tyr Phe Leu Asp Lys Phe Gln Val Ala Met Val Pro Gly Asp Ala Phe
370 375 380
Gly Asp His Ser Cys Ile Arg Ile Ser Tyr Ala Thr Ser Leu Asp Val
385 390 395 400
Leu Gln Ala Ala Val Glu Lys Ile Arg Lys Ala Leu Glu Pro Leu Arg
405 410 415
Ala Thr Val Ser Val
420

(2) INFORMATION FOR SEQ ID NO:427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1052 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1052
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

cctagtcctcaa	aaattctctca	tactataaaa	agattttttt	ttttgcttcg	ctccctcttt	60
ttcactctcgt	taacggcccc	gcctccactc	tatcctaccg	ccgacgtccg	tgatcgccga	120
aatgaactgaa	gcagagtcca	agactgttgt	tcctgagtcg	gtgttgaa	agagaaagag	180
ggaggaagaa	tgggcacttg	ccaagaagaa	ggagcttgag	gctgccaaaa	agcagaatgc	240
tgagaagagg	aaactcatat	ttaacccggc	taaacagttac	aaaggagggt	tttatgttga	300
agaaaaggaa	ttaatccagc	tgaaagctga	ggcaaaattg	aaaggagggt	tttatgttga	360
cccagaagct	aaactgcttt	tcattatccg	tatccgttgt	atcaatgcga	ttgaccctaa	420
gacaaagaa	attttgcaac	ttttgcgttt	aagacagatt	tkcaatgggt	tgktcttgaa	480
ggtcaacaag	gcaaccatta	acatgcttcg	ccgtgttgaa	ccctatgtaa	cctatggata	540
cccgaactta	aaaagtgtga	aggaattgat	ttacaaacga	ggttttggaa	agcttaacca	600
ccagagcggt	gccttaacag	acaattctat	tgtagatcag	gggctaggaa	agcatggcat	660
catctgcgtt	gaggatctga	ccatgagatg	catgacggtt	gggccacatt	tcaagggaagc	720
caataaacttt	ttgtggccat	tccagttgaa	ggctccattg	ggagggatga	agaagaagag	780
gaaccattac	gtggaagag	gagatgctgg	aaaccgcgag	aacttcacga	acgagctcgt	840
taggagaatg	aactgaagcg	taagcgttat	tgctctgaaa	ctccctagga	aacgttttctg	900
tatagtgtaa	aaactctctg	tcgcttgctt	gtgttgccat	tgaggcggaag	taaacattta	960
cggtgaaaga	ctttgatatt	ttataagttg	gcaattgtga	gaacacatca	tttatttctt	1020
ttccacattac	atcgtcaact	gcattgcatt	tt			

(2) INFORMATION FOR SEQ ID NO:428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 amino acids

```

      (B) TYPE: amino acid
      (C) STRANDEDNESS:
      (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
      (A) NAME/KEY: peptide
      (B) LOCATION: 1..244
      (D) OTHER INFORMATION: / Ceres Seq. ID 1498436
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:
Met Thr Glu Ala Glu Ser Lys Thr Val Val Pro Glu Ser Val Leu Lys
1      5      10      15
Lys Arg Lys Arg Glu Glu Glu Trp Ala Leu Ala Lys Lys Gln Glu Leu
20      25
Glu Ala Ala Lys Lys Gln Asn Ala Glu Lys Arg Lys Leu Ile Phe Asn
35      40
Arg Ala Lys Gln Tyr Ser Lys Glu Tyr Gln Glu Lys Glu Arg Glu Leu
50      55
Ile Gln Leu Lys Arg Glu Ala Lys Leu Lys Gly Gly Phe Tyr Val Asp
65      70      75      80
Pro Glu Ala Lys Leu Leu Phe Ile Ile Arg Ile Arg Gly Ile Asn Ala
85      90      95
Ile Asp Pro Lys Thr Lys Lys Ile Leu Gln Leu Leu Arg Leu Arg Gln
100      105      110
Ile Xaa Asn Gly Val Xaa Leu Lys Val Asn Lys Ala Thr Ile Asn Met
115      120      125
Leu Arg Arg Val Glu Pro Tyr Val Thr Tyr Gly Tyr Pro Asn Leu Lys
130      135      140
Ser Val Lys Glu Leu Ile Tyr Lys Arg Gly Phe Gly Lys Leu Asn His
145      150      155      160
Gln Arg Ile Ala Leu Thr Asp Asn Ser Ile Val Asp Gln Gly Leu Gly
165      170      175
Lys His Gly Ile Ile Cys Val Glu Asp Leu Ile His Glu Ile Met Thr
180      185      190
Val Gly Pro His Phe Lys Glu Ala Asn Asn Phe Leu Trp Pro Phe Gln
195      200      205
Leu Lys Ala Pro Leu Gly Gly Met Lys Lys Lys Arg Asn His Tyr Val
210      215      220
Glu Gly Gly Asp Ala Gly Asn Arg Glu Asn Phe Ile Asn Glu Leu Val
225      230      235      240
Arg Arg Met Asn

```

(2) INFORMATION FOR SEQ ID NO:429:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1252 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

```
(ix) FEATURE:
```

(A) NAME/KEY: -

(B) LOCATION: 1..1252

(D) OTHER INFORMATION: / Ceres Seq. ID 1498437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

atgtgttttgg	gatacttttaa	ctcctttgggt	gggtgtttgagc	acgatcagct	tactgtctgt	60
tccaagaagct	aagacagtgtt	gaacttttat	caaacagctga	atctcgtatgt	tgcaaatggt	120
tttaccctgt	atccggagtc	taaaaggcct	ctctctgttgc	tagtttaagaa	ggaagaggag	180
aaaaattagcc	atcttggatc	agaattttgtt	aaagtcttgc	tagtttagtt	tgttctgcc	240
gcaactcctg	cttttgctct	tgtttttcaac	agcagaagact	ctccggaaat	ttttgagagt	300
acgaatcaga	aacagcttgt	tgtgtttgtt	acgaaaaatc	aatctgaaaa	ggtctctaac	360
gaattttcaag	aacagcgcaa	atcatctaaa	ggaaaagctca	tetttgtatc	tgtgatgact	420
gcaattagag	atattggaaa	cgcaagtcgt	gaactaactgt	tgtgtctctgg	aaatgggtcct	480

aaactttattg	gctacacagg	gaatgaagac	cctaaaaaat	acttttttgcga	tggcgagatc	540
cagtcagata	aaattaaagt	atttggggag	gattttcctga	acgacaaagt	aaagcctttc	600
tataagctcag	accccatcc	tgaaaagaac	gatgaagatg	tgaataatgt	ggttggagat	660
aaactttgatg	aaattgttct	ggacgattct	aaagatgtgc	ttctcgagggt	ctacgcacca	720
tgggtgtggcc	attgccaagc	ccttgagcca	atgtataaca	aaacttgccaa	gcatttacga	780
agttattgatt	ctctcgctcat	aaccgagatg	gatggaaaca	ccaatgaaca	tcccaaggca	840
aaaggctgagg	ggttccctac	cattctcttc	ttccctgcgg	gcaacaagac	ttcagagccg	900
attactgtag	atacagaccg	cactgtgggt	gcattttaca	agttcttaag	gaacacgcga	960
acgattcccat	tcacaaactga	gaaacctgca	tcaaccgaaw	cacctaaaaac	tcagagagtcc	1020
acacacaaaag	tagaaaactac	cgagaccacaa	gaatcaccgc	atagcacgac	aaagagttagc	1080
caaaagtcatg	cgaaggacga	attgtgatca	gaaaagggtta	taatatatat	tcacatgtctc	1140
cttaagtgtg	tatatgtatg	atcagaattg	tcacatcatg	agtttggact	agataaagat	1200
gggaattaaa	gtaatttttag	ttttgagaaa	gacaaatttct	tttgatttgg	tc	

(2) INFORMATION FOR SEQ ID NO:430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..368
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

Ile	Val	Leu	Gly	Tyr	Leu	Asn	Ser	Leu	Val	Gly	Val	Glu	His	Asp	Gln
1				5					10					15	
Leu	Asn	Ala	Ala	Ser	Lys	Ala	Glu	Asp	Asp	Val	Asn	Phe	Tyr	Gln	Thr
			20					25					30		
Val	Asn	Pro	Asp	Val	Ala	Lys	Met	Phe	His	Leu	Asp	Pro	Glu	Ser	Lys
		35				40					45				
Arg	Pro	Ala	Leu	Val	Leu	Val	Lys	Lys	Glu	Glu	Glu	Lys	Ile	Ser	His
		50				55				60					
Phe	Asp	Gly	Glu	Phe	Val	Lys	Ser	Ala	Leu	Val	Ser	Phe	Val	Ser	Ala
		65			70				75					80	
Asn	Lys	Leu	Ala	Leu	Val	Ser	Val	Phe	Thr	Arg	Glu	Thr	Ala	Pro	Glu
			85					90						95	
Ile	Phe	Glu	Ser	Ala	Ile	Lys	Lys	Gln	Leu	Leu	Leu	Phe	Val	Thr	Lys
			100					105					110		
Asn	Glu	Ser	Glu	Lys	Val	Leu	Thr	Glu	Phe	Gln	Glu	Ala	Ala	Lys	Ser
		115				120						125			
Phe	Lys	Gly	Lys	Leu	Ile	Phe	Val	Ser	Val	Asp	Leu	Asp	Asn	Glu	Asp
		130				135					140				
Tyr	Gly	Lys	Pro	Val	Ala	Glu	Tyr	Phe	Gly	Val	Ser	Gly	Asn	Gly	Pro
		145			150					155				160	
Lys	Leu	Ile	Gly	Tyr	Thr	Gly	Asn	Glu	Asp	Pro	Lys	Lys	Tyr	Phe	Phe
			165					170						175	
Asp	Gly	Glu	Ile	Gln	Ser	Asp	Lys	Ile	Lys	Ile	Phe	Gly	Glu	Asp	Phe
			180					185					190		
Leu	Asn	Asp	Lys	Leu	Lys	Pro	Phe	Tyr	Lys	Ser	Asp	Pro	Ile	Pro	Glu
		195				200						205			
Lys	Asn	Asp	Glu	Asp	Val	Lys	Ile	Val	Val	Gly	Asp	Asn	Phe	Asp	Glu
		210				215					220				
Ile	Val	Leu	Asp	Asp	Ser	Lys	Asp	Val	Leu	Leu	Glu	Val	Tyr	Ala	Pro
		225				230				235				240	
Trp	Cys	Gly	His	Cys	Gln	Ala	Leu	Glu	Pro	Met	Tyr	Asn	Lys	Leu	Ala
			245					250						255	
Lys	His	Leu	Arg	Ser	Ile	Asp	Ser	Leu	Val	Ile	Thr	Glu	Met	Asp	Gly
			260					265					270		
Thr	Thr	Asn	Glu	His	Pro	Lys	Ala	Lys	Ala	Glu	Gly	Phe	Pro	Thr	Ile
		275				280						285			

Leu Phe Phe Pro Ala Gly Asn Lys Thr Ser Glu Pro Ile Thr Val Asp
290 295 300
Thr Asp Arg Thr Val Val Ala Phe Tyr Lys Phe Leu Arg Lys His Ala
305 310 315 320
Thr Ile Pro Phe Lys Leu Glu Lys Pro Ala Ser Thr Glu Xaa Pro Lys
325 330 335
Thr Ala Glu Ser Thr Pro Lys Val Glu Thr Thr Glu Thr Lys Glu Ser
340 345 350
Pro Asp Ser Thr Thr Lys Ser Ser Gln Ser Asp Ser Lys Asp Glu Leu
355 360 365

(2) INFORMATION FOR SEQ ID NO:431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..329

(D) OTHER INFORMATION: / Ceres Seq. ID 1498439

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

Met Phe His Leu Asp Pro Glu Ser Lys Arg Pro Ala Leu Val Leu Val
1 5 10 15
Lys Lys Glu Glu Glu Lys Ile Ser His Phe Asp Gly Glu Phe Val Lys
20 25 30
Ser Ala Leu Val Ser Phe Val Ser Ala Asn Lys Leu Ala Leu Val Ser
35 40 45
Val Phe Thr Arg Glu Thr Ala Pro Glu Ile Phe Glu Ser Ala Ile Lys
50 55 60
Lys Gln Leu Leu Leu Phe Val Thr Lys Asn Glu Ser Glu Lys Val Leu
65 70 75 80
Thr Glu Phe Gln Glu Ala Ala Lys Ser Phe Lys Gly Lys Leu Ile Phe
85 90 95
Val Ser Val Asp Leu Asp Asn Glu Asp Tyr Gly Lys Pro Val Ala Glu
100 105 110
Tyr Phe Gly Val Ser Gly Asn Gly Pro Lys Leu Ile Gly Tyr Thr Gly
115 120 125
Asn Glu Asp Pro Lys Lys Tyr Phe Phe Asp Gly Glu Ile Gln Ser Asp
130 135 140
Lys Ile Lys Ile Phe Gly Glu Asp Phe Leu Asn Asp Lys Leu Lys Pro
145 150 155 160
Phe Tyr Lys Ser Asp Pro Ile Pro Glu Lys Asn Asp Glu Asp Val Lys
165 170 175
Ile Val Val Gly Asp Asn Phe Asp Glu Ile Val Leu Asp Asp Ser Lys
180 185 190
Asp Val Leu Leu Glu Val Tyr Ala Pro Trp Cys Gly His Cys Gln Ala
195 200 205
Leu Glu Pro Met Tyr Asn Lys Leu Ala Lys His Leu Arg Ser Ile Asp
210 215 220
Ser Leu Val Ile Thr Glu Met Asp Gly Thr Thr Asn Glu His Pro Lys
225 230 235 240
Ala Lys Ala Glu Gly Phe Pro Thr Ile Leu Phe Phe Pro Ala Gly Asn
245 250 255
Lys Thr Ser Glu Pro Ile Thr Val Asp Thr Asp Arg Thr Val Val Ala
260 265 270
Phe Tyr Lys Phe Leu Arg Lys His Ala Thr Ile Pro Phe Lys Leu Glu
275 280 285
Lys Pro Ala Ser Thr Glu Xaa Pro Lys Thr Ala Glu Ser Thr Pro Lys

290	295	300
Val Glu Thr Thr Glu Thr Lys Glu Ser Pro Asp Ser Thr Thr Lys Ser		
305	310	315
Ser Gln Ser Asp Ser Lys Asp Glu Leu		
	325	

(2) INFORMATION FOR SEQ ID NO:432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1755 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1755
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

aaacaaaggg	tcttgctccg	acacgacaa	aaatccagat	tctgagctta	gggaaacttg	60
agaaggagaa	aaaaatgtcg	aacatagaca	tagaagggat	cttgaaggat	ctacctaagt	120
atgggagagat	cccaaagacg	aagatagttt	gcacattagg	accagcttct	cgcactgttt	180
ccatgatcga	aaagcttttt	aaagccggta	tgaatgtggc	tcgcttcaac	ttctcacatg	240
gaagccatga	ataccattcaa	gagacactcg	acaacctccg	ctctgctatg	cataataaccg	300
gcattctcga	tgctgtcatg	cttgatacta	aggggacctga	gattcgtact	ggtttcttga	360
aagatgggaa	ccctatacaa	ctgaaggaag	gtcaagagat	tactataacc	actgattatg	420
acattcaagg	agacgaatca	acgatatcca	tgagctataa	aaagctgcct	ttggatgtga	480
agcccgaa	caccatactc	tgctgcagatg	gaagcataag	tctagctgtc	ttgtcatgtg	540
atcctgagtc	tggaaactgt	aggtgccggt	gtgaaaactc	ggcgaatgct	gggtgaaagaa	600
agaatgtgaa	tcttccctggc	gtgtgtgttg	atcttccocac	tttgacagat	aaagatattg	660
aaagattctc	cggtgtgggt	gttccgaaca	gcattgatat	gattgtctct	tcgtttgtcc	720
gtaaaggttc	ggatcttggt	aaatgtccga	aggttcttgg	atctcatgct	aaagcataaa	780
tgctcatgtc	aaaggttgag	aaccaggaag	gtgtgattaa	ctttgatgat	atcttgcgtg	840
aaacagatgc	gttcatgtgt	gcccgtgggt	actctcggtg	ggagattccg	atagagaaga	900
tcttcttggc	tcaaaagtgt	atgatctaca	agtgtaacct	tgccggctaa	ccggttggtca	960
cagccactca	gatgctggag	tcaatgatca	aatcacctcg	gccaaaccga	gctgaagcca	1020
cagatgttgc	aaatgctgtt	cttgatggta	ctgactgtgt	gatgcttagc	ggtagaggtg	1080
cagcaggagc	ttatccggaa	atagctgtga	aagtcattgc	taagatatgc	attgaagccg	1140
aatctcgtct	tgattacaac	acaatcttta	aagagatgat	ccgagcaact	ccacttccaa	1200
tgagccactc	cgagagctct	gcattcatccg	ctgtacggac	tgctaacaaa	gcgagggcaa	1260
aactcatcat	tgtgttgaca	cgtggagggt	caactgctaa	tctcgtggct	aaatacacag	1320
cggtctgtcc	gattctgtca	gtgggtgtcc	cggttatgac	cactgattcc	tttgactgtg	1380
ctttagtagt	cgaagtaoct	gcaagggata	ctctgatata	cagaggttca	attccctatg	1440
tggtgtaagc	atctgcgaag	gcaacagata	gtgaagccac	cgaagtattc	attgaagctg	1500
actctgaagt	ggctactcag	agaggactgt	gcaaccgtgg	tgatgcaact	gtggcgtcgc	1560
ccctgattgg	agctgcctca	gttattaaaga	tctgtgtggt	taagtgaagt	tacagacttc	1620
tttcaatacc	tcaaatcttg	caattgttgg	aatcgtaact	gagattttgc	ttttagcat	1680
gaaataaaga	aaacagggtca	gaatagtctc	tgaaactctg	ttacttttaa	gatatctctc	1740
tctctttttt	ttttc					

(2) INFORMATION FOR SEQ ID NO:433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..534
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498441

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

Thr	Arg	Val	Leu	Ala	Pro	Thr	Arg	Gln	Gln	Ile	Leu	Ser	Leu
1				5				10					15

Gly Lys Leu Glu Lys Glu Lys Lys Met Ser Asn Ile Asp Ile Glu Gly
20 25 30
Ile Leu Lys Asp Leu Pro Asn Asp Gly Arg Ile Pro Lys Thr Lys Ile
35 40 45
Val Cys Thr Leu Gly Pro Ala Ser Arg Thr Val Ser Met Ile Glu Lys
50 55 60
Leu Leu Lys Ala Gly Met Asn Val Ala Arg Phe Asn Phe Ser His Gly
65 70 75 80
Ser His Glu Tyr His Gln Glu Thr Leu Asp Asn Leu Arg Ser Ala Met
85 90 95
His Asn Thr Gly Ile Leu Ala Ala Val Met Leu Asp Thr Lys Gly Pro
100 105 110
Glu Ile Arg Thr Gly Phe Leu Lys Asp Gly Asn Pro Ile Gln Leu Lys
115 120 125
Glu Gly Gln Glu Ile Thr Ile Thr Thr Asp Tyr Asp Ile Gln Gly Asp
130 135 140
Glu Ser Thr Thr Ile Ser Met Ser Tyr Lys Lys Leu Pro Leu Asp Val Lys
145 150 155 160
Pro Gly Asn Thr Ile Leu Cys Ala Asp Gly Ser Ile Ser Leu Ala Val
165 170 175
Leu Ser Cys Asp Pro Glu Ser Gly Thr Val Arg Cys Arg Cys Glu Asn
180 185 190
Ser Ala Met Leu Gly Glu Arg Lys Asn Val Asn Leu Pro Gly Val Val
195 200 205
Val Asp Leu Pro Thr Leu Thr Asp Lys Asp Ile Glu Asp Ile Leu Gly
210 215 220
Trp Gly Val Pro Asn Ser Ile Asp Met Ile Ala Leu Ser Phe Val Arg
225 230 235 240
Lys Gly Ser Asp Leu Val Asn Val Arg Lys Val Leu Gly Ser His Ala
245 250 255
Lys Ser Ile Met Leu Met Ser Lys Val Glu Asn Gln Glu Gly Val Ile
260 265 270
Asn Phe Asp Glu Ile Leu Arg Glu Thr Asp Ala Phe Met Val Ala Arg
275 280 285
Gly Asp Leu Gly Met Glu Ile Pro Ile Glu Lys Ile Phe Leu Ala Gln
290 295 300
Lys Leu Met Ile Tyr Lys Cys Asn Leu Ala Gly Lys Pro Val Val Thr
305 310 315 320
Ala Thr Gln Met Leu Glu Ser Met Ile Lys Ser Pro Arg Pro Thr Arg
325 330 335
Ala Glu Ala Thr Asp Val Ala Asn Ala Val Leu Asp Gly Thr Asp Cys
340 345 350
Val Met Leu Ser Gly Glu Ser Ala Ala Gly Ala Tyr Pro Glu Ile Ala
355 360 365
Val Lys Val Met Ala Lys Ile Cys Ile Glu Ala Glu Ser Ser Leu Asp
370 375 380
Tyr Asn Thr Ile Phe Lys Glu Met Ile Arg Ala Thr Pro Leu Pro Met
385 390 395 400
Ser Pro Leu Glu Ser Leu Ala Ser Ser Ala Val Arg Thr Ala Asn Lys
405 410 415
Ala Arg Ala Lys Leu Ile Ile Val Leu Thr Arg Gly Gly Ser Thr Ala
420 425 430
Asn Leu Val Ala Lys Tyr Arg Pro Ala Val Pro Ile Leu Ser Val Val
435 440 445
Val Pro Val Met Thr Thr Asp Ser Phe Asp Trp Ser Cys Ser Asp Glu
450 455 460
Ser Pro Ala Arg His Ser Leu Ile Tyr Arg Gly Leu Ile Pro Met Leu
465 470 475 480
Ala Glu Gly Ser Ala Lys Ala Thr Asp Ser Glu Ala Thr Glu Val Ile
485 490 495
Ile Glu Ala Ala Leu Lys Ser Ala Thr Gln Arg Gly Leu Cys Asn Arg

500 505 510
Gly Asp Ala Ile Val Ala Leu His Arg Ile Gly Ala Ala Ser Val Ile
515 520 525
Lys Ile Cys Val Val Lys

530

(2) INFORMATION FOR SEQ ID NO:434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..510

- (D) OTHER INFORMATION: / Ceres Seq. ID 1498442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

Met	Ser	Asn	Ile	Asp	Ile	Glu	Gly	Ile	Leu	Lys	Asp	Leu	Pro	Asn	Asp	
1			5					10						15		
Gly	Arg	Ile	Pro	Lys	Thr	Lys	Ile	Val	Cys	Thr	Leu	Gly	Pro	Ala	Ser	
			20				25						30			
Arg	Thr	Val	Ser	Met	Ile	Glu	Lys	Leu	Leu	Lys	Ala	Gly	Met	Asn	Val	
			35				40					45				
Ala	Arg	Phe	Asn	Phe	Ser	His	Gly	Ser	His	Glu	Tyr	His	Gln	Glu	Thr	
			50				55				60					
Leu	Asp	Asn	Leu	Arg	Ser	Ala	Met	His	Asn	Thr	Gly	Ile	Leu	Ala	Ala	
			65				70				75			80		
Val	Met	Leu	Asp	Thr	Lys	Gly	Pro	Glu	Ile	Arg	Thr	Gly	Phe	Leu	Lys	
			85						90				95			
Asp	Gly	Asn	Pro	Ile	Gln	Leu	Lys	Glu	Gly	Gln	Glu	Ile	Thr	Ile	Thr	
			100					105					110			
Thr	Asp	Tyr	Asp	Ile	Gln	Gly	Asp	Glu	Ser	Thr	Ile	Ser	Met	Ser	Tyr	
			115					120				125				
Lys	Lys	Leu	Pro	Leu	Asp	Val	Lys	Pro	Gly	Asn	Thr	Ile	Leu	Cys	Ala	
			130				135				140					
Asp	Gly	Ser	Ile	Ser	Leu	Ala	Val	Leu	Ser	Cys	Asp	Pro	Glu	Ser	Gly	
			145				150				155			160		
Thr	Val	Arg	Cys	Arg	Cys	Glu	Asn	Ser	Ala	Met	Leu	Gly	Glu	Arg	Lys	
			165						170				175			
Asn	Val	Asn	Leu	Pro	Gly	Val	Val	Val	Asp	Leu	Pro	Thr	Leu	Thr	Asp	
			180					185					190			
Lys	Asp	Ile	Glu	Asp	Ile	Leu	Gly	Trp	Gly	Val	Pro	Asn	Ser	Ile	Asp	
			195					200				205				
Met	Ile	Ala	Leu	Ser	Phe	Val	Arg	Lys	Gly	Ser	Asp	Leu	Val	Asn	Val	
			210					215				220				
Arg	Lys	Val	Leu	Gly	Ser	His	Ala	Lys	Ser	Ile	Met	Leu	Met	Ser	Lys	
			225					230				235				
Val	Glu	Asn	Gln	Glu	Gly	Val	Ile	Asn	Phe	Asp	Glu	Ile	Leu	Arg	Glu	
			245						250				255			
Thr	Asp	Ala	Phe	Met	Val	Ala	Arg	Gly	Asp	Leu	Gly	Met	Glu	Ile	Pro	
			260					265				270				
Ile	Glu	Lys	Ile	Phe	Leu	Ala	Gln	Lys	Leu	Met	Ile	Tyr	Lys	Cys	Asn	
			275					280				285				
Leu	Ala	Gly	Lys	Pro	Val	Thr	Ala	Thr	Gln	Met	Leu	Glu	Ser	Met		
			290					295				300				
Ile	Lys	Ser	Pro	Arg	Pro	Thr	Arg	Ala	Glu	Ala	Thr	Asp	Val	Ala	Asn	
			305					310				315			320	
Ala	Val	Leu	Asp	Gly	Thr	Asp	Cys	Val	Met	Leu	Ser	Gly	Glu	Ser	Ala	
			325						330				335			
Ala	Gly	Ala	Tyr	Pro	Glu	Ile	Ala	Val	Lys	Val	Met	Ala	Lys	Ile	Cys	
			340					345					350			

Ile Glu Ala Glu Ser Ser Leu Asp Tyr Asn Thr Ile Phe Lys Glu Met
355 360 365
Ile Arg Ala Thr Pro Leu Pro Met Ser Pro Leu Glu Ser Leu Ala Ser
370 375 380
Ser Ala Val Arg Thr Ala Asn Lys Ala Arg Ala Lys Leu Ile Ile Val
385 390 395 400
Leu Thr Arg Gly Gly Ser Thr Ala Asn Leu Val Ala Lys Tyr Arg Pro
405 410 415
Ala Val Pro Ile Leu Ser Val Val Val Pro Val Met Thr Thr Asp Ser
420 425 430
Phe Asp Trp Ser Cys Ser Asp Glu Ser Pro Ala Arg His Ser Leu Ile
435 440 445
Tyr Arg Gly Leu Ile Pro Met Leu Ala Glu Gly Ser Ala Lys Ala Thr
450 455 460
Asp Ser Glu Ala Thr Glu Val Ile Ile Glu Ala Ala Leu Lys Ser Ala
465 470 475 480
Thr Gln Arg Gly Leu Cys Asn Arg Gly Asp Ala Ile Val Ala Leu His
485 490 495
Arg Ile Gly Ala Ala Ser Val Ile Lys Ile Cys Val Val Lys
500 505 510

(2) INFORMATION FOR SEQ ID NO:435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..474
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

Met Ile Glu Lys Leu Leu Lys Ala Gly Met Asn Val Ala Arg Phe Asn
1 5 10 15
Phe Ser His Gly Ser His Glu Tyr His Gln Glu Thr Leu Asp Asn Leu
20 25 30
Arg Ser Ala Met His Asn Thr Gly Ile Leu Ala Ala Val Met Leu Asp
35 40 45
Thr Lys Gly Pro Glu Ile Arg Thr Gly Phe Leu Lys Asp Gly Asn Pro
50 55 60
Ile Gln Leu Lys Glu Gly Gln Glu Ile Thr Ile Thr Thr Asp Tyr Asp
65 70 75 80
Ile Gln Gly Asp Glu Ser Thr Ile Ser Met Ser Tyr Lys Lys Leu Pro
85 90 95
Leu Asp Val Lys Pro Gly Asn Thr Ile Leu Cys Ala Asp Gly Ser Ile
100 105 110
Ser Leu Ala Val Leu Ser Cys Asp Pro Glu Ser Gly Thr Val Arg Cys
115 120 125
Arg Cys Glu Asn Ser Ala Met Leu Gly Glu Arg Lys Asn Val Asn Leu
130 135 140
Pro Gly Val Val Val Asp Leu Pro Thr Leu Thr Asp Lys Asp Ile Glu
145 150 155 160
Asp Ile Leu Gly Trp Gly Val Pro Asn Ser Ile Asp Met Ile Ala Leu
165 170 175
Ser Phe Val Arg Lys Gly Ser Asp Leu Val Asn Val Arg Lys Val Leu
180 185 190
Gly Ser His Ala Lys Ser Ile Met Leu Met Ser Lys Val Glu Asn Gln
195 200 205
Glu Gly Val Ile Asn Phe Asp Glu Ile Leu Arg Glu Thr Thr Asp Ala Phe
210 215 220
Met Val Ala Arg Gly Asp Leu Gly Met Glu Ile Pro Ile Glu Lys Ile

[illegible]

(2) INFORMATION FOR SEQ ID NO:436:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1397 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1397
(D) OTHER INFORMATION: / Ceres Seq. ID 1498448

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

(X1) SEQUENCE						
caagctgttgc	gagattcttc	cagctctaac	atatctctac	tatactccaa	cgtaccatag	60
tctgtcatcat	caagaataatg	ggacaaactt	tgtctctatt	atgcctctct	ttgattgttt	120
ggcgcatcag	caaaaccccaa	actcatggga	actccaaatt	aagatctgtt	tgatgtcagg	180
ggacaggaag	agagatgcgcg	agttttgtgt	cttagctctc	ggagttgatg	taattgtgcg	240
gagtcgatca	ccgttcgtgt	tcagatcttt	tgtctcaatg	catataacca	caaggatatt	300
cttctgcacg	tattggccat	tcacgtcttc	tgtattatgt	ggcattgtgg	cttgtgtcaa	360
gacttttttt	ttcagcttct	ataccctcag	gacaacattt	tgtcacagtt	ctggcgcttc	420
tgatgtcgga	ttccaaatct	tcttaacggt	tgtcaaaaaa	ggaattaatg	atccaaattga	480
gagtcgcatt	ctcagactg	ataagattgg	tgctaaagtt	ataagcttgg	ctgctctcaa	540
caagaacgaa	gctctaaatg	gtgggtgaaac	actgtttgtc	atacctcatt	ctgaccttag	600
agttcgtgtg	gttctatggga	acacttttaac	tcagcagagtt	attctcagtc	aaattccaaa	660
agatgtgaat	gaggttttct	tgactggagc	caactctaac	ctgggaagag	ctattgtctc	720
ttacctttgt	ccgcctggga	tgagagttct	catgttgaca	ttgtctatgg	aaaggtttcaa	780
aaagattcat	aaagaggctc	ctgttgagtt	ccagacaacac	ctgttacaag	tgaccaataa	840
caatgtctgt	caacactgca	agacttgtag	cgtttgaaaa	tgtgtaacac	caagaagaca	900
gagctgggtg	ctgcagggga	cgattttcca	tcagttttgt	gtgcaccaca	tccttaagtt	960
tagaaggaac	tgcatcttacg	gtgatctagc	agctataaga	ctccctaaaa	atgtgtgaag	1020
actccqaact	ctgagactca	cgatggagag	aggggttgag	catcgctgac	atcgcaaggc	1080

agtggttcat atgcttgagg gttggaagca tcatgaggtt ggagccattg atgttgaccg 1140
tactgatttg gtgtgggaag cagccatgaa gtatggtctt agtgcgtgtt ctctactcac 1200
aaattgagtg aagagagaga caggtttcat tgtgtcttt tgactctccc aagattgggtc 1260
attctttgta caggtgaaag gagatgcaag caggaaaaaa aagtagaatt tcaccttatg 1320
tattgtttta tcttttatta atgatgtatt actttctttt tagatttccct taattaataat 1380
atatgcacct aatttcc

(2) INFORMATION FOR SEQ ID NO:437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..401
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498449

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

Lys	Leu	Phe	Glu	Ile	Leu	Pro	Val	Leu	Arg	Tyr	Leu	Ile	Tyr	Thr	Pro
1			5						10					15	
Thr	Tyr	His	Ser	Leu	His	His	Gln	Glu	Met	Gly	Thr	Asn	Phe	Cys	Leu
			20					25					30		
Phe	Met	Pro	Leu	Phe	Asp	Val	Leu	Gly	Asp	Thr	Gln	Asn	Pro	Asn	Ser
		35					40					45			
Trp	Glu	Leu	Gln	Lys	Lys	Ile	Arg	Leu	Ser	Ala	Gly	Glu	Arg	Lys	Arg
		50				55					60				
Val	Pro	Glu	Phe	Val	Phe	Leu	Ala	His	Gly	Val	Asp	Val	Met	Ser	Ala
65					70					75					80
Met	His	Ala	Pro	Phe	Val	Phe	Arg	Ser	Phe	Ala	Ser	Met	Pro	Tyr	Thr
			85					90					95		
Thr	Arg	Ile	Phe	Leu	Leu	Pro	Met	Trp	Pro	Phe	Thr	Phe	Cys	Val	Met
			100					105					110		
Leu	Gly	Met	Trp	Ala	Trp	Ser	Lys	Thr	Phe	Leu	Phe	Ser	Phe	Tyr	Thr
		115					120					125			
Leu	Arg	Asn	Asn	Leu	Cys	Gln	Thr	Trp	Gly	Val	Pro	Arg	Phe	Gly	Phe
		130				135					140				
Gln	Tyr	Phe	Leu	Pro	Phe	Ala	Thr	Lys	Gly	Ile	Asn	Asp	Gln	Ile	Glu
		145				150				155				160	
Ala	Ala	Ile	Leu	Arg	Ala	Asp	Lys	Ile	Gly	Val	Lys	Val	Ile	Ser	Leu
			165					170					175		
Ala	Ala	Leu	Asn	Lys	Asn	Glu	Ala	Leu	Asn	Gly	Gly	Gly	Thr	Leu	Phe
		180						185					190		
Val	Asn	Lys	His	Pro	Asp	Leu	Arg	Val	Val	His	Gly	Gly	Asn	Thr	
		195					200				205				
Leu	Thr	Ala	Ala	Val	Ile	Leu	Tyr	Glu	Ile	Pro	Lys	Asp	Val	Asn	Glu
		210				215					220				
Val	Phe	Leu	Thr	Gly	Ala	Thr	Ser	Lys	Leu	Gly	Arg	Ala	Ile	Ala	Leu
		225				230				235				240	
Tyr	Leu	Cys	Arg	Arg	Gly	Val	Arg	Val	Leu	Met	Leu	Thr	Leu	Ser	Met
			245					250					255		
Glu	Arg	Phe	Gln	Lys	Ile	Gln	Lys	Glu	Ala	Pro	Val	Glu	Phe	Gln	Asn
		260					265						270		
Asn	Leu	Val	Gln	Val	Thr	Lys	Trp	Asn	Ala	Ala	Gln	His	Cys	Lys	Thr
		275					280					285			
Trp	Ile	Val	Gly	Lys	Trp	Leu	Thr	Pro	Arg	Glu	Gln	Ser	Trp	Ala	Pro
		290				295					300				
Ala	Gly	Thr	His	Phe	His	Gln	Phe	Val	Val	Pro	Pro	Ile	Leu	Lys	Phe
		305				310				315				320	
Arg	Arg	Asn	Cys	Thr	Tyr	Gly	Asp	Leu	Ala	Ala	Met	Lys	Leu	Pro	Lys
			325					330					335		
Asp	Val	Glu	Gly	Leu	Gly	Thr	Cys	Glu	Tyr	Thr	Met	Glu	Arg	Gly	Val

(2) INFORMATION FOR SEQ ID NO:438:

(A) LENGTH: 376 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..376

(D) OTHER INFORMATION: / Ceres Seq. ID 1498450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

Met	(A1) Sequence															Gly
	Thr	Asn	Phe	Cys	Leu	Phe	Met	Pro	Leu	Phe	Asp	Val	Leu	Gly		
1	5							10					15			
Asp	Thr	Gln	Asn	Pro	Asn	Ser	Trp	Glu	Leu	Gln	Lys	Lys	Ile	Arg	Leu	
	20						25						30			
Ser	Ala	Gly	Glu	Arg	Lys	Arg	Val	Pro	Glu	Phe	Val	Phe	Leu	Ala	His	
	35						40					45				
Gly	Val	Asp	Val	Met	Ser	Ala	Met	His	Ala	Pro	Phe	Val	Phe	Arg	Ser	
	50					55					60					
Phe	Ala	Ser	Met	Pro	Tyr	Thr	Thr	Arg	Ile	Phe	Leu	Leu	Pro	Met	Trp	
65					70					75					80	
Pro	Phe	Thr	Phe	Cys	Val	Met	Leu	Gly	Met	Trp	Ala	Trp	Ser	Lys	Thr	
				85					90					95		
Phe	Leu	Phe	Ser	Phe	Tyr	Thr	Leu	Arg	Asn	Asn	Leu	Cys	Gln	Thr	Trp	
			100					105					110			
Gly	Val	Pro	Arg	Phe	Gly	Phe	Gln	Tyr	Phe	Leu	Pro	Phe	Ala	Thr	Lys	
		115					120					125				
Gly	Ile	Asn	Asp	Gln	Ile	Glu	Ala	Ala	Ile	Leu	Arg	Ala	Asp	Lys	Ile	
	130					135					140					
Gly	Val	Lys	Val	Ile	Ser	Leu	Ala	Ala	Leu	Asn	Lys	Asn	Glu	Ala	Leu	
145					150					155					160	
Asn	Gly	Gly	Gly	Thr	Leu	Phe	Val	Asn	Lys	His	Pro	Asp	Leu	Arg	Val	
				165					170					175		
Arg	Val	Val	His	Gly	Asn	Thr	Leu	Thr	Ala	Ala	Val	Ile	Leu	Tyr	Glu	
				180				185					190			
Ile	Pro	Lys	Asp	Val	Asn	Glu	Val	Phe	Leu	Thr	Gly	Ala	Thr	Ser	Lys	
		195					200					205				
Leu	Gly	Arg	Ala	Ile	Ala	Leu	Tyr	Leu	Cys	Arg	Arg	Gly	Val	Arg	Val	
	210					215					220					
Leu	Met	Leu	Thr	Leu	Ser	Met	Glu	Arg	Phe	Gln	Lys	Ile	Gln	Lys	Glu	
225					230					235					240	
Ala	Pro	Val	Glu	Phe	Gln	Asn	Asn	Leu	Val	Gln	Val	Thr	Lys	Tyr	Asn	
				245					250					255		
Ala	Ala	Gln	His	Cys	Lys	Thr	Trp	Ile	Val	Gly	Lys	Trp	Leu	Thr	Pro	
		260						265					270			
Arg	Glu	Gln	Ser	Trp	Ala	Pro	Ala	Gly	Thr	His	Phe	His	Gln	Phe	Val	
		275					280					285				
Val	Pro	Pro	Ile	Leu	Lys	Phe	Arg	Arg	Asn	Cys	Thr	Tyr	Gly	Asp	Glu	
	290					295					300					
Ala	Ala	Met	Lys	Leu	Pro	Lys	Asp	Val	Glu	Gly	Leu	Gly	Thr	Cys	Glu	
305					310					315					320	

Tyr Thr Met Glu Arg Gly Val Val His Ala Cys His Ala Gly Gly Val
325 330 335
Val His Met Leu Glu Gly Trp Lys His His Glu Val Gly Ala Ile Asp
340 345 350
Val Asp Arg Ile Asp Leu Val Trp Glu Ala Ala Met Lys Tyr Gly Leu
355 360 365
Ser Ala Val Ser Ser Leu Thr Asn
370 375

(2) INFORMATION FOR SEQ ID NO:439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..368
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498451

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

Met Pro Leu Phe Asp Val Leu Gly Asp Thr Gln Asn Pro Asn Ser Trp
1 5 10 15
Glu Leu Gln Lys Lys Ile Arg Leu Ser Ala Gly Glu Arg Lys Arg Val
20 25 30
Pro Glu Phe Val Phe Leu Ala His Gly Val Asp Val Met Ser Ala Met
35 40 45
His Ala Pro Phe Val Phe Arg Ser Phe Ala Ser Met Pro Tyr Thr Thr
50 55 60
Arg Ile Phe Leu Leu Pro Met Trp Pro Phe Thr Phe Cys Val Met Leu
65 70 75 80
Gly Met Trp Ala Trp Ser Lys Thr Phe Leu Phe Ser Phe Tyr Thr Leu
85 90 95
Arg Asn Asn Leu Cys Gln Thr Trp Gly Val Pro Arg Phe Gly Phe Gln
100 105 110
Tyr Phe Leu Pro Phe Ala Thr Lys Gly Ile Asn Asp Gln Ile Glu Ala
115 120 125
Ala Ile Leu Arg Ala Asp Lys Ile Gly Val Lys Val Ile Ser Leu Ala
130 135 140
Ala Leu Asn Lys Asn Glu Ala Leu Asn Gly Gly Gly Thr Leu Phe Val
145 150 155 160
Asn Lys His Pro Asp Leu Arg Val Arg Val Val His Gly Asn Thr Leu
165 170 175
Thr Ala Ala Val Ile Leu Tyr Glu Ile Pro Lys Asp Val Asn Glu Val
180 185 190
Phe Leu Thr Gly Ala Thr Ser Lys Leu Gly Arg Ala Ile Ala Leu Tyr
195 200 205
Leu Cys Arg Arg Gly Val Arg Val Leu Met Leu Thr Leu Ser Met Glu
210 215 220
Arg Phe Gln Lys Ile Gln Lys Glu Ala Pro Val Glu Phe Gln Asn Asn
225 230 235 240
Leu Val Gln Val Thr Lys Tyr Asn Ala Ala Gln His Cys Lys Thr Trp
245 250 255
Ile Val Gly Lys Trp Leu Thr Pro Arg Glu Gln Ser Trp Ala Pro Ala
260 265 270
Gly Thr His Phe His Gln Phe Val Val Pro Pro Ile Leu Lys Phe Arg
275 280 285
Arg Asn Cys Thr Tyr Gly Asp Leu Ala Ala Met Lys Leu Pro Lys Asp
290 295 300
Val Glu Gly Leu Gly Thr Cys Glu Tyr Thr Met Glu Arg Gly Val Val
305 310 315 320
His Ala Cys His Ala Gly Gly Val Val His Met Leu Glu Gly Trp Lys

				325					330					335			
His	His	Glu	Val	Gly	Ala	Ile	Asp	Val	Asp	Arg	Ile	Asp	Leu	Val	Trp		
			340					345					350				
Glu	Ala	Ala	Met	Lys	Tyr	Gly	Leu	Ser	Ala	Val	Ser	Ser	Leu	Thr	Asn		
		355					360					365					

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1424 base pairs

- (A) LENGTH: 1424 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

```
(ix) FEATURE:
```

- (A) NAME/KEY: -
(B) LOCATION: 1..1424
(D) OTHER INFORMATION: / Ceres Seq. ID 1498452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

(x1) SEQUENCE DESCRIPTION					60
gtatgtgtgtt	gttgagagact	gaaccataca	cgctttttcg	acaattcttc	tctttctctc
tctctctctt	catgcaaaat	cacagttaca	agaataatac	aaagattatg	aaatcaaaaac
ataaagagac	aaaaatgagt	gatgtgcgtg	ttaacgcaga	tcttcaacaa	gaagagaatac
tgtttaaacc	accggttaag	agatctctca	ctctctccat	cgtgatctac	tttttttttc
tcttcgctgt	tatcgcttgc	agctctctgc	cgaagatact	tttcgtctac	ggttgctcga
gcgctgtggg	ctccacgttg	gttcaatctg	ctgtgctttc	ctctctcttc	tctctcaatt
ctactctccc	tcaactcgtt	gttcaaaaac	cgcactgcgc	tctttctcag	cgtctcaacg
tccgcctcat	catcttctct	gtgtgtttct	ggcttcttct	cggttttcaac	aaacttctct
tctcatggag	aacccctgtac	ctctcgggtg	ccacgctgat	gcttctcttc	tcgacacaaac
tctgtcttcc	tctcattttg	ctctagatga	tgttgaacaa	gaagatcatt	tcttcaaaac
tcaactgcgt	tgtctctgtg	acgtttaagc	ctgttttgtt	gcttcttgat	tcgagttaaag
ataaacctgc	cttgtttaacc	aaaacacatt	atttctctgg	gtatgatccg	acgatcggaag
ccggttttaact	cgttctctct	tacctccccg	tgacggagaa	gctataccgt	accggtttatt
gttacgcgat	ggtcatggag	gtgcaactgt	tgatggaaat	cgcagacagg	gttttcgcga
caatcggtat	ggcttgcgaa	ggcgggttta	aggaataatg	taaagaaagc	aaccatgttt
tcaaccaaaat	accaaacatt	ttgtggacgt	ttagcgatact	agcaaatgtg	tgcacgtggc
agctctcttt	cgcgaccagc	tcaaggtagt	tttacttgac	tgcaggtagt	atcgaggata
tctgcataac	gcgcttgctc	gcgatgaatg	tgataggaag	tgtgtgtgct	tacggttgta
tgtttgtgtg	agtgaagatt	gttgcgcagg	tgcattgatat	tgtgggaatt	tctattctca
catcagggat	gtatatgaag	atgaagaagg	aggagaagga	gaaggagaga	tattctggag
taaaagcacg	gaaagacacg	gagagatagg	aggtgaaaat	gggaataatg	aaagatgcag
tgtcggcgag	gggatgatagg	gcttgaagat	atctgtgtga	ttagagacag	cgattgatgt
attttatcga	aggaaagcaa	caaaaaaaaa	caaaatagta	gtatcttttt	gtgttctttc
ttttttctgc	ctttatgttt	ttttatgaag	cttgtgtctt	tgct	

(2) INFORMATION FOR SEQ ID NO:441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(1x) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..165
(D) OTHER INFORMATION: / Ceres Seq. ID 1498453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

(XI) SEQUENCE DESCRIPTION: GBU 18															
Met	Val	Met	Glu	Val	Gln	Leu	Val	Met	Glu	Phe	Ala	Ala	Thr	Val	Phe
1				5					10					15	
Ala	Thr	Ile	Gly	Met	Ala	Cys	Glu	Gly	Phe	Lys	Glu	Met	Thr	Val	Lys
			20					25					30		
Glu	Ala	Asn	His	Val	Phe	Thr	Lys	Gly	Pro	Thr	Phe	Tyr	Trp	Thr	Phe
		35				40						45			

Ala Ile Leu Ala Asn Val Val Thr Trp Gln Leu Ser Phe Ala Ala Thr
50 55 60
Ser Gly Met Val Tyr Leu Thr Ser Gly Ile Thr Gly Gly Ile Cys Met
65 70 75 80
Thr Ala Leu Leu Ala Met Asn Val Ile Gly Gly Val Val Ala Tyr Gly
85 90 95
Asp Val Phe Gly Gly Val Lys Ile Val Ser Thr Val Leu Cys Ile Trp
100 105 110
Gly Phe Ser Ser Tyr Thr Tyr Gly Met Tyr Met Lys Met Lys Lys Glu
115 120 125
Glu Lys Glu Lys Gly Glu Tyr Ser Gly Val Lys Thr Thr Glu Asp Ser
130 135 140
Gly Glu Met Glu Val Glu Met Gly Asn Val Lys Asp Asp Val Ala Ala
145 150 155 160
Ala Asp Asp Arg Ala
165

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..163
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498454

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

Met Glu Val Gln Leu Val Met Glu Phe Ala Ala Thr Val Phe Ala Thr
1 5 10 15
Ile Gly Met Ala Cys Glu Gly Gly Phe Lys Glu Met Val Lys Glu Ala
20 25 30
Asn His Val Phe Thr Lys Gly Pro Thr Phe Tyr Trp Thr Phe Ala Ile
35 40 45
Leu Ala Asn Val Val Thr Trp Gln Leu Ser Phe Ala Ala Thr Ser Gly
50 55 60
Met Val Tyr Leu Thr Ser Gly Ile Thr Gly Gly Ile Cys Met Thr Ala
65 70 75 80
Leu Leu Ala Met Asn Val Ile Gly Gly Val Val Ala Tyr Gly Asp Val
85 90 95
Phe Gly Gly Val Lys Ile Val Ser Thr Val Leu Cys Ile Trp Gly Phe
100 105 110
Ser Ser Tyr Thr Tyr Gly Met Tyr Met Lys Met Lys Lys Glu Glu Lys
115 120 125
Glu Lys Gly Glu Tyr Ser Gly Val Lys Thr Thr Glu Asp Ser Gly Glu
130 135 140
Met Glu Val Glu Met Gly Asn Val Lys Asp Asp Val Ala Ala Ala Asp
145 150 155 160
Asp Arg Ala

(2) INFORMATION FOR SEQ ID NO:443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..157
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498455

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

Met	Glu	Phe	Ala	Ala	Thr	Val	Phe	Ala	Thr	Ile	Gly	Met	Ala	Cys	Glu
1			5					10					15		
Gly	Gly	Phe	Lys	Glu	Met	Val	Lys	Glu	Ala	Asn	His	Val	Phe	Thr	Lys
			20				25					30			
Gly	Pro	Thr	Phe	Tyr	Trp	Thr	Phe	Ala	Ile	Leu	Ala	Asn	Val	Val	Thr
		35					40				45				
Trp	Gln	Leu	Ser	Phe	Ala	Ala	Thr	Ser	Gly	Met	Val	Tyr	Leu	Thr	Ser
		50				55					60				
Gly	Ile	Thr	Gly	Gly	Ile	Cys	Met	Thr	Ala	Leu	Leu	Ala	Met	Asn	Val
		65				70				75				80	
Ile	Gly	Gly	Val	Val	Ala	Tyr	Gly	Asp	Val	Phe	Gly	Gly	Val	Lys	Ile
			85					90					95		
Val	Ser	Thr	Val	Leu	Cys	Ile	Trp	Gly	Phe	Ser	Ser	Tyr	Thr	Tyr	Gly
			100					105					110		
Met	Tyr	Met	Lys	Met	Lys	Lys	Glu	Glu	Lys	Glu	Lys	Gly	Glu	Tyr	Ser
		115				120						125			
Gly	Val	Lys	Thr	Thr	Glu	Asp	Ser	Gly	Glu	Met	Glu	Val	Glu	Met	Gly
		130				135					140				
Asn	Val	Lys	Asp	Asp	Val	Ala	Ala	Ala	Asp	Asp	Arg	Ala			
		145			150					155					

(2) INFORMATION FOR SEQ ID NO:444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1005 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1005
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

aggggtttttt	tcagcggaga	ttagcttcag	tatccattgg	cggattagcc	tcagagtgc	60
ctgatcaagg	ttttggagg	tgcatttgag	tgaggagatg	ttttcggctc	agcataaagt	120
tcataaggag	aagggtgtgg	aactttctga	attggatgag	caagttgtctc	aggcttttct	180
tgatttggag	aacaccaatc	aagaattgaa	aagtgaagctg	aaggatttat	acgtcaactc	240
ggctgttcaa	gttgatatct	ctggaggacg	caaggcaatt	gttgtcaatg	ttccttacag	300
actgagaaaa	gcttgaacag	ccgagttgrc	gtataaatcc	ttcagstcac	tttcaatttc	360
tytcatagtc	ktatggctac	taaatctcatc	accctcabtc	aaatccaccg	ccctaaaacc	420
ttactatcca	ccacaaaatc	tcgtcgacgc	ataataaaca	aaccctaaac	atccaaaacc	480
ataagcgaaa	acatgttgaa	caacgtcttt	tctggcaaaa	cgctaacaga	aatctaccat	540
aataagataa	attcacacc	acttactaat	ccactactgt	ttcttgaa	tcagttcgta	600
aaagaagagg	agacgaatca	acaagaacac	gggaagtgct	cgaacaaaga	tggttaagtc	660
ataaccgcga	caaataacgg	agatttgagg	cgtagtggtg	ctcgattaa	cttgttggtg	720
tcacatgaat	gttcataag	ccatatatta	aggaaggcaa	gagcggttta	caatgagttt	780
tggttgatga	cttatgtcga	gagtaacact	atggctgtgg	tagagccata	ttttctatt	840
ccggttaatta	attaatacct	ccaaatcgac	gtaattaaaa	attgtattta	taatatgtaa	900
aatgtttcat	tagttttgtt	gtgtgtgta	gtgatgtgct	ctctatatat	gtcatatatg	960
tgtaaacagg	acgtcaagtt	atgtaattaa	tgttatatga	aaact		

(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..160
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498457

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:
Met Ala Thr Lys Phe Ile Thr Leu Xaa Gln Ile His Arg Pro Lys Thr
1 5 10 15
Leu Leu Ser Thr Thr Lys Ser Arg Arg Asn Asn Asn Lys Pro Lys
20 25 30
Pro Ser Lys Thr Ile Ser Glu Asn Met Leu Asn Asn Val Phe Ser Gly
35 40 45
Lys Thr Leu Thr Glu Ile Tyr His Asn Lys Ile Asn Ser His Pro Leu
50 55 60
Thr Asn Pro Leu Leu Phe Leu Glu Asp Gln Phe Val Lys Glu Glu Glu
65 70 75 80
Thr Asn Gln Gln Glu His Gly Lys Val Ser Asn Lys Asp Gly Lys Ser
85 90 95
Ile Thr Ala Thr Lys Tyr Gly Asp Leu Arg Arg Asp Val Ala Arg Leu
100 105 110
Ser Leu Leu Trp Tyr Met Lys Cys Ser Ile Ser His Ile Leu Arg Lys
115 120 125
Ala Arg Ala Phe Tyr Asn Glu Phe Cys Cys Asp Thr Tyr Ala Glu Ser
130 135 140
Asn Thr Met Ala Val Val Glu Pro Tyr Phe Ser Ile Pro Val Ile Asn
145 150 155 160

(2) INFORMATION FOR SEQ ID NO:446:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1498458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

Met Leu Asn Asn Val Phe Ser Gly Lys Thr Leu Thr Glu Ile Tyr His
1 5 10 15
Asn Lys Ile Asn Ser His Pro Leu Thr Asn Pro Leu Phe Leu Glu
20 25 30
Asp Gln Phe Val Lys Glu Glu Glu Thr Asn Gln Gln Glu His Gly Lys
35 40 45
Val Ser Asn Lys Asp Gly Lys Ser Ile Thr Ala Thr Lys Tyr Gly Asp
50 55 60
Leu Arg Arg Asp Val Ala Arg Leu Ser Leu Leu Trp Tyr Met Lys Cys
65 70 75 80
Ser Ile Ser His Ile Leu Arg Lys Ala Arg Ala Phe Tyr Asn Glu Phe
85 90 95
Cys Cys Asp Thr Tyr Ala Glu Ser Asn Thr Met Ala Val Val Glu Pro
100 105 110
Tyr Phe Ser Ile Pro Val Ile Asn
115 120

(2) INFORMATION FOR SEQ ID NO:447:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1802 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

(2) INFORMATION FOR SEQ ID NO:448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..217
(D) OTHER INFORMATION

(D) OTHER INFORMATION: / Ceres seq. ID 1498460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

Met	Ile	Glu	Pro	Ser	Met	Glu	Arg	Glu	Asn	Gly	Ala	Leu	Thr	Ala	Ala
1				5					10					15	
Thr	Thr	Thr	Thr	Thr	Ala	Val	Thr	Ser	Pro	Pro	Pro	Met	Ala	Ser	Ser
			20					25				30			
Pro	Arg	Gln	Ala	Leu	Val	Glu	Arg	Leu	Lys	Asp	Tyr	Gly	Gln	Glu	Asp
		35					40					45			
Ile	Phe	Ser	Leu	Trp	Asp	Glu	Leu	Ser	Pro	Asp	Glu	Lys	Asp	Phe	Leu
	50					55					60				
Val	Arg	Asp	Ile	Glu	Asn	Leu	Asp	Leu	Pro	Arg	Ile	Asp	Arg	Ile	Ile
65					70					75				80	
Arg	Cys	Ser	Leu	His	Ser	Gln	Gly	Leu	Pro	Val	Ala	Ala	Ile	Glu	Pro
				85				90						95	
Val	Pro	Glu	Asn	Trp	Val	Ser	Thr	Val	Asp	Gly	Arg	Thr	Met	Glu	Asp
			100					105					110		
Arg	Glu	Lys	Trp	Trp	Lys	Met	Gly	Leu	Lys	Thr	Ile	Tyr	Glu	Gly	Lys
		115					120					125			

Leu Gly Val Val Leu Leu Ser Gly Gly Gln Gly Thr Arg Leu Gly Ser
130 135 140
Ser Asp Pro Lys Gly Cys Phe Asn Ile Gly Leu Pro Ser Gly Lys Ser
145 150 155 160
Leu Phe Gln Ile Gln Ala Glu Arg Ile Leu Cys Val Gln Arg Leu Ala
165 170 175
Ala Gln Val Val Ser Glu Gly Pro Ile Arg Pro Val Thr Asn Thr Leu
180 185 190
Val Tyr Tyr Asp Leu Val His Leu Leu Met Xaa Ala Thr Arg Lys Tyr
195 200 205
Phe Ser Xaa Ser Gln Val Leu Trp Ser
210 215

(2) INFORMATION FOR SEQ ID NO:449:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 266 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..266

- (D) OTHER INFORMATION: / Ceres Seq. ID 1498461

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

Met Glu Thr Pro Phe Ser Leu Ala Lys Ala Pro Asp Gly Asn Gly Gly
1 5 10 15
Val Tyr Ala Ala Leu Lys Cys Ser Arg Leu Leu Glu Asp Met Ala Ser
20 25 30
Arg Gly Ile Lys Tyr Val Asp Cys Tyr Gly Val Asp Asn Val Leu Val
35 40 45
Arg Val Ala Asp Pro Thr Phe Leu Gly Tyr Phe Ile Asp Lys Gly Ala
50 55 60
Ala Ser Ala Ala Lys Val Val Arg Lys Ala Tyr Xaa Xaa Glu Gln Val
65 70 75 80
Gly Val Xaa Val Arg Arg Gly Lys Gly Gly Pro Leu Thr Val Val Glu
85 90 95
Tyr Ser Glu Leu Asp Gln Ser Met Ala Ser Ala Ile Asn Gln Arg Thr
100 105 110
Gly Arg Leu Gln Tyr Cys Trp Ser Asn Val Cys Leu His Met Phe Thr
115 120 125
Leu Asp Phe Leu Asn Gln Val Ala Thr Gly Leu Glu Lys Asp Ser Val
130 135 140
Tyr His Leu Ala Glu Lys Lys Ile Pro Ser Met Asn Gly Tyr Thr Met
145 150 155 160
Gly Leu Lys Leu Glu Gln Phe Ile Phe Asp Ser Phe Pro Tyr Ala Pro
165 170 175
Ser Thr Ala Leu Phe Glu Val Leu Arg Glu Glu Glu Phe Ala Pro Val
180 185 190
Lys Asn Val Asn Gly Ser Asn Phe Asp Thr Pro Glu Ser Ala Arg Leu
195 200 205
Leu Val Leu Arg Leu His Thr Arg Trp Val Ile Ala Ala Gly Gly Phe
210 215 220
Leu Thr His Ser Val Pro Leu Tyr Ala Thr Gly Val Glu Val Ser Pro
225 230 235 240
Leu Cys Ser Tyr Ala Gly Glu Asn Leu Glu Ala Ile Cys Arg Gly Arg
245 250 255
Thr Phe His Ala Pro Cys Glu Ile Ser Leu
260 265

(2) INFORMATION FOR SEQ ID NO:450:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 237 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..237
(D) OTHER INFORMATION: / Ceres Seq. ID 1498462
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:
Met Ala Ser Arg Gly Ile Lys Tyr Val Asp Cys Tyr Gly Val Asp Asn
1 5 10 15
Val Leu Val Arg Val Ala Asp Pro Thr Phe Leu Gly Tyr Phe Ile Asp
20 25 30
Lys Gly Ala Ala Ser Ala Ala Lys Val Val Arg Lys Ala Tyr Xaa Xaa
35 40 45
Glu Gln Val Gly Val Xaa Val Arg Arg Gly Lys Gly Gly Pro Leu Thr
50 55 60
Val Val Glu Tyr Ser Glu Leu Asp Gln Ser Met Ala Ser Ala Ile Asn
65 70 75 80
Gln Arg Thr Gly Arg Leu Gln Tyr Cys Trp Ser Asn Val Cys Leu His
85 90 95
Met Phe Thr Leu Asp Phe Leu Asn Gln Val Ala Thr Gly Leu Glu Lys
100 105 110
Asp Ser Val Tyr His Leu Ala Glu Lys Lys Ile Pro Ser Met Asn Gly
115 120 125
Tyr Thr Met Gly Leu Lys Leu Glu Gln Phe Ile Phe Asp Ser Phe Pro
130 135 140
Tyr Ala Pro Ser Thr Ala Leu Phe Glu Val Leu Arg Glu Glu Glu Phe
145 150 155 160
Ala Pro Val Lys Asn Val Asn Gly Ser Asn Phe Asp Thr Pro Glu Ser
165 170 175
Ala Arg Leu Leu Val Leu Arg Leu His Thr Arg Trp Val Ile Ala Ala
180 185 190
Gly Gly Phe Leu Thr His Ser Val Pro Leu Tyr Ala Thr Gly Val Glu
195 200 205
Val Ser Pro Leu Cys Ser Tyr Ala Gly Glu Asn Leu Glu Ala Ile Cys
210 215 220
Arg Gly Arg Thr Phe His Ala Pro Cys Glu Ile Ser Leu
225 230 235

(2) INFORMATION FOR SEQ ID NO:451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1359 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1359
(D) OTHER INFORMATION: / Ceres Seq. ID 1498471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

ctaactctctc	tggtcatctt	ttctctctt	tatttataaa	tttatctgca	tagtactctc	60
tgaatctata	tcttcaaaaa	aaaaaaacgt	ccaagatcaa	atcaagaaac	ccattaaaaa	120
aaaaaatcag	gttttggttt	cagttttaag	ggtttaaggt	ttcttgggga	agaaacgatg	180
gagacttttt	gtgggtttca	aaaggaggaa	gagcagatgg	atttaccctc	tggtgttcagg	240
tttcatccaa	cagatgaaga	actcataaac	tcactatctc	cataagaagg	ttcttgacac	300
cagcttctca	gctaaaagcta	tcggtgaagt	tgatttaaac	aaatcagagc	catgggagtt	360
accatggatg	gcaaaaatgg	gtgagaagaa	atgggtattt	ttctgtgtga	gagacagaaa	420
gtatcccaac	gtgttaagaa	ctaaccgagc	aactgaagcc	gggtatttgg	agggcaccgg	480
gaagataaaa	gagatatacc	gaggcaaatc	acttggtggg	atgaagaaga	cactgtgttt	540
ctatagagga	agagctccta	aaggtcagaa	aaccaactgg	gtgatgcata	agtacaggct	600

tgaaaaaaat	tctctgccca	taacttgccg	aaaaccgcaa	agaatgaatg	gggtgatatgc	660
agggtgttcc	aaaagagtg	tgagggaag	aagatcccca	tttcgagttc	aatccgaatc	720
gggttcaatc	gaaccgactt	taacccttgc	cttttgccct	ctttaaccga	ttcttcgcct	780
tacaacgata	aaacccaaac	agaaccggtc	tacgtgccct	gcttctccaa	ccaaacggat	840
caaaaccaag	gaaccacact	caattgcttc	agcagccctg	ttcttaactc	gatccaagcc	900
gacatttttc	acaggattcc	actctatcaa	actcagctcc	tccagggttc	tatgaatcta	960
cgagagcccg	ttctcacgca	agaacactca	gttctacatg	ctatgatcga	gaacaacaga	1020
agacaaatgc	tcaaaacgat	gagtgctcca	caagaaacgc	gagtttcaac	tgacatgaac	1080
actgatatct	catcggtatt	tgaatttggt	aagaggcggt	ttgatttcca	agaagatccc	1140
tcttctctta	ctggaccggg	tgatcttgaa	cccttctgga	attactgaag	atgattcaag	1200
attctcatgt	ccattaatat	actgtgggtg	gttaaagttt	gtataggcta	ttgtcatata	1260
ctctcatatc	aacttccact	atatattata	acaatttaaa	gaaacttaaa	aatatgattt	1320
gatatatgac	taaagtatta	taatacaatt	ttgtacccc			

(2) INFORMATION FOR SEQ ID NO:452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

Met	Ala	Lys	Met	Gly	Glu	Lys	Glu	Trp	Tyr	Phe	Cys	Val	Arg	Asp
1				5				10				15		
Arg	Lys	Tyr	Pro	Thr	Gly	Leu	Arg	Thr	Asn	Arg	Ala	Thr	Glu	Ala
				20				25				30		
Tyr	Trp	Lys	Ala	Thr	Gly	Lys	Asp	Lys	Glu	Ile	Tyr	Arg	Gly	Lys
				35				40				45		
Leu	Val	Gly	Met	Lys	Lys	Thr	Leu	Val	Phe	Tyr	Arg	Gly	Arg	Ala
				50				55				60		
Lys	Gly	Gln	Lys	Thr	Asn	Trp	Val	Met	His	Glu	Tyr	Arg	Leu	Glu
				65				70				75		
Asn	Ser	Leu	Pro	Ile	Thr	Cys	Arg	Lys	Pro	Gln	Arg	Met	Asn	Gly
				85				90				95		

(2) INFORMATION FOR SEQ ID NO:453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498473

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

Met	Gly	Glu	Lys	Glu	Trp	Tyr	Phe	Phe	Cys	Val	Arg	Asp	Arg	Lys	Trp
1				5				10				15			
Pro	Thr	Gly	Leu	Arg	Thr	Asn	Arg	Ala	Thr	Glu	Ala	Gly	Tyr	Trp	Lys
				20				25				30			
Ala	Thr	Gly	Lys	Asp	Lys	Glu	Ile	Tyr	Arg	Gly	Lys	Ser	Leu	Val	Gly
				35				40				45			
Met	Lys	Lys	Thr	Leu	Val	Phe	Tyr	Arg	Gly	Arg	Ala	Pro	Lys	Gly	Gln
				50				55				60			
Lys	Thr	Asn	Trp	Val	Met	His	Glu	Tyr	Arg	Leu	Glu	Lys	Asn	Ser	Leu
				65				70				75			
Pro	Ile	Thr	Cys	Arg	Lys	Pro	Gln	Arg	Met	Asn	Gly				
				85				90							

(2) INFORMATION FOR SEQ ID NO:454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

Met	Asn	Leu	Gln	Ser	Pro	Val	Leu	Thr	Gln	Glu	His	Ser	Val	Leu	His
1			5					10					15		
Ala	Met	Ile	Glu	Asn	Asn	Arg	Arg	Gln	Ser	Leu	Lys	Thr	Met	Ser	Val
			20					25					30		
Ser	Gln	Glu	Thr	Gly	Val	Ser	Thr	Asp	Met	Asn	Thr	Asp	Ile	Ser	Ser
			35				40					45			
Asp	Phe	Glu	Phe	Gly	Lys	Arg	Arg	Phe	Asp	Ser	Gln	Glu	Asp	Pro	Ser
			50			55					60				
Ser	Ser	Thr	Gly	Pro	Val	Asp	Leu	Glu	Pro	Phe	Trp	Asn	Tyr		
65			70					75							

(2) INFORMATION FOR SEQ ID NO:455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1879 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1879
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498475

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

acttctctct	ctctctctct	ctctttttct	aaatcttgga	ggagaagaag	caaagaatta	60
gactactctg	caacaatggc	tatttattct	gtccataacg	cgcacaagaa	gcattggtgg	120
ttcactcaca	agaagattgt	tgataagtac	attaaggacg	caagatcttt	aatggagagt	180
gaggagcaaa	acgacgttgc	ttcagccatt	cattacttag	acgcggcttt	atcaatatcc	240
ccgcgttcgg	aaactgcgtt	agaacttaaa	gccagatctt	tgctctttct	acgtcgcttc	300
aaagatgtag	ttgatatgct	tcaagattat	atcccaagcc	tcaagcttgc	cgtgaacagag	360
gaagatggat	cttattcata	cgaagggtct	tctactctt	ctctctcttc	tcagctctcc	420
cggaaacttc	tctctgactc	atctctctgc	cgtgactcat	cttctaaagt	cttctctgtt	480
tctactccta	aaaaaataat	tatggctggg	atttgtaaaa	atcgcgatca	agataaacaa	540
tggagatacg	ttgttttagg	acaagcttgt	tgccacctag	gattaatgga	ggacgattg	600
gttctctctt	aaaccggaaa	acgtctcgca	acagtcgagt	tcgcgcgtct	aagtgtaaag	660
ttgtcagatg	atagcgtctc	actctctctc	tctgaatcgt	catcatcatc	atcctcatcc	720
tcttatgctt	ttctctccag	caaagtctcc	gaatgcggaa	ccgtcaactaa	octctcgcgc	780
cacaagaaaa	atctctctcg	gcgtcgctcc	gcgcgattcg	ccgcctttga	cgttggactt	840
ttcgccgact	cgatcagctc	cttctccaaa	attctcgacg	gtcgtcgctg	tcccgcgcca	900
caaggatctc	tcgctgattg	ctatatgcac	cgcgcgcgcc	gtgtacaaat	cgcgcggaaa	960
atcgctggag	cgatgcggca	ttgtaataaa	accttagctc	ttgagccgtc	gtgtatccat	1020
cgcttggaga	ctagagccac	ctttttggaa	acggttcggt	gtctaccgga	ttcgcttcac	1080
gatttagagc	atttgaagat	actctacac	actatcttac	gtgatccgga	acttcccgga	1140
ccaccctgga	acaagcaaca	ttgtaataac	agagagatcc	cgggaagaat	atgcgaaactg	1200
acgacgaaat	cgaagaaact	gaaagcaaaa	atggcgaatg	gagaaatcgg	aaacgttgat	1260
tattacggat	tggtcggagt	tagacgcggt	tgacagagat	cggagcttga	tcagacaaat	1320
ctcttcgtct	gtctcaggca	ttaaacggac	aaggttttag	catctatgga	acgttgcgat	1380
ttcttcgcat	agagtggagt	tagttccgtt	aaagatcgag	cgaagatgct	ttcttttgtt	1440
ctttacggat	tgattcagag	aggttatata	gctttggcgg	cagcgatagg	tgaggaggaa	1500
cagaggaaga	agatgatggt	gttgactcaa	atgtcaacga	aaacggttga	agaacatgaa	1560
cggtttgaaa	aatccggttc	aattacttta	acgatttttg	cagaaataaa	gccggggaat	1620

tcgaacgcgt accaaggagt tttctgcga ggtcttgctg ctgttgaggag ttgtttatct 1680
aggaccggat ttaaccaacc gataccaatg aaatacagatg cgatcagttg ttaaccggga 1740
attttagttt gtatatattt aagaattttt tgtcacttta aatatctgt ctcttttgag 1800
ttaattctcc tactttctct ttattctgtg gcagaaaaatg ctttacttgt cgaatatcaa 1860
atcaaaagtag tgtgagatt

(2) INFORMATION FOR SEQ ID NO:456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..203
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498476

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

Thr Ser Leu Ser Leu Ser Leu Ser Phe Leu Lys Ser Trp Arg Arg Arg
1 5 10 15
Ser Lys Glu Leu Asp Tyr Ser Ala Thr Met Ala Ile Tyr Ser Val His
20 25 30
Asn Gly Asp Lys Lys His Trp Trp Phe Thr His Lys Lys Ile Val Asp
35 40 45
Lys Tyr Ile Lys Asp Ala Arg Ser Leu Met Glu Ser Glu Glu Gln Asn
50 55 60
Asp Val Ala Ser Ala Ile His Leu Leu Asp Ala Ala Leu Ser Ile Ser
65 70 75 80
Pro Arg Ser Glu Thr Ala Leu Glu Leu Lys Ala Arg Ser Leu Leu Phe
85 90 95
Leu Arg Arg Phe Lys Asp Val Val Asp Met Leu Gln Asp Tyr Ile Pro
100 105 110
Ser Leu Lys Leu Ala Val Asn Glu Glu Asp Gly Ser Tyr Ser Tyr Glu
115 120 125
Gly Ser Ser Tyr Ser Ser Ser Ser Ser Gln Leu Ser Arg Lys Leu Leu
130 135 140
Ser Asp Ser Ser Pro Arg Arg Asp Ser Ser Phe Lys Cys Phe Ser Val
145 150 155 160
Ser Tyr Leu Lys Lys Lys Ile Met Ala Gly Ile Cys Lys Asn Arg Asp
165 170 175
Gln Asp Lys Gln Trp Arg Tyr Val Val Leu Gly Gln Ala Cys Cys His
180 185 190
Leu Gly Leu Met Glu Asp Ala Leu Val Leu Leu
195 200

(2) INFORMATION FOR SEQ ID NO:457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..178
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

Met Ala Ile Tyr Ser Val His Asn Gly Asp Lys Lys His Trp Trp Phe
1 5 10 15
Thr His Lys Lys Ile Val Asp Lys Tyr Ile Lys Asp Ala Arg Ser Leu
20 25 30
Met Glu Ser Glu Glu Gln Asn Asp Val Ala Ser Ala Ile His Leu Leu
35 40 45

Asp Ala Ala Leu Ser Ile Ser Pro Arg Ser Glu Thr Ala Leu Glu Leu
50 55 60
Lys Ala Arg Ser Leu Leu Phe Leu Arg Arg Phe Lys Asp Val Val Asp
65 70 75 80
Met Leu Gln Asp Tyr Ile Pro Ser Leu Lys Leu Ala Val Asn Glu Glu
85 90 95
Asp Gly Ser Tyr Ser Tyr Glu Gly Ser Ser Tyr Ser Ser Ser Ser
100 105 110
Gln Leu Ser Arg Lys Leu Leu Ser Asp Ser Ser Pro Arg Arg Asp Ser
115 120 125
Ser Phe Lys Cys Phe Ser Val Ser Tyr Leu Lys Lys Lys Ile Met Ala
130 135 140
Gly Ile Cys Lys Asn Arg Asp Gln Asp Lys Gln Trp Arg Tyr Val Val
145 150 155 160
Leu Gly Gln Ala Cys Cys His Leu Gly Leu Met Glu Asp Ala Leu Val
165 170 175
Leu Leu

(2) INFORMATION FOR SEQ ID NO:458:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 269 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..269

(D) OTHER INFORMATION: / Ceres Seq. ID 1498478

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

Met His Arg Ala Ala Ala Tyr Lys Ser Ala Gly Lys Ile Ala Glu Ala
1 5 10 15
Ile Ala Asp Cys Asn Lys Thr Leu Ala Leu Glu Pro Ser Cys Ile His
20 25 30
Ala Leu Glu Thr Arg Ala Thr Leu Leu Glu Thr Val Arg Cys Leu Pro
35 40 45
Asp Ser Leu His Asp Leu Glu His Leu Lys Ile Leu Tyr Asn Thr Ile
50 55 60
Leu Arg Asp Arg Lys Leu Pro Gly Pro Pro Trp Lys Arg His Asn Val
65 70 75 80
Lys Tyr Arg Glu Ile Pro Gly Lys Leu Cys Glu Leu Thr Thr Lys Ser
85 90 95
Lys Lys Leu Lys Ala Lys Met Ala Asn Gly Glu Ile Gly Asn Val Asp
100 105 110
Tyr Tyr Gly Leu Val Gly Val Arg Arg Gly Cys Thr Arg Ser Glu Leu
115 120 125
Asp Arg Ala Asn Leu Leu Leu Cys Leu Arg His Lys Pro Asp Lys Ala
130 135 140
Leu Ala Phe Met Glu Arg Cys Asp Phe Phe Asp Gln Ser Glu Ile Ser
145 150 155 160
Ser Val Lys Asp Arg Ala Lys Met Ser Ser Leu Leu Leu Tyr Arg Leu
165 170 175
Ile Gln Arg Gly Tyr Thr Ala Leu Ala Ala Ile Ala Glu Glu Glu
180 185 190
Gln Arg Lys Lys Met Met Val Leu Thr Gln Met Ser Thr Lys Thr Val
195 200 205
Glu Glu His Glu Pro Val Glu Lys Ser Gly Ser Ile Thr Leu Thr Asp
210 215 220
Phe Ala Glu Ile Lys Pro Gly Asn Ser Asn Ala Tyr Gln Gly Val Phe
225 230 235 240
Cys Arg Gly Leu Ala Ala Val Gly Ser Leu Leu Ser Arg Thr Gly Phe

245 250 255
Asn Gln Pro Ile Pro Met Lys Tyr Asp Ala Ile Ser Cys
260 265

(2) INFORMATION FOR SEQ ID NO:459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1751

(D) OTHER INFORMATION: / Ceres Seq. ID 1498487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

```
aatctctctc cctctctatc tctctcttac aaaattccat ttcacgggga aaataataat      60
acgacttttg aaactctctg ctaatatctt ccaagaaaac ctgatgaatt aaaagttcat      120
attttcttgg tgttggttgg tattagatga ctatttcttg gtattagtca attctctggt      180
tccatcttat atggatagtc tagacacaga gcaaatagtc ttctttggag aaaaagaaga      240
tgagagacga gagagatctg ttcttccacg tattggtctg agatagatct taatcgataa      300
ccatctatggc cttgactctaa ccaatcaata taaactttat ttcttctctc ttctcgatct      360
caattgttcc gaccaaacaa gatgaagaga tcacgtggaa gctcgcattc ttatccggt      420
ttcttaacca ttccgcatct tacaacagac aaacaaaataa gcccaagacc aacaactacc      480
ggctttctct attccggcgc cggagactac tcccagatgt ttgacgcatt agaagacgac      540
ggaagtctag aggacctcgg cggcgttgga caccgctctt ctacggcgccg ggagaaaaaa      600
cggcggttgg ggttagagca agtgaagacg tttagaaga atttcgagat tgataacaag      660
tttagaccag agagaaaagt gaagctggct caagagcttg ggttgacgac acgccaaagt      720
cgcatctggt ttcaaaaccc ccgctgctcg tggaaaaacaa agcagcttga acgtgattac      780
ggcgttctta agtcaaaact tgatgcactc aaacgcaccc gcgactcgct tcaacgcgat      840
aacgattcac tccttgacaa gattaaagag ctgaagacaa aacttaacaa ggaagggttt      900
aaaaggtatag aagagaacgg cgttttaaaa gtatgggaag caaatcacag ggtgatggct      960
aataatgaag tcttagagctc aagccaccgt tctccatcgc caccaccgca tattctacg      1020
gaagctccga catcgagact cgcattcgaa atgtttagca tttttccacg caccgaaaac      1080
ttcagagaag atcctgcca tagcagcgac tcaagcgccg ttttgaacga agagtatagt      1140
cccaatacgg ttgaagcagc gggcgcaagt gcggccacga ctgtagaagt gtcgacgatg      1200
gattgtttta gccaatctgt gaaaatggaa gagcatgaag atctgtttag tggagaggaa      1260
gcttgcaagt tgtttgcgga caatgagcaa tggattgctc cgcgatcagt gaattcgttaa      1320
aatgtggggg cagaaaataa aacatagaaa agtcgaaggg gatattgtga aatattactg      1380
aagtcataat gggtcggaat atgcattact caaaaatta gggtttttgg tgagaaaatg      1440
gaatatgacg cgagagggta gtaaaaacga gcgtgtggtg ttccatgcac gtgtggccgt      1500
aatcttttca aggttgaatg agaaaggaca acaatgtctg aaatcatcgg gaataaaaaa      1560
aataatgtgac gaagaaatcg tttttctctc gtttaataa ttatttgaat aatttactt      1620
aggtgaatgt aatcgtcaaa aatcttttaa ttccgaaggg ttaagattc tgagcagcac      1680
ttctatctta tctcttctta ttgttctctg cgtccattga cgactatgca caattcataa      1740
gattattccc t
```

(2) INFORMATION FOR SEQ ID NO:460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..312

(D) OTHER INFORMATION: / Ceres Seq. ID 1498488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

```
Met Lys Arg Ser Arg Gly Ser Ser Asp Ser Leu Ser Gly Phe Leu Pro
1           5           10           15
Ile Arg His Ser Thr Thr Asp Lys Gln Ile Ser Pro Arg Pro Thr Thr
20           25           30
```

Thr Gly Phe Leu Tyr Ser Gly Ala Gly Asp Tyr Ser Gln Met Phe Asp
35 40 45
Ala Leu Glu Asp Asp Gly Ser Leu Glu Asp Leu Gly Val Gly His
50 55 60
Ala Ser Ser Thr Ala Ala Glu Lys Lys Arg Arg Leu Gly Val Glu Gln
65 70 75 80
Val Lys Ala Leu Glu Lys Asn Phe Glu Ile Asp Asn Lys Leu Glu Pro
85 90 95
Glu Arg Lys Val Lys Leu Ala Gln Glu Leu Gly Leu Gln Pro Arg Gln
100 105 110
Val Ala Ile Trp Phe Gln Asn Arg Arg Ala Arg Trp Lys Thr Lys Gln
115 120 125
Leu Glu Arg Asp Tyr Gly Val Leu Lys Ser Asn Phe Asp Ala Leu Lys
130 135 140
Arg Asn Arg Asp Ser Leu Gln Arg Asp Asn Asp Ser Leu Leu Gly Gln
145 150 155 160
Ile Lys Glu Leu Lys Ala Lys Leu Asn Val Glu Gly Phe Lys Gly Ile
165 170 175
Glu Glu Asn Gly Ala Leu Lys Val Val Glu Ala Asn Gln Thr Val Met
180 185 190
Ala Asn Asn Glu Val Leu Glu Leu Ser His Arg Ser Pro Ser Pro Pro
195 200 205
Pro His Ile Pro Thr Glu Ala Pro Thr Ser Glu Leu Ala Phe Glu Met
210 215 220
Phe Ser Ile Phe Pro Arg Thr Glu Asn Phe Arg Glu Asp Pro Ala Asp
225 230 235 240
Ser Ser Asp Ser Ser Ala Val Leu Asn Glu Glu Tyr Ser Pro Asn Thr
245 250 255
Val Glu Ala Ala Gly Ala Val Ala Ala Thr Thr Val Glu Met Ser Thr
260 265 270
Met Asp Cys Phe Ser Gln Phe Val Lys Met Glu Glu His Glu Asp Leu
275 280 285
Phe Ser Gly Glu Glu Ala Cys Lys Leu Phe Ala Asp Asn Glu Gln Trp
290 295 300
Tyr Cys Ser Asp Gln Trp Asn Ser
305 310

(2) INFORMATION FOR SEQ ID NO:461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..267
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

Met Phe Asp Ala Leu Glu Asp Asp Gly Ser Leu Glu Asp Leu Gly Gly
1 5 10 15
Val Gly His Ala Ser Ser Thr Ala Ala Glu Lys Lys Arg Arg Leu Gly
20 25 30
Val Glu Gln Val Lys Ala Leu Glu Lys Asn Phe Glu Ile Asp Asn Lys
35 40 45
Leu Glu Pro Glu Arg Lys Val Lys Leu Ala Gln Glu Leu Gly Leu Gln
50 55 60
Pro Arg Gln Val Ala Ile Trp Phe Gln Asn Arg Arg Ala Arg Trp Lys
65 70 75 80
Thr Lys Gln Leu Glu Arg Asp Tyr Gly Val Leu Lys Ser Asn Phe Asp
85 90 95
Ala Leu Lys Arg Asn Arg Asp Ser Leu Gln Arg Asp Asn Asp Ser Leu

(2) INFORMATION FOR SEQ ID NO:462:

(A) LENGTH: 1140 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..1140

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION:

tttcttg agagatccaa aaaaagtatc agaaagaaga a

(2) INFORMATION FOR SEQ ID NO:463:

(A) LENGTH: 210 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..210
(D) OTHER INFORMATION: / Ceres Seq. ID 1498494
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:
Phe Phe Leu Arg Asp Pro Lys Lys Val Ser Glu Arg Arg Arg Arg Arg
1 5 10 15
Leu Gln Lys Xaa Met Pro Tyr Tyr Thr Asn Asp Asp Asn Asp Val Asp
20 25 30
Asp Phe Thr Glu Tyr Asp Pro Met Pro Tyr Ser Gly Gly Tyr Asp Ile
35 40 45
Thr Val Thr Tyr Gly Arg Ser Ile Pro Pro Ser Asp Glu Thr Cys Tyr
50 55 60
Pro Leu Ser Ser Leu Ser Gly Asp Ala Phe Glu Tyr Gln Arg Pro Asn
65 70 75 80
Phe Ser Ser Asn Asn Asp Ser Ser Ala Tyr Asp Asp Gln Ala Leu Lys
85 90 95
Thr Glu Tyr Ser Ser Tyr Ala Arg Pro Gly Pro Val Gly Ser Gly Ser
100 105 110
Asp Phe Gly Arg Lys Pro Asn Ser Gly Tyr Gly Gly Arg Thr Glu Val
115 120 125
Glu Tyr Gly Arg Lys Thr Glu Ser Glu His Gly Ser Gly Tyr Gly Gly
130 135 140
Arg Ile Glu Ser Asp Tyr Val Lys Pro Ser Tyr Gly Gly His Glu Asp
145 150 155 160
Asp Gly Asp Asp Gly His Lys Lys His Ser Gly Lys Asp Tyr Asp Asp
165 170 175
Gly Asp Glu Lys Ser Lys Lys Lys Glu Lys Lys Lys Asp Lys
180 185 190
Lys Lys Asp Gly Asn Asn Ser Glu Asp Asp Glu Phe Lys Lys Lys Lys
195 200 205
Lys Lys
210
(2) INFORMATION FOR SEQ ID NO:464:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 190 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..190
(D) OTHER INFORMATION: / Ceres Seq. ID 1498495
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:
Met Pro Tyr Tyr Thr Asn Asp Asp Asn Asp Val Asp Asp Phe Thr Glu
1 5 10 15
Tyr Asp Pro Met Pro Tyr Ser Gly Gly Tyr Asp Ile Thr Val Thr Tyr
20 25 30
Gly Arg Ser Ile Pro Pro Ser Asp Glu Thr Cys Tyr Pro Leu Ser Ser
35 40 45
Leu Ser Gly Asp Ala Phe Glu Tyr Gln Arg Pro Asn Phe Ser Ser Asn
50 55 60
Asn Asp Ser Ser Ala Tyr Asp Asp Gln Ala Leu Lys Thr Glu Tyr Ser
65 70 75 80
Ser Tyr Ala Arg Pro Gly Pro Val Gly Ser Gly Ser Asp Phe Gly Arg
85 90 95
Lys Pro Asn Ser Gly Tyr Gly Gly Arg Thr Glu Val Glu Tyr Gly Arg
100 105 110
Lys Thr Glu Ser Glu His Gly Ser Gly Tyr Gly Gly Arg Ile Glu Ser
115 120 125
Asp Tyr Val Lys Pro Ser Tyr Gly Gly His Glu Asp Asp Gly Asp Asp

130	135	140
Gly His Lys Lys His Ser Gly Lys Asp Tyr Asp Asp Gly Asp Glu Lys		
145	150	155
Ser Lys Lys Lys Glu Lys Glu Lys Lys Lys Asp Lys Lys Lys Asp Gly		
	165	170
Asn Asn Ser Glu Asp Asp Glu Phe Lys Lys Lys Lys Lys Lys		175
	180	185
		190

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..171
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

Met	Pro	Tyr	Ser	Gly	Gly	Tyr	Asp	Ile	Thr	Val	Thr	Tyr	Gly	Arg	Ser
1			5				10						15		
Ile	Pro	Pro	Ser	Asp	Glu	Thr	Cys	Tyr	Pro	Leu	Ser	Ser	Leu	Ser	Gly
			20				25						30		
Asp	Ala	Phe	Glu	Tyr	Gln	Arg	Pro	Asn	Phe	Ser	Ser	Asn	Asn	Asp	Ser
			35				40						45		
Ser	Ala	Tyr	Asp	Asp	Gln	Ala	Leu	Lys	Thr	Glu	Tyr	Ser	Ser	Tyr	Ala
			50				55						60		
Arg	Pro	Gly	Pro	Val	Gly	Ser	Gly	Ser	Asp	Phe	Gly	Arg	Lys	Pro	Asn
65					70					75				80	
Ser	Gly	Tyr	Gly	Gly	Arg	Thr	Glu	Val	Glu	Tyr	Gly	Arg	Lys	Thr	Glu
				85					90					95	
Ser	Glu	His	Gly	Ser	Gly	Tyr	Gly	Gly	Gly	Ile	Glu	Ser	Asp	Tyr	Val
			100						105					110	
Lys	Pro	Ser	Tyr	Gly	Gly	His	Glu	Asp	Asp	Gly	Asp	Asp	Gly	His	Lys
			115				120						125		
Lys	His	Ser	Gly	Lys	Asp	Tyr	Asp	Asp	Gly	Asp	Glu	Lys	Ser	Lys	Lys
			130				135						140		
Lys	Glu	Lys	Glu	Lys	Lys	Lys	Asp	Lys	Lys	Lys	Asp	Gly	Asn	Asn	Ser
145					150						155				160
Glu	Asp	Asp	Glu	Phe	Lys	Lys	Lys	Lys	Lys	Lys					
				165											170

(2) INFORMATION FOR SEQ ID NO:466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1332
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498497

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

gatacatctc	ctgctgcgcg	ttcttcggat	tttcaactctt	ctgctcgaaa	ggctctctcac	60
tcttctcttt	tttaactctat	tgaaattgaa	acttcccttc	tcttctcttc	tcttctctgt	120
agcactctcg	cttctagttt	agctgctctt	cttcttctac	ttgctgcaac	aactccaaat	180
catcatttct	ctgtgtccag	cgactgcttg	agaatcattg	aagaaggtga	tcgtgtgtgc	240
tgttttgata	actcaaagcc	gttttgctga	aagagggtta	ccaaagttag	aagctcaaaga	300
acttgagagct	gtgtctcttt	tttgtatcat	gccatatttt	attcagaggc	ttttcaatac	360
ttgcaagtca	tctctctcac	ctaattggtcc	tgtgtctgag	gaggccttag	acaaggttgc	420
caatgtcttg	gagaaaaatca	agccgtctga	tgttggtctc	gaacaggaag	ctcaattggt	480

gcgtaattgg	cctggctcctg	ggaacgagcg	taatggaaac	aatcattctc	tgccagcaat	540
aaaataccct	cagttacatg	agtgtgacag	cttctcgatt	ggaattttct	gcatgccacc	600
tggtgtctat	ataccacttc	ataatcatcc	agccatgaca	gtgctaagca	agcttgttta	660
tggttcaatg	cacgttaagt	catatgattg	ggctgagcct	gaccaatcag	agctagacga	720
tcattacaa	gcaagaccg	ogaagctggt	caaggatatt	gatatgactt	cccctagccc	780
agcaaccact	ctatatccaa	caaccgggtg	caacattcat	tggttcaaa	ccattactca	840
ttgtgcaatc	tttgacatct	tatctcctcc	atactcttct	actcatggca	gacactgcaa	900
ctacttcgca	aaatccccaa	tgctagactt	acctgggtgag	attgaagtga	tgaatggaga	960
agtgtatctca	aatgtgacat	ggcttgaaga	gtatcaacct	ccagataact	ttgtgatattg	1020
gagagtctccg	tacagaggtc	cagtgmttag	aaaatgagaa	atacaaaaag	gattaaacat	1080
attaaaaaag	agcagaaaag	gaaaggtgct	tatgatcagg	agaataattg	gtaaaaccatt	1140
cagaggtctg	ctgcataatg	gtcgaggttc	ttacataaatt	gtgaccacat	taagttccag	1200
cctatgtcgt	tgtatgataa	tgattacttc	actagtttaa	tattataatt	ttttccccc	1260
atttttatat	gcagctacac	aaaaaattgc	tcataaacag	tgttatattt	agttatcata	1320
aaatttgttt	cc					

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..242
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498498

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

Met	Pro	Tyr	Phe	Ile	Gln	Arg	Leu	Phe	Asn	Thr	Cys	Lys	Ser	Ser	Leu
1				5					10					15	
Ser	Pro	Asn	Gly	Pro	Val	Ser	Glu	Glu	Ala	Leu	Asp	Lys	Val	Arg	Asn
			20					25					30		
Val	Leu	Glu	Lys	Ile	Lys	Pro	Ser	Asp	Val	Gly	Leu	Glu	Gln	Glu	Ala
			35					40				45			
Gln	Leu	Val	Arg	Asn	Trp	Pro	Gly	Pro	Gly	Asn	Glu	Arg	Asn	Gly	Asn
			50					55				60			
Asn	His	Ser	Leu	Pro	Ala	Ile	Lys	Tyr	Leu	Gln	Leu	His	Glu	Cys	Asp
65					70				75					80	
Ser	Phe	Ser	Ile	Gly	Ile	Phe	Cys	Met	Pro	Pro	Gly	Ser	Ile	Ile	Pro
			85						90				95		
Leu	His	Asn	His	Pro	Gly	Met	Thr	Val	Leu	Ser	Lys	Leu	Val	Tyr	Gly
			100					105					110		
Ser	Met	His	Val	Lys	Ser	Tyr	Asp	Trp	Ala	Glu	Pro	Asp	Gln	Ser	Glu
			115					120				125			
Leu	Asp	Asp	Pro	Leu	Gln	Ala	Arg	Pro	Ala	Lys	Leu	Val	Lys	Asp	Ile
			130			135						140			
Asp	Met	Thr	Ser	Pro	Ser	Pro	Ala	Thr	Thr	Leu	Tyr	Pro	Thr	Thr	Gly
145					150					155					160
Gly	Asn	Ile	His	Cys	Phe	Lys	Ala	Ile	Thr	His	Cys	Ala	Ile	Phe	Asp
			165						170					175	
Ile	Leu	Ser	Pro	Pro	Tyr	Ser	Ser	Thr	His	Gly	Arg	His	Cys	Asn	Tyr
			180					185					190		
Phe	Arg	Lys	Ser	Pro	Met	Leu	Asp	Leu	Pro	Gly	Glu	Ile	Glu	Val	Met
			195				200					205			
Asn	Gly	Glu	Val	Ile	Ser	Asn	Val	Thr	Trp	Leu	Glu	Glu	Tyr	Gln	Pro
			210				215					220			
Pro	Asp	Asn	Phe	Val	Ile	Trp	Arg	Val	Pro	Tyr	Arg	Gly	Pro	Val	Xaa
225				230						235				240	
Arg	Lys														

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..154
(D) OTHER INFORMATION: / Ceres Seq. ID 1498499
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:
Met Pro Pro Gly Ser Ile Ile Pro Leu His Asn His Pro Gly Met Thr
1 5 10 15
Val Leu Ser Lys Leu Val Tyr Gly Ser Met His Val Lys Ser Tyr Asp
20 25 30
Trp Ala Glu Pro Asp Gln Ser Glu Leu Asp Asp Pro Leu Gln Ala Arg
35 40 45
Pro Ala Lys Leu Val Lys Asp Ile Asp Met Thr Ser Pro Ser Pro Ala
50 55 60
Thr Thr Leu Tyr Pro Thr Thr Gly Gly Asn Ile His Cys Phe Lys Ala
65 70 75 80
Ile Thr His Cys Ala Ile Phe Asp Ile Leu Ser Pro Pro Tyr Ser Ser
85 90 95
Thr His Gly Arg His Cys Asn Tyr Phe Arg Lys Ser Pro Met Leu Asp
100 105 110
Leu Pro Gly Glu Ile Glu Val Met Asn Gly Glu Val Ile Ser Asn Val
115 120 125
Thr Trp Leu Glu Glu Tyr Gln Pro Pro Asp Asn Phe Val Ile Trp Arg
130 135 140
Val Pro Tyr Arg Gly Pro Val Xaa Arg Lys
145 150
(2) INFORMATION FOR SEQ ID NO:469:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 140 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..140
(D) OTHER INFORMATION: / Ceres Seq. ID 1498500
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:
Met Thr Val Leu Ser Lys Leu Val Tyr Gly Ser Met His Val Lys Ser
1 5 10 15
Tyr Asp Trp Ala Glu Pro Asp Gln Ser Glu Leu Asp Asp Pro Leu Gln
20 25 30
Ala Arg Pro Ala Lys Leu Val Lys Asp Ile Asp Met Thr Ser Pro Ser
35 40 45
Pro Ala Thr Thr Leu Tyr Pro Thr Thr Gly Gly Asn Ile His Cys Phe
50 55 60
Lys Ala Ile Thr His Cys Ala Ile Phe Asp Ile Leu Ser Pro Pro Tyr
65 70 75 80
Ser Ser Thr His Gly Arg His Cys Asn Tyr Phe Arg Lys Ser Pro Met
85 90 95
Leu Asp Leu Pro Gly Glu Ile Glu Val Met Asn Gly Glu Val Ile Ser
100 105 110
Asn Val Thr Trp Leu Glu Glu Tyr Gln Pro Pro Asp Asn Phe Val Ile
115 120 125
Trp Arg Val Pro Tyr Arg Gly Pro Val Xaa Arg Lys
130 135 140
(2) INFORMATION FOR SEQ ID NO:470:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 984 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..984

(D) OTHER INFORMATION: / Ceres Seq. ID 1498501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

agattcgcga	gttcttctgt	cttcgttctg	cccttttttt	ttttattttt	tttgtgtgtt	60
tgagagatgt	ctgcctttga	agacgattcc	ttcgtcatca	tcaacgatga	tgcgtctgag	120
tctgttccag	tctcaggctc	ttttgacgcc	actgattctt	tctcagcttt	cgacggctca	180
ctccaagtcg	aggactccgt	cgacgatgtt	tttgacgcgc	cgctctctga	ctacggtgct	240
tactccaacg	gtgacggcat	cttcggatcc	aacggggatc	acgacggtcc	tatcttgcca	300
ccacggtcgg	agatgggaat	agatgagggg	tttgctctta	gagaaatggg	aagacaaaat	360
gcaattcaac	ttgaggagaa	ggagaagaga	gaaaaggaaat	tgttgaaaca	aattattgag	420
gaagctgata	aatacaaaag	agagtttcat	aagaagattg	aagtaacttg	tgaaaaacac	480
aaagcagcta	acagagagaa	ggaaaaagctg	tatctggaga	accaagagaa	gtcttaccgcg	540
gaatccagca	agaattactg	gaaggcaata	gcagagctag	ttcctaaga	agttccaaca	600
atagagaaaa	ggagaggaaa	aaaagagcaa	caagatccta	agaagccaac	agtcctctgt	660
attcaaggtc	caaaagcccg	taagccaacc	gatctaacaa	gaatgagaca	aattattggtg	720
aagctcaaac	acaaacccac	ttctcacctg	aaactcaact	ctcaacctcc	atcgaggagg	780
gcggctgtct	ctccaaaaga	tgttcccggaa	accaagccca	ctgaggcagt	tactgtcgtc	840
taaaaacctc	ttttgttttc	ttattcgttg	cttacatctg	tgtgaattca	gtctttgcat	900
ttcattatgt	gtttataaca	gctgagagat	tttatgtgtc	atgtgtgtta	ttaacataat	960
tatgtcatat	tggaatgata	actt				

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1498502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

Asp	Ser	Arg	Val	Leu	Arg	Ser	Ser	Phe	Cys	Leu	Xaa	Phe	Phe	Thr	Phe
1				5					10					15	
Phe	Cys	Val	Phe	Glu	Arg	Cys	Leu	Pro	Leu	Lys	Thr	Ile	Pro	Ser	Ser
				20				25					30		
Thr	Ser	Thr	Met	Met	Arg	Leu	Ser	Leu	Phe	Gln	Ser	Gln	Ala	Leu	Leu
				35				40					45		
Thr	Pro	Leu	Ile	Leu	Ser	Gln	Leu	Ser	Thr	Ala	His	Ser	Lys	Ser	Arg
				50				55				60			
Thr	Pro	Ser	Thr	Met	Phe	Leu	Gln	Arg	Arg	Leu	Leu	Thr	Thr	Val	Leu
65					70					75				80	
Thr	Pro	Thr	Val	Thr	Ala	Ser	Ser	Asp	Pro	Thr	Gly	Ile	Thr	Thr	Val
				85				90					95		
Leu	Ser	Cys	His	His	Arg	Arg	Arg	Trp	Asn	Gln	Met	Arg	Asp	Leu	Leu
				100				105					110		
Leu	Glu	Asn	Gly	Glu	Asp	Lys	Met	Gln	Phe	Asn	Leu	Arg	Arg	Arg	Arg
				115				120					125		
Arg	Glu	Lys	Arg	Asn	Cys										
				130											

(2) INFORMATION FOR SEQ ID NO:472:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 258 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..258
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498503
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:
Met Ser Ala Phe Glu Asp Asp Ser Phe Val Ile Leu Asn Asp Asp Ala
1 5 10 15
Ser Glu Ser Val Pro Val Ser Gly Ser Phe Asp Ala Thr Asp Ser Phe
 20 25 30
Ser Ala Phe Asp Gly Ser Leu Gln Val Glu Asp Ser Val Asp Asp Val
 35 40 45
Phe Ala Ala Pro Ser Ser Asp Tyr Gly Ala Tyr Ser Asn Gly Asp Gly
50 55 60
Ile Phe Gly Ser Asn Gly Asp His Asp Gly Pro Ile Leu Pro Pro Pro
65 70 75 80
Ser Glu Met Glu Ser Asp Glu Gly Phe Ala Leu Arg Glu Trp Arg Arg
 85 90 95
Gln Asn Ala Ile Gln Leu Glu Glu Lys Glu Lys Arg Glu Lys Glu Leu
 100 105 110
Leu Lys Gln Ile Ile Glu Glu Ala Asp Gln Tyr Lys Glu Glu Phe His
 115 120 125
Lys Lys Ile Glu Val Thr Cys Glu Asn Asn Lys Ala Ala Asn Arg Glu
130 135 140
Lys Glu Lys Leu Tyr Leu Glu Asn Gln Glu Lys Phe Tyr Ala Glu Ser
145 150 155 160
Ser Lys Asn Tyr Trp Lys Ala Ile Ala Glu Leu Val Pro Lys Glu Val
 165 170 175
Pro Thr Ile Glu Lys Arg Arg Gly Lys Lys Glu Gln Gln Asp Pro Lys
180 185 190
Lys Pro Thr Val Ser Val Ile Gln Gly Pro Lys Pro Gly Lys Pro Thr
195 200 205
Asp Leu Thr Arg Met Arg Gln Ile Leu Val Lys Leu Lys His Asn Pro
210 215 220
Pro Ser His Leu Lys Leu Thr Ser Gln Pro Pro Ser Glu Glu Ala Ala
225 230 235 240
Ala Pro Pro Lys Asn Val Pro Glu Thr Lys Pro Thr Glu Ala Val Thr
 245 250 255
Ala Ala

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..176
(D) OTHER INFORMATION: / Ceres Seq. ID 1498504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

Met Glu Ser Asp Glu Gly Phe Ala Leu Arg Glu Trp Arg Arg Gln Asn
1 5 10 15
Ala Ile Gln Leu Glu Glu Lys Glu Lys Arg Glu Lys Glu Leu Leu Lys
 20 25 30
Gln Ile Ile Glu Glu Ala Asp Gln Tyr Lys Glu Glu Phe His Lys Lys
35 40 45

(2) INFORMATION FOR SEQ ID NO:474:

(A) LENGTH: 1308 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1308

(D) OTHER INFORMATION: / Ceres Seq. ID 1498509

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

(X1) SEQUENCE DESCRIPTION						
cattcttttt	tctctttatt	tataaaattt	tctgcatagt	actctctgaa	tctatatctt	60
cgaaattaaa	aaacgctcaa	gatacaaatc	aggaacccat	taaaaaaaaa	aatacaggtt	120
ttttttcaagt	tttaaagggtt	taaggtttctt	tggtggagaag	acgatggaga	ctttttgtgt	180
tttttcaaaag	gagggaagag	agatgtgattt	acctctctgt	tcaggtttct	atccacaaga	240
tgaagaatac	ataactcact	atctccataa	gaaggtttct	gaacacagct	tcctcagtaa	300
agctatcgtg	gaagttgtgt	taacaacaat	agagccatgt	gagttaccat	ggatggcaaa	360
aatgggtgtg	aaagaatggt	attttttctg	tgtgagagac	agaagaatct	ccacgggttc	420
aagaactaac	cgagacaactg	aagccgggtta	tggaaagcgc	accgggaagg	ataaagagat	480
ataccggagc	aaatcactct	tgtgggtgaa	gaactacact	gtttcttata	gagggaagag	540
tcctaaaggt	cagaaaaaaa	actgggtgat	gcattgagtc	agggcttaag	gaaattcttc	600
tgcctcatac	tgtccgaaaa	cgcgaagaag	tgaatgggtg	atatgcaggg	tgttccaaaa	660
gagtgctgga	gggcagaag	atcccgattt	cgagttcta	ccgaatcgtt	tcactcgaaa	720
ccgactttta	acctctgctt	ttgcctcttt	taacgccttc	ttgcctcttc	aacgataaar	780
ccraaacaga	ccgctgtctac	tgccctgctt	tctccaaaca	aacgatccaa	aaccaaggaa	840
ccacactcaa	ttgtctcagc	agccctgttc	taaacctgat	ccaagccgac	attttcmca	900
ggattccact	ctatacaact	cagtcctctc	aggtttctat	gaattcacag	agcccggttc	960
taacgcgaag	acactccagt	ctacatcgta	tgatcagaaa	caacgaaga	caaagtctca	1020
aaacgatgag	tgtctcaaaa	gaaacccggg	tttcaactga	catgaacact	gatatctcat	1080
cggaatttga	atttgcgtag	agacgggttg	attctcaaga	agatccggtt	tcctcactgt	1140
gacgggttga	tcttgaacct	tctctgaaat	actcaagatg	attcaagatt	ctcatgtcca	1200
ttaatttact	gtgtgtgtgt	aaagtttgtg	taggcttatg	tcataacttc	tcatatcaac	1260
tttccactata	tattataaga	attttaaaga	actttaaaat	atgattgtt		

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 188 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..188

(D) OTHER INFORMATION: / Ceres Seq. ID 1498510

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

Met Glu Thr Phe Cys Gly Phe Gln Lys Glu Glu Gln Met Asp Leu
1 5 10 15
Pro Pro Gly Phe Arg Phe His Pro Thr Asp Glu Glu Leu Ile Thr His
20 25 30
Tyr Leu His Lys Lys Val Leu Asp Thr Ser Phe Ser Ala Lys Ala Ile
35 40 45
Gly Glu Val Asp Leu Asn Lys Ser Glu Pro Trp Glu Leu Pro Trp Met
50 55 60
Ala Lys Met Gly Glu Lys Glu Trp Tyr Phe Phe Cys Val Arg Asp Arg
65 70 75 80
Lys Tyr Pro Thr Gly Leu Arg Thr Asn Arg Ala Thr Glu Ala Gly Tyr
85 90 95
Trp Lys Ala Thr Gly Lys Asp Lys Glu Ile Tyr Arg Gly Lys Ser Leu
100 105 110
Val Gly Met Lys Lys Thr Leu Val Phe Tyr Arg Gly Arg Ala Pro Lys
115 120 125
Gly Gln Lys Thr Asn Trp Val Met His Glu Tyr Arg Leu Glu Gly Lys
130 135 140
Phe Ser Ala His Asn Leu Pro Lys Thr Ala Lys Asn Glu Trp Val Ile
145 150 155 160
Cys Arg Val Xaa Gln Lys Ser Ala Gly Gly Gln Glu Asp Pro Asp Phe
165 170 175
Glu Ser Asn Pro Asn Arg Phe Thr Arg Asn Arg Leu
180 185

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1498511

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

Met Asp Leu Pro Pro Gly Phe Arg Phe His Pro Thr Asp Glu Glu Leu
1 5 10 15
Ile Thr His Tyr Leu His Lys Lys Val Leu Asp Thr Ser Phe Ser Ala
20 25 30
Lys Ala Ile Gly Glu Val Asp Leu Asn Lys Ser Glu Pro Trp Glu Leu
35 40 45
Pro Trp Met Ala Lys Met Gly Glu Lys Glu Trp Tyr Phe Phe Cys Val
50 55 60
Arg Asp Arg Lys Tyr Pro Thr Gly Leu Arg Thr Asn Arg Ala Thr Glu
65 70 75 80
Ala Gly Tyr Trp Lys Ala Thr Gly Lys Asp Lys Glu Ile Tyr Arg Gly
85 90 95
Lys Ser Leu Val Gly Met Lys Lys Thr Leu Val Phe Tyr Arg Gly Arg
100 105 110
Ala Pro Lys Gly Gln Lys Thr Asn Trp Val Met His Glu Tyr Arg Leu
115 120 125
Glu Gly Lys Phe Ser Ala His Asn Leu Pro Lys Thr Ala Lys Asn Glu
130 135 140
Trp Val Ile Cys Arg Val Xaa Gln Lys Ser Ala Gly Gly Gln Glu Asp
145 150 155 160
Pro Asp Phe Glu Ser Asn Pro Asn Arg Phe Thr Arg Asn Arg Leu
165 170 175

(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498512

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

```
Met Ala Lys Met Gly Glu Lys Glu Trp Tyr Phe Phe Cys Val Arg Asp
1      5      10      15
Arg Lys Tyr Pro Thr Gly Leu Arg Thr Asn Arg Ala Thr Glu Ala Gly
20      25      30
Tyr Trp Lys Ala Thr Gly Lys Asp Lys Glu Ile Tyr Arg Gly Lys Ser
35      40      45
Leu Val Gly Met Lys Lys Thr Leu Val Phe Tyr Arg Gly Arg Ala Pro
50      55      60
Lys Gly Gln Lys Thr Asn Trp Val Met His Glu Tyr Arg Leu Glu Gly
65      70      75      80
Lys Phe Ser Ala His Asn Leu Pro Lys Thr Ala Lys Asn Glu Trp Val
85      90      95
Ile Cys Arg Val Xaa Gln Lys Ser Ala Gly Gly Gln Glu Asp Pro Asp
100      105      110
Phe Glu Ser Asn Pro Asn Arg Phe Thr Arg Asn Arg Leu
115      120      125
```

(2) INFORMATION FOR SEQ ID NO:478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1465
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498517

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

```
attctctaga tgcgtgaaag ctgtgtaggg attgtagaag agggagcgat atttttcaat 60
cgctgcctgt ttgggaaatt cctcacatct cagatgaact ccaatcgctt cgagaaactc 120
taattctcgt ggaattttcg atagcatcat cgagaaattg tttcccggtt gaacaatgga 180
tggtacaaca gatgacgcgt tgaatgcctt aaaaatcggt aaggatgcta taaaagcagg 240
agatagatct cgcgctttga aattctttga gaaagcttgt cgtcttgatc caaatcttct 300
gatcgatgat ctgtgttcgg atctgaagaa gcaatcggat gaaccagcgg cgaggaggga 360
ttcgctcgga tctggcgcca acgagctctt taagccgtcg gatcgacctt ctctctgtca 420
acgtggatct tcgtcatcag ccgcggggatc gtcactatct tgcctctcca cggaagaaca 480
acgaacgcat gtgaggggaga taaagtcgaa gaaggattac tatgagatcc ttgatttgaa 540
aagaaactgt tcaagtggaa atttgaggaa atcttatcgg aaactctcgt tgaaagtcca 600
tcccgataag aataaagctc ctgcttctga agaagctttt aaattcgtct ctaaaagctt 660
ccaatgctta aagcaacaaa gacactagcc gaaagtaaca attcaacggc ttctctgatg 720
ctgcttatca accatgccga gctgcgagaa gaaacaacgg attcaacggc ttctctgatg 780
atgaatttga tgcgtgatgag attttcagaa gcttctttgg tgggtgtgga atgaactcgt 840
ctactactca attccgatca ttcaatttgc gtggaggaaac tagaacagct aattaagctt 900
ctgatacagg attcaaatct cctgtactcc ttcaaatact tcctgttgtg ttcatactac 960
tttcaactt ttgtccttct ccctcaacaaa ttactcgcgt ttctccatcg tataactacg 1020
agcacaaatt caccactcat aggggtgtcca attactttg gagatcagcc aagttcgagc 1080
aggaataccc gataagtagt ttctagagac agaggggtga agagcaagtt gatagagatt 1140
acttgtctat acttgccag aattgtgcc atgagcttca gagacaacaa tggggatata 1200
tccgcgaagc gccacattgt gacatgatga agaggtttga tgcagctgct gcataaacca 1260
```

tccatgtcag agagagactg aagcaccaag ttagtaaaact caaatccaag aaacttgggt 1320
ggattgttct gagacatagc tatggctactt actaacttct gagcattttt gtgtgatgctt 1380
cagtgaggtt gatttctaag tcccaaaactc atatacgttg attactgtgc tccttatgat 1440
gttagtaga aacatattat gtgtg

(2) INFORMATION FOR SEQ ID NO:479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..170
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498518

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

Met	Asp	Gly	Asn	Lys	Asp	Asp	Ala	Leu	Lys	Cys	Leu	Lys	Ile	Gly	Lys
1			5						10					15	
Asp	Ala	Ile	Lys	Ala	Gly	Asp	Arg	Ser	Arg	Ala	Leu	Lys	Phe	Leu	Glu
			20					25					30		
Lys	Ala	Cys	Arg	Leu	Asp	Pro	Asn	Leu	Leu	Ile	Asp	Asp	Leu	Val	Ser
			35				40					45			
Asp	Leu	Lys	Lys	Gln	Ser	Asp	Glu	Pro	Ala	Ala	Glu	Glu	Asp	Ser	Pro
			50			55					60				
Gly	Ser	Gly	Ala	Asn	Glu	Ser	Ser	Lys	Pro	Ser	Asp	Arg	Pro	Ser	Leu
			65		70					75				80	
Arg	Gln	Arg	Gly	Ser	Ser	Ser	Ser	Ala	Ala	Gly	Ser	Ser	Ser	Ser	Ser
			85					90						95	
Ser	Ser	Thr	Glu	Glu	Gln	Arg	Thr	Ile	Val	Arg	Glu	Ile	Lys	Ser	Lys
			100				105						110		
Lys	Asp	Tyr	Tyr	Glu	Ile	Leu	Gly	Leu	Lys	Arg	Asn	Cys	Ser	Val	Glu
			115				120					125			
Asp	Leu	Arg	Lys	Ser	Tyr	Arg	Lys	Leu	Ser	Leu	Lys	Val	His	Pro	Asp
			130			135					140				
Lys	Asn	Lys	Ala	Pro	Ala	Ser	Glu	Glu	Ala	Phe	Lys	Phe	Val	Ser	Lys
			145			150				155					160
Ala	Phe	Gln	Cys	Leu	Lys	Gln	Gln	Arg	His						
			165					170							

(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..778
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

ctctctcttta	ggtttttttt	ccctctctcc	aatctcatct	tctccgaaaa	cctttctttt	60
ctcaaatctc	tggtgaaaac	atgtctgacg	acgagcacca	ctttgaggcc	agcgatcccg	120
gagcttccaa	gacctatcct	caatcagccg	gtaacatccg	taaaagtggt	cacatcgctc	180
tcaaaaacgc	tccttgcaag	gtttgtgagg	tttcgacttc	caaaaactggc	aagcacggtc	240
acgccaatgt	tcactttgtt	gctattgata	tcttcactgc	taagaagcct	gaagatattg	300
ttccatcttc	ccacaattgt	gatgtccac	atgtgaaccg	tggtgattac	cagttgattg	360
atatacctga	ggatggcttc	gtgagccttc	tcactgacag	tggtggcacc	aaggatgac	420
tcaagcttcc	caccgatgat	ggctctcacc	nccagttgtt	gtgtttttgt	aatgcacatg	480
agactgtgat	tcgatgagg	aaagatat	gtgtgtctct	tcactgtctc	cattggagag	540
gagcagatct	gtgccgtcaa	ggaagtgtgt	ggtggcaagt	aaacaagtat	cattcgatat	600
attattacca	gtttgacaac	ggacgtcaat	gttataagaa	ccaaaagatg	ttttcttttt	660

tctcaatttta gaccctttgt gtgtgtttct tgttgcaaga caaccataatc tattggtttt
ggattgttgg aaaagtttgt gtggaacat tcaaagtttc ttatgagatg ttattctc

720

(2) INFORMATION FOR SEQ ID NO:481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1498520

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

Leu	Ser	Leu	Arg	Phe	Phe	Phe	Pro	Ser	Pro	Asn	Leu	Ile	Phe	Ser	Glu
1															15
Asn	Leu	Ser	Ser	Leu	Lys	Phe	Leu	Val	Lys	Thr	Cys	Leu	Thr	Thr	Ser
															30
Thr	Thr	Leu	Arg	Pro	Ala	Asn	Pro	Glu	Leu	Pro	Arg	Pro	Ile	Leu	Asn
															45
Gln	Pro	Val	Thr	Ser	Val	Lys	Val	Val	Thr	Ser	Ser	Ser	Lys	Thr	Val
															60
Pro	Ala	Arg	Leu	Leu	Arg	Phe	Arg	Leu	Pro	Lys	Leu	Ala	Ser	Thr	Val
															75
Thr	Pro	Asn	Val	Thr	Leu	Leu	Leu	Leu	Ile	Ser	Ser	Leu	Leu	Arg	Ser
															90
Leu	Lys	Ile	Leu	Phe	His	Leu	Pro	Thr	Ile	Val	Met	Phe	His	Met	
															110

(2) INFORMATION FOR SEQ ID NO:482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1498521

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

Met	Ser	Asp	Asp	Glu	His	His	Phe	Glu	Ala	Ser	Glu	Ser	Gly	Ala	Ser
1															15
Lys	Thr	Tyr	Pro	Gln	Ser	Ala	Gly	Asn	Ile	Arg	Lys	Gly	Gly	His	Ile
															30
Val	Ile	Lys	Asn	Arg	Pro	Cys	Lys	Val	Val	Glu	Val	Ser	Thr	Ser	Lys
															45
Thr	Gly	Lys	His	Gly	His	Ala	Lys	Cys	His	Phe	Val	Ala	Ile	Asp	Ile
															60
Phe	Thr	Ala	Lys	Lys	Leu	Glu	Asp	Ile	Val	Pro	Ser	Ser	His	Asn	Cys
															75
Asp	Val	Pro	His	Val	Asn	Arg	Val	Asp	Tyr	Gln	Leu	Ile	Asp	Ile	Thr
															90
Glu	Asp	Gly	Phe	Val	Ser	Leu	Leu	Thr	Asp	Ser	Gly	Gly	Thr	Lys	Asp
															105
Asp	Leu	Lys	Leu	Pro	Thr	Asp	Asp	Gly	Leu	Thr	Xaa	Gln	Leu	Leu	Cys
															120
Phe	Val	Asn	Ala	His	Glu	Xaa	Trp	Ile	Arg						
															135

(2) INFORMATION FOR SEQ ID NO:483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1212 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..1212
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498522
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:
ctgtctctct tcagtgacac aaacccaaag aaaagtagtg agaaacaaaa tcgaggtaac 60
tactagatga agacgatgac gcaataaaat attgcggttg trgttgtagt gacggttctt 120
attggaatgt tgagatcatc ggaggctcaa cttcaaatga atttctacgc gaagactctt 180
ccaaacgcag agaaaatcat ttcagatcat attcaaaatc atatccacaa tggctctctt 240
cttgcagctc ctctcatccg aatgcacttc catgattgct tcgttagggg atgtgacgga 300
tcgggtgttg taaattcaac atctggtaac gcagagagag atgcaccacc gaatctaaca 360
cttagaggat tcggtttcgt ggaaaggatt aaggctcttc ttgaaaaagt gtgtcctaag 420
actgtttctt gcgcagatat cattgctttg actgctagag acacagttgt ccccaccgga 480
ggctctctcat ggagtgttcc aacgggaaga agagacggta ggatctcaaa tttgaaggag 540
gctacgaata acattccacc tccaacgagt aatttcacga ctttacgacg acttttcaaa 600
aaccaaggcc ttaattccaa ggacctgttt ctgctctctg gggctcacac gatttggtgc 660
tcacattgtt cttccatgaa tactcgtctc tacaacttct cgactacagt caaacaagat 720
ccatctctcg atagccaagta cgcagctaat ctaaaaggcta acaaatgtaa gaggcctaac 780
gacaatagca ccattcctga gatggatccc gatggagctt ttccaatctg attctgcctt gaccacgaac 840
tataggctgt tcttgaagag gatggagctt ttccaatctg attctgcctt gaccacgaac 900
tcagcgcagt tgaagggtgat caacgacttg gtcaacgggt ctgaaaaaga ttctttcaaa 960
gcttttgcta agtcaatgrg agaagatggg gagagttaaaw gtgacagact ggcctcagctg 1020
gtgtgatcag gacacgggtgt tctgtcgctg gaagttagta agcttggtgc gaattgggtg 1080
tgtttatggtc attgtgtttt tgtgtgactt tcggaaaaaa caaatgttgt taaattaatt 1140
tgtgtgtgtg ttgattgtg tttatgcacc caagaatgat gtgttatggt tcaattaata 1200
tgtgaatcat tt
(2) INFORMATION FOR SEQ ID NO:484:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 310 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..310
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498523
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:
Met Lys Thr Met Thr Gln Leu Asn Ile Ala Val Xaa Val Val Val Thr
1 5 10 15
Val Leu Ile Gly Met Leu Arg Ser Ser Glu Ala Gln Leu Gln Met Asn
20 25 30
Phe Tyr Ala Lys Ser Cys Pro Asn Ala Glu Lys Ile Ile Ser Asp His
35 40 45
Ile Gln Asn His Ile His Asn Gly Pro Ser Leu Ala Ala Pro Leu Ile
50 55 60
Arg Met His Phe His Asp Cys Phe Val Arg Gly Cys Asp Gly Ser Val
65 70 75 80
Leu Ile Asn Ser Thr Ser Gly Asn Ala Glu Arg Asp Ala Pro Pro Asn
85 90 95
Leu Thr Leu Arg Gly Phe Gly Phe Val Glu Arg Ile Lys Ala Leu Leu
100 105 110
Glu Lys Val Cys Pro Lys Thr Val Ser Cys Ala Asp Ile Ile Ala Leu
115 120 125
Thr Ala Arg Asp Thr Val Val Ala Thr Gly Gly Pro Ser Trp Ser Val
130 135 140
Pro Thr Gly Arg Arg Asp Gly Arg Ile Ser Asn Leu Lys Glu Ala Thr

145 150 155 160
Asn Asn Ile Pro Pro Pro Thr Ser Asn Phe Thr Thr Leu Arg Arg Leu
165 170 175
Phe Lys Asn Gln Gly Leu Asn Leu Lys Asp Leu Val Leu Leu Ser Gly
180 185 190
Ala His Thr Ile Gly Val Ser His Cys Ser Ser Met Asn Thr Arg Leu
195 200 205
Tyr Asn Phe Ser Thr Thr Val Lys Gln Asp Pro Ser Leu Asp Ser Gln
210 215 220
Tyr Ala Ala Asn Leu Lys Ala Asn Lys Cys Lys Ser Leu Asn Asp Asn
225 230 235 240
Ser Thr Ile Leu Glu Met Asp Pro Gly Ser Ser Arg Ser Phe Asp Leu
245 250 255
Ser Tyr Tyr Arg Leu Val Leu Lys Arg Gly Leu Phe Gln Ser Asp
260 265 270
Ser Ala Leu Thr Thr Asn Ser Ala Thr Leu Lys Val Ile Asn Asp Leu
275 280 285
Val Asn Gly Ser Glu Lys Lys Phe Phe Lys Ala Phe Ala Lys Ser Met
290 295 300
Xaa Glu Asp Gly Glu Ser
305 310

(2) INFORMATION FOR SEQ ID NO:485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..307
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498524

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

Met Thr Gln Leu Asn Ile Ala Val Xaa Val Val Val Thr Val Leu Ile
1 5 10 15
Gly Met Leu Arg Ser Ser Glu Ala Gln Leu Gln Met Asn Phe Tyr Ala
20 25 30
Lys Ser Cys Pro Asn Ala Glu Lys Ile Ile Ser Asp His Ile Gln Asn
35 40 45
His Ile His Asn Gly Pro Ser Leu Ala Ala Pro Leu Ile Arg Met His
50 55 60
Phe His Asp Cys Phe Val Arg Gly Cys Asp Gly Ser Val Leu Ile Asn
65 70 75 80
Ser Thr Ser Gly Asn Ala Glu Arg Asp Ala Pro Pro Asn Leu Thr Leu
85 90 95
Arg Gly Phe Gly Phe Val Glu Arg Ile Lys Ala Leu Leu Glu Lys Val
100 105 110
Cys Pro Lys Thr Val Ser Cys Ala Asp Ile Ile Ala Leu Thr Ala Arg
115 120 125
Asp Thr Val Val Ala Thr Gly Gly Pro Ser Trp Ser Val Pro Thr Gly
130 135 140
Arg Arg Asp Gly Arg Ile Ser Asn Leu Lys Glu Ala Thr Asn Asn Ile
145 150 155 160
Pro Pro Pro Thr Ser Asn Phe Thr Thr Leu Arg Arg Leu Phe Lys Asn
165 170 175
Gln Gly Leu Asn Leu Lys Asp Leu Val Leu Leu Ser Gly Ala His Thr
180 185 190
Ile Gly Val Ser His Cys Ser Ser Met Asn Thr Arg Leu Tyr Asn Phe
195 200 205
Ser Thr Thr Val Lys Gln Asp Pro Ser Leu Asp Ser Gln Tyr Ala Ala
210 215 220

Asn Leu Lys Ala Asn Lys Cys Lys Ser Leu Asn Asp Asn Ser Thr Ile
225 230 235 240
Leu Glu Met Asp Pro Gly Ser Ser Arg Ser Phe Asp Leu Ser Tyr Tyr
245 250 255
Arg Leu Val Leu Lys Arg Arg Gly Leu Phe Gln Ser Asp Ser Ala Leu
260 265 270
Thr Thr Asn Ser Ala Thr Leu Lys Val Ile Asn Asp Leu Val Asn Gly
275 280 285
Ser Glu Lys Lys Phe Phe Lys Ala Phe Ala Lys Ser Met Xaa Glu Asp
290 295 300
Gly Glu Ser
305

(2) INFORMATION FOR SEQ ID NO:486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..290

(D) OTHER INFORMATION: / Ceres Seq. ID 1498525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

Met Leu Arg Ser Ser Glu Ala Gln Leu Gln Met Asn Phe Tyr Ala Lys
1 5 10 15
Ser Cys Pro Asn Ala Glu Lys Ile Ile Ser Asp His Ile Gln Asn His
20 25 30
Ile His Asn Gly Pro Ser Leu Ala Ala Pro Leu Ile Arg Met His Phe
35 40 45
His Asp Cys Phe Val Arg Gly Cys Asp Gly Ser Val Leu Ile Asn Ser
50 55 60
Thr Ser Gly Asn Ala Glu Arg Asp Ala Pro Pro Asn Leu Thr Leu Arg
65 70 75 80
Gly Phe Gly Phe Val Glu Arg Ile Lys Ala Leu Leu Glu Lys Val Cys
85 90 95
Pro Lys Thr Val Ser Cys Ala Asp Ile Ile Ala Leu Thr Ala Arg Asp
100 105 110
Thr Val Val Ala Thr Gly Gly Pro Ser Trp Ser Val Pro Thr Gly Arg
115 120 125
Arg Asp Gly Arg Ile Ser Asn Leu Lys Glu Ala Thr Asn Asn Ile Pro
130 135 140
Pro Pro Thr Ser Asn Phe Thr Thr Leu Arg Arg Leu Phe Lys Asn Gln
145 150 155 160
Gly Leu Asn Leu Lys Asp Leu Val Leu Ser Gly Ala His Thr Ile
165 170 175
Gly Val Ser His Cys Ser Ser Met Asn Thr Arg Leu Tyr Asn Phe Ser
180 185 190
Thr Thr Val Lys Gln Asp Pro Ser Leu Asp Ser Gln Tyr Ala Ala Asn
195 200 205
Leu Lys Ala Asn Lys Cys Lys Ser Leu Asn Asp Asn Ser Thr Ile Leu
210 215 220
Glu Met Asp Pro Gly Ser Ser Arg Ser Phe Asp Leu Ser Tyr Tyr Arg
225 230 235 240
Leu Val Leu Lys Arg Arg Gly Leu Phe Gln Ser Asp Ser Ala Leu Thr
245 250 255
Thr Asn Ser Ala Thr Leu Lys Val Ile Asn Asp Leu Val Asn Gly Ser
260 265 270
Glu Lys Lys Phe Phe Lys Ala Phe Ala Lys Ser Met Xaa Glu Asp Gly
275 280 285
Glu Ser

- 290
(2) INFORMATION FOR SEQ ID NO:487:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1734 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..1734
(D) OTHER INFORMATION: / Ceres Seq. ID 1498526
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:
atcaatggct ctggatgcat tcttctctat tttcttctgt ttccgtcacc 60
atcccgcgta gaatccacta ctcagttttg tagtgcaggg agagagaatg gtgtggggatc 120
ttgtgggggt tcatcgacga ggattttgat taaaggaggg actgtgtgca atgcacacca 180
tcaagaaactt gctgatgttt atgtggaaaa ttgtattatt gtctgtgtgc agccaaacat 240
taaggttggg gatgaagtca ctgtccctga tgctactgga aagttgtgca tgccaggagg 300
aattgacccc cacacgcacc tcgcgatgga atttatgggt accgagacta ttgatgattt 360
cttcagtggt caggcagcgg cattagctgg tggaacaact atgcataatag actttgttat 420
acctgtcaat gggaaatctgg ttgctgggtt tgaagcctat gaaaacaaat cttagaattt 480
ttgtatggat tacggttttc atatggcaat cacaagtggt gatgaaggtg ttccaggaga 540
catggagatg ttggtcaaag aaaagggtat caactcttcc aagtttttcc tagcgtataa 600
aggatctctt atggttaactg atgacctact ctagaaggga cttaaagat gcaaatccct 660
cggtgccttg gccatgttgc atgctgaaaa tggagatgca gtattcgaa gacagaaaag 720
aatgattgar ctgggcattt acaggctcag agggctcagc tcttttcaag gccctctgtg 780
ctcgagggag aggcactgac tagagcaatt cggttggttc gttttattaa cagcctctc 840
tatgttgttc atgtgatgca tgttgatgca atggacgaga ttgtctaaag tcgaaaatca 900
ggacagaagg ttattggaga gccctgtgtg tctggattaa tctctgatga ctattggctt 960
tgggtacctg acttcacact tgcgtccaag tatgtcatga gtccacctat cagaccagta 1020
ggacatggga aagccctaca agatgccctt tccacaggaa tctctcagct ttgaggaaat 1080
gatcatgca ctttcaattc tacacaaaaa gctctaggac ttgatgattt ccgcaaaaaa 1140
cctaattggtg ttaattggcct tgaggaaagg atgcacttga tatgggacac gatgtggagg 1200
ttctggccac tctcagctac tgattatggt cgaataacca gcactgagtg tcttagaatt 1260
ttcaacatat atccacaggaa aggaactatc cttgctggct cggatgcaga tattatcata 1320
ttgaatccaa actcaagcta cgagattagc tcaagctct atcattcaag atcagacaca 1380
aacgtctacg agggcagaga aggaaaggga aaagttaga tgacaatagc agggaggaga 1440
attgtgtggg aaaacgagga acttaaaagt gtcccaagaa gtggccaagta tctatcttct 1500
ctctctttca gttacctttt cgatgggtatt gagaaatcag atgcttaatta tctatcttct 1560
ctctgagctc cagttaaagg tgtcagaact gaagctacgt aaagtgcagg tatctatctt 1620
tcgtgattct gtaagaacaa ttgtacataa ttgttattaa aagatttgaa agatcgatta 1680
tgaataatgt gcatgtagtc ttggttttgag aaaaaataaa agattgttaa attt

- (2) INFORMATION FOR SEQ ID NO:488:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 284 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..284
(D) OTHER INFORMATION: / Ceres Seq. ID 1498527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:
Ser Met Ala Leu Asp Ala Phe Phe Phe Ile Val Ser Leu Phe Leu Leu
1 5 10 15
Phe Pro Ser Pro Ser Ala Ser Glu Ser Thr Thr Gln Phe Cys Ser Ala
20 25 30
Gly Arg Glu Asn Gly Val Gly Ser Cys Gly Val Ser Ser Thr Arg Ile
35 40 45
Leu Ile Lys Gly Gly Thr Val Val Asn Ala His His Gln Glu Leu Ala

50	55	60
Asp Val Tyr Val Glu Asn Gly Ile Ile Val Ala Val Gln Pro Asn Ile		
65	70	75
Lys Val Gly Asp Glu Val Thr Val Leu Asp Ala Thr Gly Lys Phe Val		80
	85	90
Met Pro Gly Gly Ile Asp Pro His Thr His Leu Ala Met Glu Phe Met		95
	100	105
Gly Thr Glu Thr Ile Asp Asp Phe Phe Ser Gly Gln Ala Ala Ala Leu		110
	115	120
Ala Gly Gly Thr Thr Met His Ile Asp Phe Val Ile Pro Val Asn Gly		125
	130	135
Asn Leu Val Ala Gly Phe Glu Ala Tyr Glu Asn Lys Ser Arg Glu Ser		140
	145	150
Cys Met Asp Tyr Gly Phe His Met Ala Ile Thr Lys Trp Asp Glu Gly		155
	165	170
Val Ser Arg Asp Met Glu Met Leu Val Lys Glu Lys Gly Ile Asn Ser		175
	180	185
Phe Lys Phe Phe Leu Ala Tyr Lys Gly Ser Leu Met Val Thr Asp Asp		190
	195	200
Leu Leu Leu Glu Gly Leu Lys Arg Cys Lys Ser Leu Gly Ala Leu Ala		205
	210	215
Met Val His Ala Glu Asn Gly Asp Ala Val Phe Glu Gly Gln Lys Arg		220
	225	230
Met Ile Xaa Leu Gly Ile Tyr Arg Ser Arg Gly Ser Cys Ser Phe Gln		235
	245	250
Gly Leu Leu Cys Ser Arg Glu Arg Pro Leu Leu Glu Gln Phe Val Trp		255
	260	265
Leu Val Leu Leu Thr Arg Leu Ser Met Leu Phe Met		270
	275	280

(2) INFORMATION FOR SEQ ID NO:489:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 283 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..283

(D) OTHER INFORMATION: / Ceres Seq. ID 1498528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

Met Ala Leu Asp Ala Phe Phe Phe Ile Val Ser Leu Phe Leu Leu Phe		
1	5	10
Pro Ser Pro Ser Ala Ser Glu Ser Thr Thr Gln Phe Cys Ser Ala Gly		15
	20	25
Arg Glu Asn Gly Val Gly Ser Cys Gly Val Ser Ser Thr Arg Ile Leu		30
	35	40
Ile Lys Gly Gly Thr Val Val Asn Ala His His Gln Glu Leu Ala Asp		45
	50	55
Val Tyr Val Glu Asn Gly Ile Ile Val Ala Val Gln Pro Asn Ile Lys		60
	65	70
Val Gly Asp Glu Val Thr Val Leu Asp Ala Thr Gly Lys Phe Val Met		75
	85	90
Pro Gly Gly Ile Asp Pro His Thr His Leu Ala Met Glu Phe Met Gly		95
	100	105
Thr Glu Thr Ile Asp Asp Phe Phe Ser Gly Gln Ala Ala Ala Leu Ala		110
	115	120
Gly Gly Thr Thr Met His Ile Asp Phe Val Ile Pro Val Asn Gly Asn		125
	130	135
Leu Val Ala Gly Phe Glu Ala Tyr Glu Asn Lys Ser Arg Glu Ser Cys		140
	145	150
		155
		160

Met Asp Tyr Gly Phe His Met Ala Ile Thr Lys Trp Asp Glu Gly Val
165 170 175
Ser Arg Asp Met Glu Met Leu Val Lys Glu Lys Gly Ile Asn Ser Phe
180 185 190
Lys Phe Phe Leu Ala Tyr Lys Gly Ser Leu Met Val Thr Asp Asp Leu
195 200 205
Leu Leu Glu Gly Leu Lys Arg Cys Lys Ser Leu Gly Ala Leu Ala Met
210 215 220
Val His Ala Glu Asn Gly Asp Ala Val Phe Glu Gly Gln Lys Arg Met
225 230 235 240
Ile Xaa Leu Gly Ile Tyr Arg Ser Arg Gly Ser Cys Ser Phe Gln Gly
245 250 255
Leu Leu Cys Ser Arg Glu Arg Pro Leu Leu Glu Gln Phe Val Trp Leu
260 265 270
Val Leu Leu Thr Arg Leu Ser Met Leu Phe Met
275 280

(2) INFORMATION FOR SEQ ID NO:490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..281
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

Met Leu Phe Ser Arg Pro Pro Val Leu Glu Gly Glu Ala Thr Ala Arg
1 5 10 15
Ala Ile Arg Leu Ala Arg Phe Ile Asn Thr Pro Leu Tyr Val Val His
20 25 30
Val Met Ser Val Asp Ala Met Asp Glu Ile Ala Lys Ala Arg Lys Ser
35 40 45
Gly Gln Lys Val Ile Gly Glu Pro Val Val Ser Gly Leu Ile Leu Asp
50 55 60
Asp His Trp Leu Trp Asp Pro Asp Phe Thr Ile Ala Ser Lys Tyr Val
65 70 75 80
Met Ser Pro Pro Ile Arg Pro Val Gly His Gly Lys Ala Leu Gln Asp
85 90 95
Ala Leu Ser Thr Gly Ile Leu Gln Leu Val Gly Thr Asp His Cys Thr
100 105 110
Phe Asn Ser Thr Gln Lys Ala Leu Gly Leu Asp Asp Phe Arg Lys Ile
115 120 125
Pro Asn Gly Val Asn Gly Leu Glu Glu Arg Met His Leu Ile Trp Asp
130 135 140
Thr Met Val Glu Ser Gly Gln Leu Ser Ala Thr Asp Tyr Val Arg Ile
145 150 155 160
Thr Ser Thr Glu Cys Ala Arg Ile Phe Asn Ile Tyr Pro Arg Lys Gly
165 170 175
Ala Ile Leu Ala Gly Ser Asp Ala Asp Ile Ile Ile Leu Asn Pro Asn
180 185 190
Ser Ser Tyr Glu Ile Ser Ser Lys Ser His His Ser Arg Ser Asp Thr
195 200 205
Asn Val Tyr Glu Gly Arg Arg Gly Lys Gly Lys Val Glu Val Thr Ile
210 215 220
Ala Gly Gly Arg Ile Val Trp Glu Asn Glu Glu Leu Lys Val Val Pro
225 230 235 240
Arg Ser Gly Lys Tyr Ile Glu Met Pro Pro Phe Ser Tyr Leu Phe Asp
245 250 255
Gly Ile Glu Lys Ser Asp Ala Asn Tyr Leu Ser Ser Leu Arg Ala Pro

260 265 270
Val Lys Arg Val Arg Thr Glu Ala Thr
275 280

(2) INFORMATION FOR SEQ ID NO:491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1193 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1193

(D) OTHER INFORMATION: / Ceres Seq. ID 1498530

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

```
atcaccttact taacatacta agagagttat tagaacttgc aaaaaaatggc ttccaaggct      60
ttgattctgt tagtctctct ctcagttctt ctcgtcgtct ccgaagtgtc tgcccgaagg      120
maatcgggca tgggtgaagcc agagagttag gaaactgtgc aaactgaagg ttatggcggt      180
ggccacggga gacatgggtg tcacggaggc ggaggaggcc acggacatgg aggacacaa      240
ggaggagggg gccacgggact tgacggatac rgaggagggtg gaggggcacta tggaggagggt      300
ggaggacact acggagggtg tggaggaggga tacggagggtg gaggagggaca ccacggaaagg      360
cgcgaaagca ctcccctaaa gccccctaagc taccagttcc tccggtgacc gtcctctaagc      420
taaccagttcc tccggtgacc gtcctctaagc taccagttcc taagctaccc gtccccccgg      480
taactgtacc taagctaccc gttcctccag tgaccgtccc taagctaccc cttcctccga      540
tttcaggggc acccatacct ccagttggtag gtcccaatct gccattgccca ctttggccaa      600
ttgtagggtcc tatttttcca ccgggaaacaa cccccaccag cacaggagggg aaggactgtc      660
ctccaccggc agggagcgta aagccaccat cagggggcggg gaaggcgaca tgtccaatag      720
acacagtgaa gttaggtgct tgcgtgcact tgttgggagg tttagtaaaag ataggcgctgt      780
gggatccagc agttaacaaa tgttgcctgt tacttaaaagg cctcgttgaa atcgaagccg      840
cggttggctc ctgcactacc ctcaagctca aagctcttga cctcaatctt tatgtccctg      900
ttgtctttca gcttctcctt acctgtggca aaaatccacc tccgggctac acttgttcca      960
tatgataaac tcactccact tataaaggat gctttggaaa aaaaagttag aagagaatgg      1020
cagagctcca atctttcctg ctcttggtta ccaaatacat catatcaaat cctatccctt      1080
tgattcttcc ctctatcggt ccttatgctt tgtatcatta attaatgtgt gctttttaga      1140
ttaatgatcc ttctcttgta ttaaagtatg atttgaatc cttttttttt ctc
```

(2) INFORMATION FOR SEQ ID NO:492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1498531

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

```
Met Ala Ser Lys Ala Leu Ile Leu Leu Gly Leu Phe Ser Val Leu Leu
1 5 10 15
Val Val Ser Glu Val Ser Ala Ala Arg Xaa Ser Gly Met Val Lys Pro
20 25 30
Glu Ser Glu Gly Thr Val Gln Pro Glu Gly Tyr Gly Gly His Gly
35 40 45
Gly His Gly Gly His Gly Gly Gly His Gly His Gly Gly His
50 55 60
Asn Gly Gly Gly Gly His Gly Leu Asp Gly Tyr Xaa Gly Gly Gly
65 70 75 80
His Tyr Gly Gly Gly Gly His Tyr Gly Gly Gly Gly Gly Tyr
85 90 95
Gly Gly Gly Gly Gly His His Gly Arg Ala Glu Ser Thr Pro Leu Lys
100 105 110
```

Pro Leu Ser Tyr Gln Phe Leu Arg
115 120

(2) INFORMATION FOR SEQ ID NO:493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92

(D) OTHER INFORMATION: / Ceres Seq. ID 1498532

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

Met Val Lys Pro Glu Ser Glu Glu Thr Val Gln Pro Glu Gly Tyr Gly
1 5 10 15
Gly Gly His Gly Gly His Gly Gly His Gly Gly Gly Gly Gly His Gly
20 25 30
His Gly Gly His Asn Gly Gly Gly Gly His Gly Leu Asp Gly Tyr Xaa
35 40 45
Gly Gly Gly Gly His Tyr Gly Gly Gly Gly Gly His Tyr Gly Gly Gly
50 55 60
Gly Gly Gly Tyr Gly Gly Gly Gly His His Gly Arg Ala Glu Ser
65 70 75 80
Thr Pro Leu Lys Pro Leu Ser Tyr Gln Phe Leu Arg
85 90

(2) INFORMATION FOR SEQ ID NO:494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..68

(D) OTHER INFORMATION: / Ceres Seq. ID 1498533

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

Met Ala Val Ala Thr Glu Asp Met Val Thr Glu Gly Glu Glu Ala
1 5 10 15
Thr Asp Met Glu Asp Thr Thr Glu Glu Gly Ala Thr Asp Leu Thr Asp
20 25 30
Xaa Glu Glu Val Glu Gly Thr Met Glu Glu Val Glu Asp Thr Thr Glu
35 40 45
Val Val Glu Glu Asp Thr Glu Val Glu Glu Asp Thr Thr Glu Gly Arg
50 55 60
Lys Ala Leu Pro
65

(2) INFORMATION FOR SEQ ID NO:495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1669 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1669
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

accgtgatta ctgattactg tgттаattat ttttattctg cgtacgttac gtaagagaga

tattgaggaa	tggtctgcgaa	gaaggttttt	ggatcgccgg	aagcgagtaa	tttgtgtacg	120
gagcttcgtc	ggagttttga	tgatggtgtg	acacgtggtt	atgaatggag	agtgaactac	180
cttaagaaac	tgatgattat	tttgtataat	catgagccctg	agatcgctgc	ggctcttcgc	240
gatgatcttg	gtaagcctca	gcttgaatct	tctgtttatg	aggtatctct	actgagaaac	300
tctatcaagt	tggtctctaa	gcagctaaaag	aactgggatg	ctccggagaa	ggcaaaagact	360
tctctaaaca	cggtttccctg	atcccgaggag	attgtgtctg	agcctctctg	tggttgctca	420
gtgatctcgg	cttggaaacta	tccttttctg	ttgtctattg	atcctgttat	tggtgcaatt	480
tctgctggga	atgctgttgtt	tttaaagcca	tcagaattgg	ctccagcttc	gtcagctctg	540
ctcactaagt	tactggaaca	gtatcttgat	cctctcgagg	tgcgagttgt	cgaaggagct	600
gtttaccgaaa	caagtgcctc	gctagagcag	aagtgggaca	agatatctca	cacaggtagt	660
tcaaaaatcg	gacgtgtcat	aatggcgcca	gctgcgaagc	atctcacacc	gggttgctca	720
gagctgtgag	gaaaaatctc	tgctgttgta	gactcggata	ccgatttgaa	agttaccgtc	780
agggcggata	tcgtagcaaa	atgggggttg	aacaacggac	agggcgtcgt	ttcccgccgac	840
tatatcttga	cgacaaaaga	atatgctcct	aaattgattg	atgccatgaa	gcttgaattg	900
gagaaaaatt	atgggaagaa	ccctatatag	tcgaaaagata	tgtaacgtat	cgtaaaactg	960
aatcactttg	atgcctgttc	taagttgtta	gacgagaagg	aagtttctga	caaaattgtc	1020
tatggtgggt	aaaaggacag	agaaaaactg	aaaattgctc	cgacaactct	gtcgtgatga	1080
ccattagatt	ctctgatcat	gagtgaaaga	atatttgccc	ctctctctcc	aatcctcacg	1140
cttaacaact	tggaagagag	ctttgacgtg	attcgttctc	gacctaaagc	acttgccgca	1200
tactttgttta	cacataacaa	gaagttgaaa	gagagattca	cagcgacagt	ctccgctgga	1260
ggcatagtag	tcaatgacat	agctgttcat	cttgacattc	acacattgoc	atccggagga	1320
gttggtgaaa	gtggaatggg	tgcttaccat	ggtaaaattc	catttgatgc	ttttagtcac	1380
aagaagcgcg	ttctctacag	aagccttttc	ggtgattcag	ccgtcaggtg	ttccgccatc	1440
tcgagaggaa	agcttagatt	gttaaaagcc	cttgctcgaca	gcaatatatt	cgatttatct	1500
aaagtccttc	tcggtttagc	ttaaaccgta	aaaagaccga	ggacactctc	ctttgtacct	1560
tatttacttg	ttttattttt	caaacatgga	cttagttggg	taatatgttt	tggtttgggt	1620
tgattctcat	gaattattga	gttgataaat	aaaagatttt	cggttggttt		

(2) INFORMATION FOR SEQ ID NO:496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..484
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498535

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

Met	Ala	Ala	Lys	Lys	Val	Phe	Gly	Ser	Ala	Glu	Ala	Ser	Asn	Leu	Val
1			5					10					15		
Thr	Glu	Leu	Arg	Arg	Ser	Phe	Asp	Asp	Gly	Val	Thr	Arg	Gly	Tyr	Glu
			20				25					30			
Trp	Arg	Val	Thr	Gln	Leu	Lys	Lys	Leu	Met	Ile	Ile	Cys	Asp	Asn	His
			35				40					45			
Glu	Pro	Glu	Ile	Val	Ala	Ala	Leu	Arg	Asp	Asp	Leu	Gly	Lys	Pro	Glu
			50			55					60				
Leu	Glu	Ser	Ser	Val	Tyr	Glu	Val	Ser	Leu	Leu	Arg	Asn	Ser	Ile	Lys
			65			70				75				80	
Leu	Ala	Leu	Lys	Gln	Leu	Lys	Asn	Trp	Met	Ala	Pro	Glu	Lys	Ala	Lys
			85					90					95		
Thr	Ser	Leu	Thr	Thr	Phe	Pro	Ala	Ser	Ala	Glu	Ile	Val	Ser	Glu	Pro
			100				105					110			
Leu	Gly	Val	Val	Leu	Val	Ile	Ser	Ala	Trp	Asn	Tyr	Pro	Phe	Leu	Leu
			115			120				125					
Ser	Ile	Asp	Pro	Val	Ile	Gly	Ala	Ile	Ser	Ala	Gly	Asn	Ala	Val	Val
			130			135				140					
Leu	Lys	Pro	Ser	Thr	Glu	Leu	Ala	Pro	Ala	Ser	Ser	Ala	Leu	Leu	Thr
			145			150				155					
Leu	Leu	Glu	Gln	Tyr	Leu	Leu	Asp	Pro	Ser	Ala	Val	Arg	Val	Val	Glu
			165					170						175	

Ala Val Thr Glu Thr Ser Ala Leu Leu Glu Gln Lys Trp Asp Lys Ile
180 185 190
Phe Tyr Thr Gly Ser Ser Lys Ile Gly Arg Val Ile Met Ala Ala Ala
195 200 205
Ala Lys His Leu Thr Pro Val Val Leu Glu Leu Gly Gly Lys Ser Pro
210 215 220
Val Val Val Asp Ser Asp Thr Asp Leu Lys Val Thr Val Arg Arg Ile
225 230 235 240
Ile Val Gly Lys Trp Gly Cys Asn Asn Gly Gln Ala Cys Val Ser Pro
245 250 255
Asp Tyr Ile Leu Thr Thr Lys Glu Tyr Ala Pro Lys Leu Ile Asp Ala
260 265 270
Met Lys Leu Glu Leu Glu Lys Phe Tyr Gly Lys Asn Pro Ile Glu Ser
275 280 285
Lys Asp Met Ser Arg Ile Val Asn Ser Asn His Phe Asp Arg Leu Ser
290 295 300
Lys Leu Leu Asp Glu Lys Glu Val Ser Asp Lys Ile Val Tyr Gly Gly
305 310 315 320
Glu Lys Asp Arg Glu Asn Leu Lys Ile Ala Pro Thr Ile Leu Leu Asp
325 330 335
Val Pro Leu Asp Ser Leu Ile Met Ser Glu Glu Ile Phe Gly Pro Leu
340 345 350
Leu Pro Ile Leu Thr Leu Asn Asn Leu Glu Glu Ser Phe Asp Val Ile
355 360 365
Arg Ser Arg Pro Lys Pro Leu Ala Ala Tyr Leu Phe Thr His Asn Lys
370 375 380
Lys Leu Lys Glu Arg Phe Thr Ala Thr Val Ser Ala Gly Gly Ile Val
385 390 395 400
Val Asn Asp Ile Ala Val His Leu Ala Leu His Thr Leu Pro Phe Gly
405 410 415
Gly Val Gly Glu Ser Gly Met Gly Ala Tyr His Gly Lys Phe Ser Phe
420 425 430
Asp Ala Phe Ser His Lys Lys Ala Val Leu Tyr Arg Ser Leu Phe Gly
435 440 445
Asp Ser Ala Val Arg Tyr Pro Pro Tyr Ser Arg Gly Lys Leu Arg Leu
450 455 460
Leu Lys Ala Leu Val Asp Ser Asn Ile Phe Asp Leu Phe Lys Val Leu
465 470 475 480
Leu Gly Leu Ala

(2) INFORMATION FOR SEQ ID NO:497:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 443 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..443

(D) OTHER INFORMATION: / Ceres Seq. ID 1498536

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

Met Ile Ile Cys Asp Asn His Glu Pro Glu Ile Val Ala Ala Leu Arg
1 5 10 15
Asp Asp Leu Gly Lys Pro Glu Leu Glu Ser Ser Val Tyr Glu Val Ser
20 25 30
Leu Leu Arg Asn Ser Ile Lys Leu Ala Leu Lys Gln Leu Lys Asn Trp
35 40 45
Met Ala Pro Glu Lys Ala Lys Thr Ser Leu Thr Thr Phe Pro Ala Ser
50 55 60
Ala Glu Ile Val Ser Glu Pro Leu Gly Val Val Leu Val Ile Ser Ala

65					70					75					80
Trp	Asn	Tyr	Pro	Phe	Leu	Leu	Ser	Ile	Asp	Pro	Val	Ile	Gly	Ala	Ile
				85					90					95	
Ser	Ala	Gly	Asn	Ala	Val	Val	Leu	Lys	Pro	Ser	Glu	Leu	Ala	Pro	Ala
			100					105					110		
Ser	Ser	Ala	Leu	Leu	Thr	Lys	Leu	Leu	Glu	Gln	Tyr	Leu	Asp	Pro	Ser
		115					120					125			
Ala	Val	Arg	Val	Val	Glu	Gly	Ala	Val	Thr	Glu	Thr	Ser	Ala	Leu	Leu
						135					140				
Glu	Gln	Lys	Trp	Asp	Lys	Ile	Phe	Tyr	Thr	Gly	Ser	Ser	Lys	Ile	Gly
145					150					155				160	
Arg	Val	Ile	Met	Ala	Ala	Ala	Ala	Lys	His	Leu	Thr	Pro	Val	Val	Leu
			165						170					175	
Glu	Leu	Gly	Gly	Lys	Ser	Pro	Val	Val	Val	Asp	Ser	Asp	Thr	Asp	Leu
			180					185					190		
Lys	Val	Thr	Val	Arg	Arg	Ile	Ile	Val	Gly	Lys	Trp	Gly	Cys	Asn	Asn
		195				200						205			
Gly	Gln	Ala	Cys	Val	Ser	Pro	Asp	Tyr	Ile	Leu	Thr	Thr	Lys	Glu	Tyr
	210					215					220				
Ala	Pro	Lys	Leu	Ile	Asp	Ala	Met	Lys	Leu	Glu	Leu	Glu	Lys	Phe	Tyr
225					230					235					240
Gly	Lys	Asn	Pro	Ile	Glu	Ser	Lys	Asp	Met	Ser	Arg	Ile	Val	Asn	Ser
			245						250					255	
Asn	His	Phe	Asp	Arg	Leu	Ser	Lys	Leu	Leu	Asp	Glu	Lys	Glu	Val	Ser
			260						265					270	
Asp	Lys	Ile	Val	Tyr	Gly	Gly	Glu	Lys	Asp	Arg	Glu	Asn	Leu	Lys	Ile
		275						280				285			
Ala	Pro	Thr	Ile	Leu	Leu	Asp	Val	Pro	Leu	Asp	Ser	Leu	Ile	Met	Ser
	290					295					300				
Glu	Glu	Ile	Phe	Gly	Pro	Leu	Leu	Pro	Ile	Leu	Thr	Leu	Asn	Asn	Leu
				310					315						320
Glu	Glu	Ser	Phe	Asp	Val	Ile	Arg	Ser	Arg	Pro	Lys	Pro	Leu	Ala	Ala
			325						330				335		
Tyr	Leu	Phe	Thr	His	Asn	Lys	Lys	Leu	Lys	Glu	Arg	Phe	Thr	Ala	Thr
		340					345					350			
Val	Ser	Ala	Gly	Gly	Ile	Val	Val	Asn	Asp	Ile	Ala	Val	His	Leu	Ala
		355					360					365			
Leu	His	Thr	Leu	Pro	Phe	Gly	Gly	Val	Gly	Glu	Ser	Gly	Met	Gly	Ala
	370					375					380				
Tyr	His	Gly	Lys	Phe	Ser	Phe	Asp	Ala	Phe	Ser	His	Lys	Lys	Ala	Val
385					390					395					400
Leu	Tyr	Arg	Ser	Leu	Phe	Gly	Asp	Ser	Ala	Val	Arg	Tyr	Pro	Pro	Tyr
			405						410				415		
Ser	Arg	Gly	Lys	Leu	Arg	Leu	Leu	Lys	Ala	Leu	Val	Asp	Ser	Asn	Ile
		420					425						430		
Phe	Asp	Leu	Phe	Lys	Val	Leu	Leu	Gly	Leu	Ala					
		435					440								

(2) INFORMATION FOR SEQ ID NO:498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..395
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498537

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

Met	Ala	Pro	Glu	Lys	Ala	Lys	Thr	Ser	Leu	Thr	Thr	Phe	Pro	Ala	Ser
1				5				10						15	

Ala Glu Ile Val Ser Glu Pro Leu Gly Val Val Leu Val Ile Ser Ala
20 25 30
Trp Asn Tyr Pro Phe Leu Leu Ser Ile Asp Pro Val Ile Gly Ala Ile
35 40 45
Ser Ala Gly Asn Ala Val Val Leu Lys Pro Ser Glu Leu Ala Pro Ala
50 55 60
Ser Ser Ala Leu Leu Thr Lys Leu Leu Glu Gln Tyr Leu Asp Pro Ser
65 70 75 80
Ala Val Arg Val Val Glu Gly Ala Val Thr Glu Thr Ser Ala Leu Leu
85 90 95
Glu Gln Lys Trp Asp Lys Ile Phe Tyr Thr Gly Ser Ser Lys Ile Gly
100 105 110
Arg Val Ile Met Ala Ala Ala Ala Lys His Leu Thr Pro Val Val Leu
115 120 125
Glu Leu Gly Gly Lys Ser Pro Val Val Val Asp Ser Asp Thr Asp Leu
130 135 140
Lys Val Thr Val Arg Arg Ile Ile Val Gly Lys Trp Gly Cys Asn Asn
145 150 155 160
Gly Gln Ala Cys Val Ser Pro Asp Tyr Ile Leu Thr Thr Lys Glu Tyr
165 170 175
Ala Pro Lys Leu Ile Asp Ala Met Lys Leu Glu Leu Glu Lys Phe Tyr
180 185 190
Gly Lys Asn Pro Ile Glu Ser Lys Asp Met Ser Arg Ile Val Asn Ser
195 200 205
Asn His Phe Asp Arg Leu Ser Lys Leu Leu Asp Glu Lys Glu Val Ser
210 215 220
Asp Lys Ile Val Tyr Gly Gly Glu Lys Asp Arg Glu Asn Leu Lys Ile
225 230 235 240
Ala Pro Thr Ile Leu Leu Asp Val Pro Leu Asp Ser Leu Ile Met Ser
245 250 255
Glu Glu Ile Phe Gly Pro Leu Leu Pro Ile Leu Thr Leu Asn Asn Leu
260 265 270
Glu Glu Ser Phe Asp Val Ile Arg Ser Arg Pro Lys Pro Leu Ala Ala
275 280 285
Tyr Leu Phe Thr His Asn Lys Lys Leu Lys Glu Arg Phe Thr Ala Thr
290 295 300
Val Ser Ala Gly Gly Ile Val Val Asn Asp Ile Ala Val His Leu Ala
305 310 315 320
Leu His Thr Leu Pro Phe Gly Gly Val Gly Glu Ser Gly Met Gly Ala
325 330 335
Tyr His Gly Lys Phe Ser Phe Asp Ala Phe Ser His Lys Lys Ala Val
340 345 350
Leu Tyr Arg Ser Leu Phe Gly Asp Ser Ala Val Arg Tyr Pro Pro Tyr
355 360 365
Ser Arg Gly Lys Leu Arg Leu Lys Ala Leu Val Asp Ser Asn Ile
370 375 380
Phe Asp Leu Phe Lys Val Leu Leu Gly Leu Ala
385 390 395

(2) INFORMATION FOR SEQ ID NO:499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1111
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498542

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

aggaattcgc acaagaccat tacystagaa catcmtaatc acaaaaaatca aatccatctc

```

ccactcttct agcatcttga agcttaaatc tcagccgtcc gatcatgccg atcagaataa 120
tcgcccattgg ccgtccagat gaagcaacc ccgccgatgc cttaaaggcg gggttggctg 180
agtcactttc aacttttgatc ttgtgtctgc ccggttcagg ctctggcatg gctttcaaca 240
agctcaatga aaacggagcc accactcctt ctggtctcgt agctgctgca ctggctcatg 300
cctttggact ctctgtgcgt gtctcagttg gtgccaacat ctctggtgga cacgttaacc 360
ctgcccgtcac tttcgggtgtc ttcattgggt gtaacatcac tctctccgtt ggtatcctct 420
actggattgc tcagcttctc ggctccgtgc tcgcttgccct catccttaaa ttgcgccacc 480
gtggcttggc tgtgcccgtc ttgtgtctct ctctgggagt aggagtgttg aacgctttcg 540
ttttcgagat cgtgatgaca ttccgggcttg ttacaccgtc ctacgctaca gccattgacc 600
ctggaaacct taccttggctg ctacaagacc aagtcgggtg attacaaggc acacgtgaca 660
atggcaagac ctggattacg gttcagcctg tgaaggagag gtttgcgtc aatctggcg 720
accacggtca ttttttgagc aatgggaggt tcaagaatgc tgatcatcag ccgctggtga 780
actctaacct gagcagatta tccatagcca cgttccagaa ccccgcgccg gatgccacag 840
tgtatcactc gaaagtaaga gaaggagaga aggcaatatt ggaggagcca atcagctttg 900
cggagatgta taagagaaag atgggaagag atttggagct tgcctgcctc aagaagcttg 960
ctaaagagga gcgtgaccac aaagaagttg ccaagcctgt cgaccaaatc ttgccttaga 1020
atctctgtgt tcttgtttac ttgttgggtc gttggttctg tttgtactgt tggtagttaa 1080
aattatgcta ggctcggtgt gttttgtgtt c

```

(2) INFORMATION FOR SEQ ID NO:500:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 304 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..304

(D) OTHER INFORMATION: / Ceres Seq. ID 1498543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

```

Met Pro Ile Arg Asn Ile Ala Ile Gly Arg Pro Asp Glu Ala Thr Arg
1      5      10      15
Pro Asp Ala Leu Lys Ala Ala Leu Ala Glu Phe Ile Ser Thr Leu Ile
20     25     30
Phe Val Val Ala Gly Ser Gly Ser Gly Met Ala Phe Asn Lys Leu Thr
35     40     45
Glu Asn Gly Ala Thr Thr Pro Ser Gly Leu Val Ala Ala Ala Leu Ala
50     55     60
His Ala Phe Gly Leu Phe Val Ala Val Ser Val Gly Ala Asn Ile Ser
65     70     75
Gly Gly His Val Asn Pro Ala Val Thr Phe Gly Ala Phe Ile Gly Gly
85     90     95
Asn Ile Thr Leu Leu Arg Gly Ile Leu Tyr Trp Ile Ala Gln Leu Leu
100    105   110
Gly Ser Val Val Ala Cys Leu Ile Leu Lys Phe Ala Thr Gly Gly Leu
115    120   125
Ala Val Pro Ala Phe Gly Leu Ser Ala Gly Val Gly Val Leu Asn Ala
130    135   140
Phe Val Phe Glu Ile Val Met Thr Phe Gly Leu Val Tyr Thr Val Tyr
145    150   155
Ala Thr Ala Ile Asp Pro Gly Thr Ile Thr Leu Leu Leu Gln Asp Gln
165    170   175
Val Gly Gly Leu Gln Ala Thr Arg Asp Asn Gly Lys Thr Trp Ile Thr
180    185   190
Val Gln Pro Val Glu Gly Ala Phe Val Val Asn Leu Gly Asp His Gly
195    200   205
His Phe Leu Ser Asn Gly Arg Phe Lys Asn Ala Asp His Gln Ala Val
210    215   220
Val Asn Ser Asn Ser Ser Arg Leu Ser Ile Ala Thr Phe Gln Asn Pro
225    230   235
Ala Pro Asp Ala Thr Val Tyr Pro Leu Lys Val Arg Glu Gly Gly Lys

```


	245		250		255										
Ala	Ile	Leu	Glu	Pro	Ile	Thr	Phe	Ala	Glu	Met	Tyr	Lys	Arg	Lys	
	260		265		270										
Met	Gly	Arg	Asp	Leu	Glu	Leu	Ala	Arg	Leu	Lys	Lys	Leu	Ala	Lys	Glu
	275		280		285										
Glu	Arg	Asp	His	Lys	Glu	Val	Ala	Lys	Pro	Val	Asp	Gln	Ile	Phe	Ala
	290		295		300										

(2) INFORMATION FOR SEQ ID NO:501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..263
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

Met	Ala	Phe	Asn	Lys	Leu	Thr	Glu	Asn	Gly	Ala	Thr	Thr	Pro	Ser	Gly
1			5					10					15		
Leu	Val	Ala	Ala	Ala	Leu	Ala	His	Ala	Phe	Gly	Leu	Phe	Val	Ala	Val
			20					25					30		
Ser	Val	Gly	Ala	Asn	Ile	Ser	Gly	Gly	His	Val	Asn	Pro	Ala	Val	Thr
			35					40					45		
Phe	Gly	Ala	Phe	Ile	Gly	Gly	Asn	Ile	Thr	Leu	Leu	Arg	Gly	Ile	Leu
			50				55				60				
Tyr	Trp	Ile	Ala	Gln	Leu	Leu	Gly	Ser	Val	Val	Ala	Cys	Leu	Ile	Leu
							70				75			80	
Lys	Phe	Ala	Thr	Gly	Gly	Leu	Ala	Val	Pro	Ala	Phe	Gly	Leu	Ser	Ala
							85				90			95	
Gly	Val	Gly	Val	Leu	Asn	Ala	Phe	Val	Phe	Glu	Ile	Val	Met	Thr	Phe
														110	
Gly	Leu	Val	Tyr	Thr	Val	Tyr	Ala	Thr	Ala	Ile	Asp	Pro	Gly	Thr	Ile
														125	
Thr	Leu	Leu	Leu	Gln	Asp	Gln	Val	Gly	Gly	Leu	Gln	Ala	Thr	Arg	Asp
														140	
Asn	Gly	Lys	Thr	Trp	Ile	Thr	Val	Gln	Pro	Val	Glu	Gly	Ala	Phe	Val
														155	
Val	Asn	Leu	Gly	Asp	His	Gly	His	Phe	Leu	Ser	Asn	Gly	Arg	Phe	Lys
														170	
Asn	Ala	Asp	His	Gln	Ala	Val	Val	Asn	Ser	Asn	Ser	Ser	Arg	Leu	Ser
														185	
Ile	Ala	Thr	Phe	Gln	Asn	Pro	Ala	Pro	Asp	Ala	Thr	Val	Tyr	Pro	Leu
														200	
Lys	Val	Arg	Glu	Gly	Glu	Lys	Ala	Ile	Leu	Glu	Glu	Pro	Ile	Thr	Phe
														215	
Ala	Glu	Met	Tyr	Lys	Arg	Lys	Met	Gly	Arg	Asp	Leu	Glu	Leu	Ala	Arg
														230	
Leu	Lys	Lys	Leu	Ala	Lys	Glu	Glu	Arg	Asp	His	Lys	Glu	Val	Ala	Lys
														245	
Pro	Val	Asp	Gln	Ile	Phe	Ala								250	

(2) INFORMATION FOR SEQ ID NO:502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1498545

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

Met Thr Phe Gly Leu Val Tyr Thr Val Tyr Ala Thr Ala Ile Asp Pro
1 5 10 15
Gly Thr Ile Thr Leu Leu Leu Gln Asp Gln Val Gly Gly Leu Gln Ala
20 25 30
Thr Arg Asp Asn Gly Lys Thr Trp Ile Thr Val Gln Pro Val Glu Gly
35 40 45
Ala Phe Val Val Asn Leu Gly Asp His Gly His Phe Leu Ser Asn Gly
50 55 60
Arg Phe Lys Asn Ala Asp His Gln Ala Val Val Asn Ser Asn Ser Ser
65 70 75 80
Arg Leu Ser Ile Ala Thr Phe Gln Asn Pro Ala Pro Asp Ala Thr Val
85 90 95
Tyr Pro Leu Lys Val Arg Glu Gly Glu Lys Ala Ile Leu Glu Glu Pro
100 105 110
Ile Thr Phe Ala Glu Met Tyr Lys Arg Lys Met Gly Arg Asp Leu Glu
115 120 125
Leu Ala Arg Leu Lys Lys Leu Ala Lys Glu Glu Arg Asp His Lys Glu
130 135 140
Val Ala Lys Pro Val Asp Gln Ile Phe Ala
145 150

(2) INFORMATION FOR SEQ ID NO:503:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 382 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..382

(D) OTHER INFORMATION: / Ceres Seq. ID 1498550

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

aaacacaaac aaaactcata ttttcaatct ccagggtgctt tacaccaaca gaggcgcaag 60
aaaacaaaaa ccaaaactcgg atttagtttg acagaagaag gaatcgagag tcggggtatgc 120
attatcttaa caacagaacc gaattcgctcg gagctccagc cccaaccggg tatcaaaaagg 180
agcagttgtc accggagcaa gagctttcag ttattgtctc tgctttgcaa cacgtgatct 240
caggggaaaaa cgaaacggcg csgtgtcagg gtttttccag tgacagcaca gtgataagcg 300
cgggaaatgcs tcggttgat ccagacactt gtcaagtcgt taggatcgaa ggatgtctcg 360
gctgtaacta ctitttcgcg cc

(2) INFORMATION FOR SEQ ID NO:504:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1498551

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

Lys His Lys Gln Asn Ser Tyr Phe Gln Ser Pro Gly Ala Leu His Gln
1 5 10 15
Gln Ser Arg Lys Lys Thr Lys Thr Lys Leu Gly Phe Ser Leu Thr Glu
20 25 30

Glu Gly Ile Glu Ser Arg Val Cys Ile Ile Leu Thr Thr Glu Pro Asn
35 40 45
Ser Ser Glu Leu Gln Pro Gln Pro Gly Ile Lys Arg Ser Ser Cys His
50 55 60
Arg Ser Lys Ser Phe Gln Leu Leu Ser Leu Leu Cys Asn Thr
65 70 75

(2) INFORMATION FOR SEQ ID NO:505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88

(D) OTHER INFORMATION: / Ceres Seq. ID 1498552

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

Met His Tyr Pro Asn Asn Arg Thr Glu Phe Val Gly Ala Pro Ala Pro
1 5 10 15
Thr Arg Tyr Gln Lys Glu Gln Leu Ser Pro Glu Gln Glu Leu Ser Val
20 25 30
Ile Val Ser Ala Leu Gln His Val Ile Ser Gly Glu Asn Glu Thr Ala
35 40 45
Xaa Cys Gln Gly Phe Ser Ser Asp Ser Thr Val Ile Ser Ala Gly Met
50 55 60
Xaa Arg Leu Asp Ser Asp Thr Cys Gln Val Cys Arg Ile Glu Gly Cys
65 70 75 80
Leu Gly Cys Asn Tyr Phe Phe Ala
85

(2) INFORMATION FOR SEQ ID NO:506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1396

(D) OTHER INFORMATION: / Ceres Seq. ID 1498553

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

attattattt ccagagaagc ttctcttttg attctctgc tctctcttcc ttcacgcgct 60
cttcgagatt cgaatggttg gaattattctg gtgaccggtg gtgtcggtta catcggaagt 120
cacacggttc ttccagcttct tctcggaggc tataacacccg tcgttataga caacctcgac 180
aattcctctc tcgttttcgat ccaacgcgctc aaggatctcg ccggagatca tggacaaaaa 240
ctcacgctcc accaggttga ccttcgcgat aaacccgcac ttgagaaggt ttctccgaa 300
acaaagtgtg atgcagtaat gcatttttgc ggattgaaag cagtgggtga gagcgtggcg 360
aaaccacttc tgtattataa caataaacttg attgcgacta ttacactttt ggaagttaatg 420
gctgcacacg gatgtaaaaa gcttgtattt tcttcgtccg ctactgtgta tggctggcca 480
aaggagggtc ctgttacaga agagtctccc ctgtctggaa tgagtcccta tggacggaca 540
aagctgttca tagaggacat ttgccgtgat gtacaacgtg gtgatcccta atggagaatc 600
ataatgctga ggtactttaa cctcgtggga gctcaccccta gcggtcgcat tggtaggagt 660
ccttggtggg ctccaaaata tctcatgcct tatgtccagc aagtogttgt tgggaggcta 720
cctaaccataa aaatttatgg aactgactat accactaaag atggcactgg tgcacgacac 780
tatattcatg ttgttgatcg agcagatggc catatatatt cgcttcaaaa gctagacgat 840
actgaaatag gtgttgaggt atacaacctg ggaacccgaa aaggaaacac agtgttgagg 900
atggttgatg catttgagaa agctctctga atgaaaaatc cactggtgaa ggttggaagg 960
agacacaggt atgcagagaa cgtctatgcg tcaacagaaa aagctgaacg ggaactaaac 1020
tggaaggcaa attttggaat cgaagaaatg ttagggatc agtggaaact ggcaagcaac 1080
aatcctttcg gttacggttc ttacacaaac tcaacataac taatccaacac 1140

tccattcttt	ttcttttggg	tcgtcggtg	ttatctttat	gttacacact	caggttttag	1200
ctttaagacc	taaacacagt	gagggagaag	ttactttctt	attcatatat	ctgctttctc	1260
cttttggta	ttatataat	cttatatacg	cataggttta	acttaagcgg	atccttttgt	1320
tttttgatt	tgtataact	ctcttaggaa	attaattgtc	atgggattat	atttgtatta	1380
aatagaaact gaattc						

(2) INFORMATION FOR SEQ ID NO:507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..372
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498554

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

Ile	Ile	Ile	Ser	Arg	Glu	Ala	Ser	Leu	Leu	Ile	Leu	Ser	Leu	Ser	Leu
1			5					10					15		
Ser	Ser	Ser	Pro	Leu	Arg	Ala	Ser	Met	Val	Gly	Asn	Ile	Leu	Val	Thr
			20					25					30		
Gly	Gly	Ala	Gly	Tyr	Ile	Gly	Ser	His	Thr	Val	Leu	Gln	Leu	Leu	Leu
			35					40				45			
Gly	Gly	Tyr	Asn	Thr	Val	Val	Ile	Asp	Asn	Leu	Asp	Asn	Ser	Ser	Leu
			50					55			60				
Val	Ser	Ile	Gln	Arg	Val	Lys	Asp	Leu	Ala	Gly	Asp	His	Gly	Gln	Asn
			65					70			75			80	
Leu	Thr	Val	His	Gln	Val	Asp	Leu	Arg	Asp	Lys	Pro	Ala	Leu	Glu	Lys
			85					90					95		
Val	Phe	Ser	Glu	Thr	Lys	Phe	Asp	Ala	Val	Met	His	Phe	Ala	Gly	Leu
			100					105					110		
Lys	Ala	Val	Gly	Glu	Ser	Val	Ala	Lys	Pro	Leu	Leu	Tyr	Tyr	Asn	Asn
			115					120				125			
Asn	Leu	Ile	Ala	Thr	Ile	Thr	Leu	Leu	Glu	Val	Met	Ala	Ala	His	Gly
			130				135				140				
Cys	Lys	Lys	Leu	Val	Phe	Ser	Ser	Ser	Ala	Thr	Val	Tyr	Gly	Trp	Pro
			145				150				155			160	
Lys	Glu	Val	Pro	Cys	Thr	Glu	Glu	Ser	Pro	Leu	Ser	Gly	Met	Ser	Pro
			165					170						175	
Tyr	Gly	Arg	Thr	Lys	Leu	Phe	Ile	Glu	Asp	Ile	Cys	Arg	Asp	Val	Gln
			180					185					190		
Arg	Gly	Asp	Pro	Glu	Trp	Arg	Gly	Ile	Met	Leu	Arg	Tyr	Phe	Asn	Pro
			195					200					205		
Val	Gly	Ala	His	Pro	Ser	Gly	Arg	Ile	Gly	Glu	Asp	Pro	Cys	Gly	Thr
			210					215				220			
Pro	Asn	Asn	Leu	Met	Pro	Tyr	Val	Gln	Gln	Val	Val	Val	Gly	Arg	Leu
			225					230				235			240
Pro	Asn	Leu	Lys	Ile	Tyr	Gly	Thr	Asp	Tyr	Thr	Thr	Lys	Asp	Gly	Thr
			245					250					255		
Gly	Val	Arg	Asp	Tyr	Ile	His	Val	Val	Asp	Leu	Ala	Asp	Gly	His	Ile
			260					265					270		
Phe	Ala	Leu	Gln	Lys	Leu	Asp	Asp	Thr	Glu	Ile	Gly	Cys	Glu	Val	Tyr
			275					280				285			
Asn	Leu	Gly	Thr	Gly	Lys	Gly	Thr	Thr	Val	Leu	Glu	Met	Val	Asp	Ala
			290				295				300				
Phe	Glu	Lys	Ala	Ser	Gly	Met	Lys	Ile	Pro	Leu	Val	Lys	Val	Gly	Arg
			305				310			315				320	
Arg	Pro	Gly	Asp	Ala	Glu	Thr	Val	Tyr	Ala	Ser	Thr	Glu	Lys	Ala	Glu
			325					330						335	
Arg	Glu	Leu	Asn	Trp	Lys	Ala	Asn	Phe	Gly	Ile	Glu	Glu	Met	Cys	Arg
			340					345						350	

Asp Gln Trp Asn Trp Ala Ser Asn Asn Pro Phe Gly Tyr Gly Ser Ser
355 360 365
Pro Asn Ser Thr
370

(2) INFORMATION FOR SEQ ID NO:508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..348

(D) OTHER INFORMATION: / Ceres Seq. ID 1498555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

Met Val Gly Asn Ile Leu Val Thr Gly Ala Gly Tyr Ile Gly Ser
1 5 10 15
His Thr Val Leu Gln Leu Leu Leu Gly Gly Tyr Asn Thr Val Val Ile
20 25 30
Asp Asn Leu Asp Asn Ser Ser Leu Val Ser Ile Gln Arg Val Lys Asp
35 40 45
Leu Ala Gly Asp His Gly Gln Asn Leu Thr Val His Gln Val Asp Leu
50 55 60
Arg Asp Lys Pro Ala Leu Glu Lys Val Phe Ser Glu Thr Lys Phe Asp
65 70 75 80
Ala Val Met His Phe Ala Gly Leu Lys Ala Val Gly Glu Ser Val Ala
85 90 95
Lys Pro Leu Leu Tyr Tyr Asn Asn Asn Leu Ile Ala Thr Ile Thr Leu
100 105 110
Leu Glu Val Met Ala Ala His Gly Cys Lys Lys Leu Val Phe Ser Ser
115 120 125
Ser Ala Thr Val Tyr Gly Trp Pro Lys Glu Val Pro Cys Thr Glu Glu
130 135 140
Ser Pro Leu Ser Gly Met Ser Pro Tyr Gly Arg Thr Lys Leu Phe Ile
145 150 155 160
Glu Asp Ile Cys Arg Asp Val Gln Arg Gly Asp Pro Glu Trp Arg Ile
165 170 175
Ile Met Leu Arg Tyr Phe Asn Pro Val Gly Ala His Pro Ser Gly Arg
180 185 190
Ile Gly Glu Asp Pro Cys Gly Thr Pro Asn Asn Leu Met Pro Tyr Val
195 200 205
Gln Gln Val Val Val Gly Arg Leu Pro Asn Leu Lys Ile Tyr Gly Thr
210 215 220
Asp Tyr Thr Thr Lys Asp Gly Thr Gly Val Arg Asp Tyr Ile His Val
225 230 235 240
Val Asp Leu Ala Asp Gly His Ile Phe Ala Leu Gln Lys Leu Asp Asp
245 250 255
Thr Glu Ile Gly Cys Glu Val Tyr Asn Leu Gly Thr Gly Lys Gly Thr
260 265 270
Thr Val Leu Glu Met Val Asp Ala Phe Glu Lys Ala Ser Gly Met Lys
275 280 285
Ile Pro Leu Val Lys Val Gly Arg Arg Pro Gly Asp Ala Glu Thr Val
290 295 300
Tyr Ala Ser Thr Glu Lys Ala Glu Arg Glu Leu Asn Trp Lys Ala Asn
305 310 315 320
Phe Gly Ile Glu Glu Met Cys Arg Asp Gln Trp Asn Trp Ala Ser Asn
325 330 335
Asn Pro Phe Gly Tyr Gly Ser Ser Pro Asn Ser Thr
340 345

(2) INFORMATION FOR SEQ ID NO:509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..266

(D) OTHER INFORMATION: / Ceres Seq. ID 1498556

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

Met	His	Phe	Ala	Gly	Leu	Lys	Ala	Val	Gly	Glu	Ser	Val	Ala	Lys	Pro
1				5				10						15	
Leu	Leu	Tyr	Tyr	Asn	Asn	Asn	Leu	Ile	Ala	Thr	Ile	Thr	Leu	Leu	Glu
			20				25						30		
Val	Met	Ala	Ala	His	Gly	Cys	Lys	Lys	Leu	Val	Phe	Ser	Ser	Ser	Ala
			35				40						45		
Thr	Val	Tyr	Gly	Trp	Pro	Lys	Glu	Val	Pro	Cys	Thr	Glu	Glu	Ser	Pro
			50			55				60					
Leu	Ser	Gly	Met	Ser	Pro	Tyr	Gly	Arg	Thr	Lys	Leu	Phe	Ile	Glu	Asp
65					70					75				80	
Ile	Cys	Arg	Asp	Val	Gln	Arg	Gly	Asp	Pro	Glu	Trp	Arg	Ile	Ile	Met
			85					90					95		
Leu	Arg	Tyr	Phe	Asn	Pro	Val	Gly	Ala	His	Pro	Ser	Gly	Arg	Ile	Gly
			100					105					110		
Glu	Asp	Pro	Cys	Gly	Thr	Pro	Asn	Asn	Leu	Met	Pro	Tyr	Val	Gln	Gln
			115				120						125		
Val	Val	Val	Gly	Arg	Leu	Pro	Asn	Leu	Lys	Ile	Tyr	Gly	Thr	Asp	Tyr
			130				135					140			
Thr	Thr	Lys	Asp	Gly	Thr	Gly	Val	Arg	Asp	Tyr	Ile	His	Val	Val	Asp
			145			150				155				160	
Leu	Ala	Asp	Gly	His	Ile	Phe	Ala	Leu	Gln	Lys	Leu	Asp	Asp	Thr	Glu
			165					170						175	
Ile	Gly	Cys	Glu	Val	Tyr	Asn	Leu	Gly	Thr	Gly	Lys	Gly	Thr	Thr	Val
			180				185						190		
Leu	Glu	Met	Val	Asp	Ala	Phe	Glu	Lys	Ala	Ser	Gly	Met	Lys	Ile	Pro
			195				200					205			
Leu	Val	Lys	Val	Gly	Arg	Arg	Pro	Gly	Asp	Ala	Glu	Thr	Val	Tyr	Ala
			210			215					220				
Ser	Thr	Glu	Lys	Ala	Glu	Arg	Glu	Leu	Asn	Trp	Lys	Ala	Asn	Phe	Gly
225					230					235				240	
Ile	Glu	Glu	Met	Cys	Arg	Asp	Gln	Trp	Asn	Trp	Ala	Ser	Asn	Asn	Pro
			245					250						255	
Phe	Gly	Tyr	Gly	Ser	Ser	Pro	Asn	Ser	Thr						
			260					265							

(2) INFORMATION FOR SEQ ID NO:510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..558

(D) OTHER INFORMATION: / Ceres Seq. ID 1498561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

rysgtcgctt	attgccggga	gattaccggg	aagaacagat	aacgagataa	agaactattg	60
gaacacacat	atacgaagaa	agctttataa	cagagggatt	gatccaacga	gtcacagacc	120
aatcccaagaa	tcatacagctt	ctcaagattc	taaacctaca	caactagAAC	cagttacgag	180
taacaccatt	aatatctcat	tcacttctgc	tccaaaggtc	gaaacgttcc	atgaaagtat	240

(2) INFORMATION FOR SEQ ID NO:511:

(A) LENGTH: 185 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(D) OTHER INFORMATION: / Ceres Seq. ID 1498562

Xaa	1	Arg	Ser	Leu	Ile	Ala	Gly	Arg	Leu	Pro	Gly	Arg	Thr	Asp	Asn	Glu	Ile
					5						10					15	
Lys	Asn	Ser	Tyr	Trp	Asn	Thr	His	Ile	Arg	Arg	Lys	Leu	Ile	Asn	Arg	Gly	
				20					25					30			
Ile	Asp	Pro	Thr	Ser	His	Arg	Pro	Ile	Gln	Glu	Ser	Ser	Ala	Ser	Gln		
		35					40					45					
Asp	Ser	Lys	Pro	Thr	Gln	Leu	Glu	Pro	Val	Thr	Ser	Asn	Thr	Ile	Asn		
		50				55					60						
Ile	Ser	Phe	Thr	Ser	Ala	Pro	Lys	Val	Glu	Thr	Phe	His	Glu	Ser	Ile		
					70					75					80		
Ser	Phe	Pro	Gly	Lys	Ser	Glu	Lys	Ile	Ser	Met	Leu	Thr	Phe	Lys	Glu		
				85					90					95			
Glu	Lys	Asp	Glu	Cys	Pro	Val	Gln	Glu	Lys	Phe	Pro	Asp	Leu	Asn	Leu		
			100					105					110				
Glu	Leu	Arg	Ile	Ser	Leu	Pro	Asp	Asp	Val	Asp	Arg	Ser	Gln	Gly	His		
			115				120					125					
Gly	Lys	Ser	Thr	Thr	Pro	Arg	Cys	Phe	Lys	Cys	Ser	Leu	Gly	Met	Ile		
			130			135					140						
Asn	Gly	Met	Glu	Cys	Arg	Cys	Gly	Arg	Met	Arg	Cys	Asp	Val	Val	Gly		
					150					155				160			
Gly	Ser	Ser	Lys	Gly	Ser	Asp	Met	Ser	Asn	Gly	Phe	Asp	Phe	Leu	Gly		
				165					170					175			
Leu	Ala	Lys	Lys	Glu	Thr	Thr	Ser	Leu									
			180					185									

(D) OTHER INFORMATION: / Ceres Seq. ID 1498563

Met	Leu	Thr	Phe	5	Asn	Glu	Glu	Lys	Asp	Glu	Cys	Pro	Val	Gln	Glu	Lys	15
Phe	Pro	Asp	Leu	20	Asn	Leu	Glu	Leu	Arg	Ile	Ser	Leu	Pro	Asp	Asp	Val	15
Asp	Arg	Leu	Gln	35	Gly	His	Gly	Lys	Ser	Thr	Thr	Pro	Arg	Cys	Phe	Lys	45
Cys	Ser	Leu	Gly	Met	Ile	Asn	Gly	Met	Glu	Cys	Arg	Cys	Gly	Arg	Met		

50	55	60
Arg Cys Asp Val Val Gly Gly Ser Ser Lys Gly Ser Asp Met Ser Asn		
65	70	75
Gly Phe Asp Phe Leu Gly Leu Ala Lys Lys Glu Thr Thr Ser Leu		
85	90	95

(2) INFORMATION FOR SEQ ID NO:513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..802
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498564

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

aacacatttc	aagcatttga	ttaatcaaa	g	cgaaaatggt	ggcaaatattt	60
cagaaaagctt	ttgctcaccc	accggaagaa	ctcaacagtc	cggtctctca	tttctccggc	120
aaaactccta	aacttcccg	cgaaactctc	tccgacttcc	tctctcatca	ccaaaacaat	180
gctttctcta	tgaacttcgg	cgactccgcc	gtcttagctt	acgtcgcaca	agaaacctct	240
cttcgtcaaa	ggttggtctg	tggactagat	gggatctact	gtatgtttct	aggagagattg	300
aataatctct	gtacattgaa	tcgacaatac	ggtttatctg	ggaagaagat	tgagaaggag	360
cccaagtctt	tgaagaatgg	tgatgctggt	atggtgaaga	tgactccaac	caagcccatg	420
gttggtggaga	cctctctctg	gtacccacca	cttgagcgtt	tcgctgtgca	gggacatgag	480
gcagactggt	gcagtcgggt	ttatcaagag	tggtgacaag	aaggaccaca	ccggagccaa	540
ggttaccaa	gctgcgctca	agaagggtgc	gaagtgaacc	atctcaaaa	ctctatctgc	600
cgcaggtgaa	tcaaaggaca	gtgttagttt	tattacaata	gtttgtgatt	tggtcgcgtg	660
tctgtgttct	gttttctgtt	tctcccgctc	agagcgttgt	tctcgttaatt	gggtctctga	720
tcggagggtg	cggatctaca	cacacattct	tctgtttttt	tgctttttat	ttgtttttctc	780
attttgaa	gtttaaaatg	ag				

(2) INFORMATION FOR SEQ ID NO:514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..156
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

Met Leu Ala Ile Phe Gln Lys Ala Phe Ala His Pro Pro Glu Glu Leu		
1	5	10
Asn Ser Pro Ala Ser His Phe Ser Gly Lys Thr Pro Lys Leu Pro Gly		
20	25	30
Glu Thr Leu Ser Asp Phe Leu Ser His His Gln Asn Asn Ala Phe Ser		
35	40	45
Met Asn Phe Gly Asp Ser Ala Val Leu Ala Tyr Ala Arg Gln Glu Thr		
50	55	60
Ser Leu Arg Gln Arg Leu Phe Cys Gly Leu Asp Gly Ile Tyr Cys Met		
65	70	75
Phe Leu Gly Arg Leu Asn Asn Leu Cys Thr Leu Asn Arg Gln Tyr Gly		
85	90	95
Leu Ser Gly Lys Lys Ile Glu Lys Glu Pro Lys Phe Leu Lys Asn Gly		
100	105	110
Asp Ala Gly Met Val Lys Met Thr Pro Thr Lys Pro Met Val Val Glu		
115	120	125
Thr Phe Ser Glu Tyr Pro Pro Leu Gly Arg Phe Ala Val Gln Gly His		
130	135	140

Glu Ala Asp Cys Cys Ser Arg Cys Tyr Gln Glu Cys
145 150 155

(2) INFORMATION FOR SEQ ID NO:515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..108
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

Met Asn Phe Gly Asp Ser Ala Val Leu Ala Tyr Ala Arg Gln Glu Thr
1 5 10 15
Ser Leu Arg Gln Arg Leu Phe Cys Gly Leu Asp Gly Ile Tyr Cys Met
20 25 30
Phe Leu Gly Arg Leu Asn Asn Leu Cys Thr Leu Asn Arg Gln Tyr Gly
35 40 45
Leu Ser Gly Lys Lys Ile Glu Lys Glu Pro Lys Phe Leu Lys Asn Gly
50 55 60
Asp Ala Gly Met Val Lys Met Thr Pro Thr Lys Pro Met Val Val Glu
65 70 75 80
Thr Phe Ser Glu Tyr Pro Pro Leu Gly Arg Phe Ala Val Gln Gly His
85 90 95
Glu Ala Asp Cys Cys Ser Arg Cys Tyr Gln Glu Cys
100 105

(2) INFORMATION FOR SEQ ID NO:516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..534
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

aaaccaagtt ttcttctaag ctgtatttga aagggtatat atttcacaca ccaaacagat 60
cagaagcnaa aaggtataata tataatggcg gatttgaggg acgaaaaagg taacccaatc 120
catctaaccg acacacaggg aaacccaatt gtgcacctga ctgatgagca cggtaacccc 180
atgtacctaa ccggtgttgt tagctccact cctcagcagt aaggagagha ctaccagcga 240
cattgcagag caccctacta gcaccgttgg agaaacacat ccggcagctg ctccagctgg 300
tgctggtgct gccaccgctg ccactgcgac aggagtctct gctggtactg gagcaaccac 360
cacagggcag caacaccatg ggtcgcttga agagcatctt cgtcggtctg gaagttcatc 420
tagctctagc tcggaggatg acgggcaagg agggaggagg aagaagagca taaaggagaa 480
aattaaagag aagctcaaa cgcaccaaga attccaagaa actgattgtt ggat

(2) INFORMATION FOR SEQ ID NO:517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..45
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

Met Ala Asp Leu Arg Asp Glu Lys Gly Asn Pro Ile His Leu Thr Asp
1 5 10 15
Thr Gln Gly Asn Pro Ile Val Asp Leu Thr Asp Glu His Gly Asn Pro
20 25 30
Met Tyr Leu Thr Gly Val Val Ser Ser Thr Pro Gln Gln
35 40 45

(2) INFORMATION FOR SEQ ID NO:518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..31
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

Met Gly Arg Leu Lys Ser Ile Phe Val Gly Leu Glu Val His Leu Ala
1 5 10 15
Leu Ala Arg Arg Met Thr Gly Lys Glu Gly Gly Arg Arg Ala
20 25 30

(2) INFORMATION FOR SEQ ID NO:519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1548 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1548
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

aaaatttaggg	cttttatctta	tcttcgcgat	tctctcatct	cctccctccta	aaattctccg	60
jcgacacagt	tcaccggaaa	tcgtagacga	aatcagattc	ttctctctta	gtatgaaaca	120
atgaatttga	tctcaagaac	attgacaaga	gcagtgtctt	cgctactata	ccactcaaaa	180
cgagcgaaagc	tccccactca	aaaatggata	atctcgcagc	aaatccgtgt	ttcttcgcgc	240
acagctcatca	gcggtggagg	aaagaaaacct	ctggcaaaag	tatccgtgaa	accacgccta	300
aatgtagcga	cggagaaga	atcgactccg	ccgaagacaa	ttaggtacaa	accggaaatt	360
tcaaaactgta	tcaacctaat	cggattcggt	gaacaaccag	ttcaattcgg	tctctgtctc	420
gatggaaaaa	tctgggctgg	aacagttatt	tctcagcggt	ctgggtcaaa	atcatctaat	480
ttctgcgattc	cgattatatt	cgaaggagat	ttagctaaaa	ttgcagttca	acatgtaaa	540
aaagaagatc	ggattcatgt	ttccgggaag	ctgtttattg	attcgctctc	tccaaatgtg	600
acataattctc	aatccaatgt	tcaggttatg	gttcagaatc	ttaactctgt	acaagctgct	660
acttctacga	ctaagacagt	ctcaccactt	gaaaaagaag	ttaccagcat	caagaaaaag	720
cccgcaagat	ccaaaaaggt	taaagtcata	gatgaagaaa	cctctaatct	ttggaaagcat	780
cttatttga	atctctaaag	gtggttggat	caccgtggga	ataaagctaa	cggattggta	840
aagccaggac	atccccgattt	caagatgaag	gttggttggt	tgtccctgtg	gctcagcaca	900
gctcctgatt	gggctttgct	aaaactcgaa	gagcttaagt	ttgatgtatt	agtcctctaaa	960
ggaacactca	aactgaatca	acttaaaagg	gaggaaatct	ggaaggattt	ggttcagaca	1020
ccagacaaat	gggttagacaa	cagatcagat	aagacaaaag	tgaaataacc	tgacttcaag	1080
cataaagaga	ctggttgaagc	actgtggatg	accaattctc	ctatttgggt	actgtcaaa	1140
ttaccacctc	taaaagaagaa	ccaagaaaga	cctctcatgt	ctaataaagt	ctcgcagctt	1200
gagcttgacg	ttgaagtacc	taaaggaaat	ctgaaccagc	ttaaaagaga	ggaattttgg	1260
aagaacttgg	ttgagaaccc	cagtaaatgt	tgggataaca	gattagacaa	gagaaaccc	1320
aaaggccctg	acttttaagca	taaggagacc	ggtagaacac	tgttgatagg	tgattctcgc	1380
actgtggcgc	tgtcaaaagt	accacctcta	aagaaaaaac	aagaagaacc	tgctatggcc	1440
taagctcttc	tagcagcctt	attgttaatt	tggccccccac	tatgtaaaaa	ggccctatga	1500
ctttattatc	cagctcttata	caaagagaat	tgctatagta	tcagtgccc		

(2) INFORMATION FOR SEQ ID NO:520:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 440 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..440
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498575

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

Met	Asn	Leu	Ile	Ser	Arg	Thr	Leu	Thr	Arg	Ala	Val	Ser	Ser	Ser	Leu
1				5				10						15	
Tyr	His	Ser	Lys	Ala	Ala	Lys	Leu	Pro	Thr	Gln	Lys	Trp	Ile	Ile	Ser
			20				25						30		
Gln	Gln	Ile	Arg	Val	Phe	Ser	Ala	Thr	Val	Ile	Ser	Gly	Gly	Gly	Lys
		35					40					45			
Lys	Pro	Leu	Ala	Lys	Val	Ser	Val	Lys	Pro	Pro	Leu	Asn	Val	Ala	Thr
	50					55					60				
Glu	Lys	Glu	Ser	Thr	Pro	Pro	Lys	Thr	Ile	Glu	Tyr	Lys	Pro	Glu	Ile
65				70					75						
Ser	Asn	Trp	Ile	Asn	Leu	Ile	Gly	Phe	Val	Glu	Gln	Pro	Val	Gln	Phe
				85					90					95	
Gly	Pro	Cys	Ser	Asp	Gly	Lys	Phe	Trp	Ala	Gly	Thr	Val	Ile	Ser	Gln
		100					105						110		
Arg	Ser	Gly	Ser	Lys	Ser	Ser	Asn	Phe	Trp	Ile	Pro	Ile	Ile	Phe	Glu
		115					120					125			
Gly	Asp	Leu	Ala	Lys	Ile	Ala	Val	Gln	His	Val	Lys	Lys	Glu	Asp	Arg
	130					135					140				
Ile	His	Val	Ser	Gly	Lys	Leu	Phe	Ile	Asp	Ser	Pro	Pro	Pro	Asn	Val
145					150					155				160	
Thr	Tyr	Ser	Gln	Ser	Asn	Val	Gln	Val	Met	Val	Gln	Asn	Leu	Asn	Phe
			165						170					175	
Val	Gln	Ala	Ala	Thr	Ser	Thr	Thr	Lys	Thr	Ile	Ser	Pro	Pro	Glu	Lys
		180						185					190		
Glu	Val	Thr	Ser	Ile	Lys	Lys	Lys	Pro	Ala	Arg	Ser	Lys	Lys	Val	Lys
		195					200					205			
Val	Ile	Asp	Glu	Glu	Thr	Ser	Asn	Ser	Trp	Lys	His	Leu	Ile	Glu	Asn
	210					215					220				
Pro	Lys	Glu	Trp	Leu	Asp	His	Arg	Gly	Asn	Lys	Ala	Asn	Gly	Leu	Val
225				230						235				240	
Lys	Pro	Gly	His	Pro	Asp	Phe	Lys	Met	Lys	Val	Gly	Gly	Leu	Ser	Leu
			245						250				255		
Trp	Leu	Ser	Thr	Ala	Pro	Asp	Trp	Ala	Leu	Leu	Lys	Leu	Glu	Glu	Leu
		260					265						270		
Lys	Phe	Asp	Val	Leu	Val	Pro	Lys	Gly	Asn	Ile	Lys	Leu	Asn	Gln	Leu
		275					280					285			
Lys	Gly	Glu	Glu	Ser	Trp	Lys	Asp	Leu	Val	Gln	Asn	Pro	Asp	Lys	Trp
	290					295					300				
Leu	Asp	Asn	Arg	Ser	Asp	Lys	Thr	Asn	Val	Lys	Tyr	Pro	Asp	Phe	Lys
305					310					315				320	
His	Lys	Glu	Thr	Gly	Glu	Ala	Leu	Trp	Met	Thr	Asn	Ser	Pro	Ile	Trp
			325						330					335	
Val	Leu	Ser	Lys	Leu	Pro	Pro	Leu	Lys	Lys	Asn	Gln	Glu	Arg	Pro	Leu
		340						345					350		
Met	Ser	Asn	Lys	Val	Ser	Gln	Leu	Glu	Leu	Asp	Val	Glu	Val	Pro	Lys
		355					360					365			
Gly	Asn	Leu	Lys	Gln	Leu	Lys	Arg	Glu	Glu	Ile	Trp	Lys	Asn	Leu	Val
	370					375					380				
Glu	Asn	Pro	Ser	Lys	Trp	Trp	Asp	Asn	Arg	Leu	Asp	Lys	Arg	Asn	Pro
385					390					395				400	

Lys Gly Pro Asp Phe Lys His Lys Glu Thr Gly Glu Ala Leu Trp Ile
405 410 415
Gly Asp Ser Pro Thr Trp Ala Leu Ser Lys Leu Pro Pro Leu Lys Lys
420 425 430
Asn Gln Glu Arg Pro Val Met Ala
435 440

(2) INFORMATION FOR SEQ ID NO:521:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..271
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

Met Val Gln Asn Leu Asn Phe Val Gln Ala Ala Thr Ser Thr Lys
1 5 10 15
Thr Ile Ser Pro Pro Glu Lys Glu Val Thr Ser Ile Lys Lys Lys Pro
20 25 30
Ala Arg Ser Lys Lys Val Lys Val Ile Asp Glu Glu Thr Ser Asn Ser
35 40 45
Trp Lys His Leu Ile Glu Asn Pro Lys Glu Trp Leu Asp His Arg Gly
50 55 60
Asn Lys Ala Asn Gly Leu Val Lys Pro Gly His Pro Asp Phe Lys Met
65 70 75 80
Lys Val Gly Gly Leu Ser Leu Trp Leu Ser Thr Ala Pro Asp Trp Ala
85 90 95
Leu Leu Lys Leu Glu Glu Leu Lys Phe Asp Val Leu Val Pro Lys Gly
100 105 110
Asn Ile Lys Leu Asn Gln Leu Lys Gly Glu Glu Ser Trp Lys Asp Leu
115 120 125
Val Gln Asn Pro Asp Lys Trp Leu Asp Asn Arg Ser Asp Lys Thr Asn
130 135 140
Val Lys Tyr Pro Asp Phe Lys His Lys Glu Thr Gly Glu Ala Leu Trp
145 150 155 160
Met Thr Asn Ser Pro Ile Trp Val Leu Ser Lys Leu Pro Pro Leu Lys
165 170 175
Lys Asn Gln Glu Arg Pro Leu Met Ser Asn Lys Val Ser Gln Leu Glu
180 185 190
Leu Asp Val Glu Val Pro Lys Gly Asn Leu Lys Gln Leu Lys Arg Glu
195 200 205
Glu Ile Trp Lys Asn Leu Val Glu Asn Pro Ser Lys Trp Trp Asp Asn
210 215 220
Arg Leu Asp Lys Arg Asn Pro Lys Gly Pro Asp Phe Lys His Lys Glu
225 230 235 240
Thr Gly Glu Ala Leu Trp Ile Gly Asp Ser Pro Thr Trp Ala Leu Ser
245 250 255
Lys Leu Pro Pro Leu Lys Lys Asn Gln Glu Arg Pro Val Met Ala
260 265 270

(2) INFORMATION FOR SEQ ID NO:522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 607 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..607

(D) OTHER INFORMATION: / Ceres Seq. ID 1498577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

atcaacttca	gatactttca	ccagcaaacac	aagttatatt	caaaagatga	tgccaaattc	60
tagatcgggc	acaataactc	cgacgacaga	atcaaccacc	acgacaacaa	caacaacaac	120
gactctaacg	acgtcgattt	gggtttacag	ttgtacacga	ttcatcagcg	tttggaaga	180
tcaagacgca	aacgtcgagg	tcttatgtcc	ttattgcaac	gggtgattca	tcgaagagat	240
tgaagattct	tctaattcca	ccgtcgcgcc	gattccggct	tcgactccgg	aagttagatc	300
gggtgaggaa	acacatagat	ctataattag	acgtcgtaga	tctaatacgcc	ggacgtccct	360
taatccggtg	atcgctcttac	acggcgaggag	aggaggagga	gccgggtgaga	gagttgagaa	420
cgaagaaggt	gacggagcta	ctagagaacg	acgagcttat	gagtyttatt	acgatgatgg	480
atctggttca	gggtctaagac	ctcttctcga	ttctgtatct	gagatcttga	ttggatctgg	540
attcgaacgg	ttacttgaac	aattgagtca	gatcgaagcg	tcaggtaaacg	gaatcggtag	600
atctggg						

(2) INFORMATION FOR SEQ ID NO:523:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 202 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..202

(D) OTHER INFORMATION: / Ceres Seq. ID 1498578

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

Ser	Thr	Ser	Asp	Pro	Phe	Thr	Ser	Asn	Thr	Ser	Tyr	Phe	Gln	Lys	Met
1			5					10						15	
Met	Pro	Asn	Ser	Arg	Ser	Ala	Thr	Ile	Thr	Pro	Thr	Thr	Glu	Ser	Thr
			20					25					30		
Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Leu	Thr	Thr	Ser	Tyr	Trp	Cys	
			35					40				45			
Tyr	Ser	Cys	Thr	Arg	Phe	Ile	Ser	Val	Trp	Glu	Asp	Gln	Asp	Ala	Asn
			50			55					60				
Ala	Gly	Val	Leu	Cys	Pro	Tyr	Cys	Asn	Gly	Gly	Phe	Ile	Glu	Glu	Ile
			65			70				75				80	
Glu	Asp	Ser	Ser	Asn	Ser	Thr	Val	Ala	Ala	Ile	Pro	Ala	Ser	Thr	Pro
			85					90					95		
Glu	Val	Arg	Ser	Val	Glu	Glu	Thr	His	Arg	Ser	Ile	Ile	Arg	Arg	Arg
			100					105					110		
Arg	Ser	Asn	Arg	Arg	Thr	Ser	Phe	Asn	Pro	Val	Ile	Val	Leu	His	Gly
			115				120					125			
Gly	Gly	Gly	Gly	Ala	Gly	Glu	Arg	Val	Glu	Asn	Glu	Glu	Gly	Asp	
			130			135				140					
Gly	Ala	Thr	Arg	Glu	Arg	Ala	Tyr	Glu	Xaa	Tyr	Tyr	Asp	Asp	Gly	
			145			150			155					160	
Ser	Gly	Ser	Gly	Leu	Arg	Pro	Leu	Pro	Asp	Ser	Val	Ser	Glu	Ile	Leu
			165					170					175		
Ile	Gly	Ser	Gly	Phe	Glu	Arg	Leu	Leu	Glu	Gln	Leu	Ser	Gln	Ile	Glu
			180				185					190			
Ala	Ser	Gly	Asn	Gly	Ile	Gly	Arg	Ser	Gly						
			195			200									

(2) INFORMATION FOR SEQ ID NO:524:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..187

(D) OTHER INFORMATION: / Ceres Seq. ID 1498579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

Met	Met	Pro	Asn	Ser	Arg	Ser	Ala	Thr	Ile	Thr	Pro	Thr	Thr	Glu	Ser
1			5						10					15	
Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Leu	Thr	Thr	Ser	Tyr	Trp	
			20					25					30		
Cys	Tyr	Ser	Cys	Thr	Arg	Phe	Ile	Ser	Val	Trp	Glu	Asp	Gln	Asp	Ala
			35				40					45			
Asn	Ala	Gly	Val	Leu	Cys	Pro	Tyr	Cys	Asn	Gly	Gly	Phe	Ile	Glu	Glu
			50				55				60				
Ile	Glu	Asp	Ser	Ser	Asn	Ser	Thr	Val	Ala	Ala	Ile	Pro	Ala	Ser	Thr
65					70					75				80	
Pro	Glu	Val	Arg	Ser	Val	Glu	Glu	Thr	His	Arg	Ser	Ile	Ile	Arg	Arg
					85			90						95	
Arg	Arg	Ser	Asn	Arg	Arg	Thr	Ser	Phe	Asn	Pro	Val	Ile	Val	Leu	His
			100					105					110		
Gly	Gly	Gly	Gly	Gly	Gly	Ala	Gly	Glu	Arg	Val	Glu	Asn	Glu	Glu	Gly
			115				120								
Asp	Gly	Ala	Thr	Arg	Glu	Arg	Arg	Ala	Tyr	Glu	Xaa	Tyr	Tyr	Asp	Asp
			130				135				140				
Gly	Ser	Gly	Ser	Gly	Leu	Arg	Pro	Leu	Pro	Asp	Ser	Val	Ser	Glu	Ile
145					150					155				160	
Leu	Ile	Gly	Ser	Gly	Phe	Glu	Arg	Leu	Leu	Glu	Gln	Leu	Ser	Gln	Ile
					165				170					175	
Glu	Ala	Ser	Gly	Asn	Gly	Ile	Gly	Arg	Ser	Gly					
					180				185						

(2) INFORMATION FOR SEQ ID NO:525:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..186

(D) OTHER INFORMATION: / Ceres Seq. ID 1498580

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

Met	Pro	Asn	Ser	Arg	Ser	Ala	Thr	Ile	Thr	Pro	Thr	Thr	Glu	Ser	Thr
1			5						10					15	
Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Leu	Thr	Thr	Ser	Tyr	Trp	Cys	
			20					25					30		
Tyr	Ser	Cys	Thr	Arg	Phe	Ile	Ser	Val	Trp	Glu	Asp	Gln	Asp	Ala	Asn
			35				40					45			
Ala	Gly	Val	Leu	Cys	Pro	Tyr	Cys	Asn	Gly	Gly	Phe	Ile	Glu	Glu	Ile
			50				55				60				
Glu	Asp	Ser	Ser	Asn	Ser	Thr	Val	Ala	Ala	Ile	Pro	Ala	Ser	Thr	Pro
65					70				75					80	
Glu	Val	Arg	Ser	Val	Glu	Glu	Thr	His	Arg	Ser	Ile	Ile	Arg	Arg	Arg
					85			90						95	
Arg	Ser	Asn	Arg	Arg	Thr	Ser	Phe	Asn	Pro	Val	Ile	Val	Leu	His	Gly
			100					105					110		
Gly	Gly	Gly	Gly	Ala	Gly	Glu	Arg	Val	Glu	Asn	Glu	Glu	Gly	Asp	
			115				120				125				
Gly	Ala	Thr	Arg	Glu	Arg	Ala	Tyr	Glu	Xaa	Tyr	Tyr	Asp	Asp	Gly	
			130				135				140				
Ser	Gly	Ser	Gly	Leu	Arg	Pro	Leu	Pro	Asp	Ser	Val	Ser	Glu	Ile	Leu
145					150				155					160	
Ile	Gly	Ser	Gly	Phe	Glu	Arg	Leu	Leu	Glu	Gln	Leu	Ser	Gln	Ile	Glu
					165				170					175	

Ala Ser Gly Asn Gly Ile Gly Arg Ser Gly
180 185

(2) INFORMATION FOR SEQ ID NO:526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1303
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

aaagctcaga	tatctgaata	actcgtcttc	gtgcctctct	ctctctaaaa	gcccatctct	60
ttctctctct	cctctccat	tgaagaagaa	acctaccttc	gtaattattc	ctcaattacg	120
atcatgtgtga	atgttaaagg	gtcaaccaaa	aaatcgaaat	ttgatcgatt	ccttcattgc	180
ataacacccct	tagtgccacc	ccaatctctc	cccaagacgg	agattagaac	cctaataatga	240
ttgtggcatc	catgggagag	acaaaagggt	gagtttttca	ggttgagtga	ttgtggggat	300
gtttatgatg	aatggagcgc	ttatggagct	agcgttctca	ttcatgttac	caacggagaaa	360
ctctctgttc	aatactatgt	tccttatctc	cttgccatcc	agattttcac	ctctcattcc	420
tccttgatcc	gcttaaggga	agagttctga	gatggggaat	gtgagggtag	agatccgttt	480
agcgattcac	gtagcgatga	gagtgctctc	gagggaaggac	ttgagaacaa	caacgtcttg	540
catccaagtg	atcgtttggg	ttatctttat	ctccaatact	ttgagagatc	agctccttat	600
accagagttc	ctctgatgga	taagatcaat	gaattggctc	aaagatcccc	gggattgatg	660
tcgttgagaa	gcgttgatct	ttctccagct	agttggatgt	cagtgcgatg	gtaccggatt	720
taccatatac	caatgggaag	aaccattaaa	gacttatcca	cggtgttctc	caattataac	780
actctttctc	ctctttttca	agatatggaa	cgggaagaaa	atggtgggga	caaggagaga	840
gtgctggagg	aaggggaaga	tataactctg	ctccattttg	ggatggctac	ttacaagatg	900
caaggcgatg	tttggctttc	gcaggaccac	gatgatcaag	agagattggc	ttcgctttac	960
agtggttcgg	attcttggtc	taaacagctc	agggtccaac	atcatgactt	caactacttc	1020
tgcaatatgt	caatgactca	tcgtggctaa	acctcgggtg	gatgaaccca	tgatgtttgc	1080
ttgtttcttc	atatatagtc	taattcttgc	tttgttctgg	aaccgcgttg	gttttgtaaa	1140
acgcaatgga	gcgattcgct	ttgcagtggt	ttggttagaa	tagcgttttg	agctctttaa	1200
cccttgagag	agtatatgtc	gtatatagag	ttttgttgct	tggtgaaaca	gagtacaatt	1260
gtgtgtgtgt	gttaaaaaaa	gagtgatgtt	ttcttataag	ttg		

(2) INFORMATION FOR SEQ ID NO:527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..308
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

Met	Val	Asn	Val	Lys	Gly	Ser	Thr	Lys	Lys	Ser	Asn	Leu	Asp	Arg	Phe
1			5					10					15		
Leu	His	Cys	Ile	Thr	Pro	Leu	Val	Pro	Pro	Gln	Ser	Leu	Pro	Lys	Thr
			20					25				30			
Glu	Ile	Arg	Thr	Leu	Asn	Arg	Leu	Trp	His	Pro	Trp	Glu	Arg	Gln	Lys
			35				40					45			
Val	Glu	Phe	Phe	Arg	Leu	Ser	Asp	Leu	Trp	Asp	Cys	Tyr	Asp	Glu	Trp
			50			55					60				
Ser	Ala	Tyr	Gly	Ala	Ser	Val	Pro	Ile	His	Val	Thr	Asn	Gly	Glu	Ser
			65			70				75				80	
Leu	Val	Gln	Tyr	Tyr	Val	Pro	Tyr	Leu	Ser	Ala	Ile	Gln	Ile	Phe	Thr
			85					90				95			
Ser	His	Ser	Ser	Leu	Ile	Arg	Leu	Arg	Glu	Ser	Glu	Asp	Gly	Glu	

	100		105		110	
Cys	Glu	Gly	Arg	Asp	Pro	Phe
	115		120		125	
Ser	Glu	Glu	Gly	Leu	Glu	Asn
	130		135		140	
Leu	Gly	Tyr	Leu	Tyr	Gln	Tyr
	145		150		155	
Arg	Val	Pro	Leu	Met	Asp	Lys
			165		170	
Gly	Leu	Met	Ser	Leu	Arg	Ser
		180		185		
Ser	Val	Ala	Trp	Tyr	Pro	Ile
		195		200		
Lys	Asp	Leu	Ser	Thr	Cys	Phe
		210		215		
Phe	Gln	Asp	Met	Glu	Pro	Glu
		225		230		
Arg	Arg	Glu	Gly	Glu	Asp	Ile
		245		250		
Tyr	Lys	Met	Gln	Gly	Asp	Val
		260		265		
Glu	Arg	Leu	Ala	Ser	Leu	Tyr
		275		280		
Leu	Arg	Val	Gln	His	His	Asp
		290		295		
Thr	His	Arg	Gly			
		305				

(2) INFORMATION FOR SEQ ID NO:528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..518
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498595

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

gtccgagtc	cgatgagtc	actcggagat	ttgcttagag	aatcagaaga	tggacaaga	60
agtgaagag	cgatgatgat	gagtttgctc	gaagaagatc	aaatcaacgg	tggagataga	120
acgatgagc	aatggactac	gttaaagcaa	cggctgagat	ttgatgggtg	tggtgtgtgt	180
ggtaagctc	ttactctgcg	tctcagacaa	cgggagacac	caatcgtcgt	cgatgatgat	240
gacgacga	aagaaagtca	aaaccaggtc	gttgactttt	cggtaccggg	tacgggtacg	300
gagttggatt	gtttgagacg	cagagtaaga	ggcttaccac	aacaaccaac	ccaatcaaat	360
ctcagccgtt	gcttttaacgt	agtacttttg	tggtttatgt	tttggggcca	tgtaacagcct	420
ctgataaata	attgatcgac	tatgtttccg	ttttctttcat	ctctcttttc	tttcaaacaa	480
caaatggaac	ttattctcta	ttgcaattat	ctcttttgc			

(2) INFORMATION FOR SEQ ID NO:529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498596

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

Val Arg Val Thr Met Ser Gln Leu Gly Asp Leu Leu Arg Glu Ser Glu

1	5	10	15
Asp Gly Thr Arg Ser Glu Arg Thr Met Met Ser Leu Leu Glu Glu			
	20	25	30
Asp Gln Ile Asn Gly Gly Asp Arg Thr Met Ser Lys Trp Thr Thr Leu			
	35	40	45
Lys Gln Arg Leu Arg Phe Asp Trp Val Gly Cys Xaa Gly Lys Pro Leu			
	50	55	60
Thr Leu Arg Leu Arg Gln Ala Glu Thr Pro Ile Val Val Asp Asp Asp			
	65	70	75
Asp Asp Glu Glu Glu Ser Gln Asn Gln Val Val Asp Phe Ser Asp Pro			
	85	90	95
Gly Thr Gly Thr Glu Leu Asp Cys Leu Arg Arg Arg Val Arg Gly Leu			
	100	105	110
Pro Gln Gln Pro Thr Gln Ser Asn Leu Ser Arg Cys Phe Asn Val Val			
	115	120	125
Leu Trp Trp Phe Met Phe Trp Gly His Val Gln Pro Leu Ile Asn Asn			
	130	135	140

(2) INFORMATION FOR SEQ ID NO:530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1498597

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

Met Ser Gln Leu Gly Asp Leu Leu Arg Glu Ser Gly Asp Gly Thr Arg			
	5	10	15
Ser Glu Arg Thr Met Met Met Ser Leu Glu Glu Asp Gln Ile Asn			
	20	25	30
Gly Gly Asp Arg Thr Met Ser Lys Trp Thr Thr Leu Lys Gln Arg Leu			
	35	40	45
Arg Phe Asp Trp Val Gly Cys Xaa Gly Lys Pro Leu Thr Leu Arg Leu			
	50	55	60
Arg Gln Ala Glu Thr Pro Ile Val Val Asp Asp Asp Asp Glu Glu			
	65	70	75
Glu Ser Gln Asn Gln Val Val Asp Phe Ser Asp Pro Gly Thr Gly Thr			
	85	90	95
Glu Leu Asp Cys Leu Arg Arg Arg Val Arg Gly Leu Pro Gln Gln Pro			
	100	105	110
Thr Gln Ser Asn Leu Ser Arg Cys Phe Asn Val Val Leu Trp Trp Phe			
	115	120	125
Met Phe Trp Gly His Val Gln Pro Leu Ile Asn Asn			
	130	135	140

(2) INFORMATION FOR SEQ ID NO:531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1498598

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

Met Met Met Ser Leu Leu Glu Glu Asp Gln Ile Asn Gly Gly Asp Arg
1 5 10 15
Thr Met Ser Lys Trp Thr Thr Leu Lys Gln Arg Leu Arg Phe Asp Trp
20 25 30
Val Gly Cys Xaa Gly Lys Pro Leu Thr Leu Arg Leu Arg Gln Ala Glu
35 40 45
Thr Pro Ile Val Val Ser Asp Asp Asp Glu Glu Ser Gln Asn
50 55 60
Gln Val Val Asp Phe Ser Asp Pro Gly Thr Gly Thr Glu Leu Asp Cys
65 70 75 80
Leu Arg Arg Arg Val Arg Gly Leu Pro Gln Gln Pro Thr Gln Ser Asn
85 90 95
Leu Ser Arg Cys Phe Asn Val Val Leu Trp Trp Phe Met Phe Trp Gly
100 105 110
His Val Gln Pro Leu Ile Asn Asn
115 120

(2) INFORMATION FOR SEQ ID NO:532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1919 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1919
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498599

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

cattaagagc	aaaaactagt	tttgctttca	tttttttttg	gtaggaaagg	gttaattata	60
cgtaacacag	aaacaaaaac	aattctcttt	tcctctagaa	aaagagatta	aaaaaaaaat	120
ggaggggagc	ttattgacgg	tggttggtctg	cctcgtctct	acggtggcga	tcgtgaacgc	180
cgggtgactg	tacttcttcc	atacatggaa	cgtgaacttac	ggaactgcct	caacctctgg	240
tgttctctcaa	aaggtgattc	tcatcaacgg	tcaattccct	ggctctaacc	ttacctcaac	300
ctctaaacac	aacgtcgtca	tcaatgtctt	caaccaccta	gacgaacctt	tcctcttgac	360
ctggagtggg	attcagcctc	ggaagaactg	ctggcaagat	ggtgtggctg	gaacttcatg	420
ccccatccca	gctggacaga	actttactta	ccatttccaa	cctaaggacc	agattgggtt	480
ctaactctat	tacccaacca	cttctctcca	ccgctttgct	ggtggttttg	gtggctctcg	540
gtgcaacagc	cgtctcctaa	ttcccgcttc	ttatgtctgat	cctgaagatg	actacactgt	600
cccttcgggt	gactgggtaca	cagctggcca	cactgctctc	aagaacttcc	ttgacagttg	660
acgcaccctt	ggattgccta	acggtgtttt	gatcaatgga	aagtctggaa	aggttggagg	720
aaagaacagc	ccctttgttca	caatgaagcc	tggaagagct	tacaagtaca	ggctctgcaa	780
tggtgggttg	aagctctacac	ttaaacttcag	gatccagaac	cacaagatga	agctcgtgga	840
gatggaagga	tcocatgtta	tcagaacga	ctatgactct	ctcgatgtcc	atgttggcca	900
gtgcttttca	gttctctgtga	ctgctaacca	agcagctaag	gattactaca	tggttgcatc	960
gactagggtc	ctcaaaagag	agttgagcac	cgtgggtgtg	atccggtatg	agggaaagcaa	1020
cgttcaggct	tcaactgagc	tacccaaggc	tcctgttgga	tggtgtgtgt	ctttgaacca	1080
gttcagggtc	tccagtggtga	accttaacct	taacgtgca	agggcctaacc	ccaaaggctc	1140
ataccattac	gaaagaatca	atattaccgc	tagcatcaag	cttgtoaact	cttaaaagtgt	1200
gggtgacggt	aaagtccggt	ttggttttcaa	tggtgtatca	cacgttgaca	ccgagactcc	1260
tttgaagctt	gctgagtact	tccaaatgtc	agagaaggtt	ttcaagtaca	atgtgatcaa	1320
ggaagagcct	ggaagcctaaa	tcaacagcatt	gactgtacaa	cctaattgtc	tcaacatcac	1380
tttccgtacc	ttttagagaa	tcatatttga	gaaccaacag	aaagaccatgc	agctcatcca	1440
tttggatggc	tactcctctt	tcgctgtcgc	ttctgagcca	gggaggtgga	cgctgcctaaa	1500
gagagagaac	tacaactctg	tcgatgcggt	tcgacagac	accgtgtcaa	cttaccgccaa	1560
gtctgttgca	gctatccttt	tgacatttga	caacgcgggt	atgtgtgaaca	tcaggtctga	1620
gaacttggag	aggaaatacc	taggcgagca	attgtatgtc	agtggtttat	cccggtgaga	1680
atcgtcaagg	gacgagtaca	acatccccct	caacacaaac	ctctgtggca	tcgtcaaggg	1740
cttgccattt	cctgcacact	actcctaata	caatatataa	ttactactta	ctctacaaag	1800
tggtgtgcga	tattaaatta	actaataata	cttttctcga	atttttaagt	taatttttaa	1860
accccttctt	tcataatacta	tcatataaac	ataatcata	accaagtttt	gctttcatt	

(2) INFORMATION FOR SEQ ID NO:533:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 341 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..341
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498600
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

Met	Lys	Pro	Gly	Lys	Thr	Tyr	Lys	Tyr	Arg	Leu	Cys	Asn	Val	Gly	Phe
1				5				10					15		
Lys	Ser	Thr	Leu	Asn	Phe	Arg	Ile	Gln	Asn	His	Lys	Met	Lys	Leu	Val
			20				25					30			
Glu	Met	Glu	Gly	Ser	His	Val	Ile	Gln	Asn	Asp	Tyr	Asp	Ser	Leu	Asp
		35				40					45				
Val	His	Val	Gly	Gln	Cys	Phe	Ser	Val	Leu	Val	Thr	Ala	Asn	Gln	Ala
	50				55					60					
Ala	Lys	Asp	Tyr	Tyr	Met	Val	Ala	Ser	Thr	Arg	Phe	Leu	Lys	Lys	Glu
65				70					75						80
Leu	Ser	Thr	Val	Gly	Val	Ile	Arg	Tyr	Glu	Gly	Ser	Asn	Val	Gln	Ala
			85					90				95			
Ser	Thr	Glu	Leu	Pro	Lys	Ala	Pro	Val	Gly	Trp	Ala	Trp	Ser	Leu	Asn
		100					105					110			
Gln	Phe	Arg	Ser	Phe	Arg	Trp	Asn	Leu	Thr	Ser	Asn	Ala	Ala	Arg	Pro
		115				120					125				
Asn	Pro	Gln	Gly	Ser	Tyr	His	Tyr	Gly	Lys	Ile	Asn	Ile	Thr	Arg	Ser
	130				135					140					
Ile	Lys	Leu	Val	Asn	Ser	Lys	Ser	Val	Val	Asp	Gly	Lys	Val	Arg	Phe
145				150					155						160
Gly	Phe	Asn	Gly	Val	Ser	His	Val	Asp	Thr	Glu	Thr	Pro	Leu	Lys	Leu
		165						170					175		
Ala	Glu	Tyr	Phe	Gln	Met	Ser	Glu	Lys	Val	Phe	Lys	Tyr	Asn	Val	Ile
	180						185						190		
Lys	Asp	Glu	Pro	Ala	Ala	Lys	Ile	Thr	Ala	Leu	Thr	Val	Gln	Pro	Asn
	195					200						205			
Val	Leu	Asn	Ile	Thr	Phe	Arg	Thr	Phe	Val	Glu	Ile	Ile	Phe	Glu	Asn
	210					215					220				
His	Glu	Lys	Thr	Met	Gln	Ser	Phe	His	Leu	Asp	Gly	Tyr	Ser	Phe	Phe
225				230						235					240
Ala	Val	Ala	Ser	Glu	Pro	Gly	Arg	Trp	Thr	Pro	Glu	Lys	Arg	Glu	Asn
		245						250						255	
Tyr	Asn	Leu	Leu	Asp	Ala	Val	Ser	Arg	His	Thr	Val	Gln	Val	Tyr	Pro
	260						265					270			
Lys	Ser	Trp	Ser	Ala	Ile	Leu	Leu	Thr	Phe	Asp	Asn	Ala	Gly	Met	Trp
	275					280						285			
Asn	Ile	Arg	Ser	Glu	Asn	Leu	Glu	Arg	Lys	Tyr	Leu	Gly	Glu	Gln	Leu
	290				295						300				
Tyr	Val	Ser	Val	Leu	Ser	Pro	Glu	Lys	Ser	Leu	Arg	Asp	Glu	Tyr	Asn
	305				310					315				320	
Ile	Pro	Leu	Asn	Thr	Asn	Leu	Cys	Gly	Ile	Val	Lys	Gly	Leu	Pro	Leu
		325						330					335		
Pro	Ala	His	Tyr	Ser											
		340													

(2) INFORMATION FOR SEQ ID NO:534:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 313 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..313

(D) OTHER INFORMATION: / Ceres Seq. ID 1498601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:

Met Lys Leu Val Glu Met Glu Gly Ser His Val Ile Gln Asn Asp Tyr
1 5 10 15
Asp Ser Leu Asp Val His Val Gly Gln Cys Phe Ser Val Leu Val Thr
20 25 30
Ala Asn Gln Ala Ala Lys Asp Tyr Tyr Met Val Ala Ser Thr Arg Phe
35 40 45
Leu Lys Lys Glu Leu Ser Thr Val Gly Val Ile Arg Tyr Glu Gly Ser
50 55 60
Asn Val Gln Ala Ser Thr Glu Leu Pro Lys Ala Pro Val Gly Trp Ala
65 70 75 80
Trp Ser Leu Asn Gln Phe Arg Ser Phe Arg Trp Asn Leu Thr Ser Asn
85 90 95
Ala Ala Arg Pro Asn Pro Gln Gly Ser Tyr His Tyr Gly Lys Ile Asn
100 105 110
Ile Thr Arg Ser Ile Lys Leu Val Asn Ser Lys Ser Val Val Asp Gly
115 120 125
Lys Val Arg Phe Gly Phe Asn Gly Val Ser His Val Asp Thr Glu Thr
130 135 140
Pro Leu Lys Leu Ala Glu Tyr Phe Gln Met Ser Glu Lys Val Phe Lys
145 150 155 160
Tyr Asn Val Ile Lys Asp Glu Pro Ala Ala Lys Ile Thr Ala Leu Thr
165 170 175
Val Gln Pro Asn Val Leu Asn Ile Thr Phe Arg Thr Phe Val Glu Ile
180 185 190
Ile Phe Glu Asn His Glu Lys Thr Met Gln Ser Phe His Leu Asp Gly
195 200 205
Tyr Ser Phe Phe Ala Val Ala Ser Glu Pro Gly Arg Trp Thr Pro Glu
210 215 220
Lys Arg Glu Asn Tyr Asn Leu Leu Asp Ala Val Ser Arg His Thr Val
225 230 235 240
Gln Val Tyr Pro Lys Ser Trp Ser Ala Ile Leu Leu Thr Phe Asp Asn
245 250 255
Ala Gly Met Trp Asn Ile Arg Ser Glu Asn Leu Glu Arg Lys Tyr Leu
260 265 270
Gly Glu Gln Leu Tyr Val Ser Val Leu Ser Pro Glu Lys Ser Leu Arg
275 280 285
Asp Glu Tyr Asn Ile Pro Leu Asn Thr Asn Leu Cys Gly Ile Val Lys
290 295 300
Gly Leu Pro Leu Pro Ala His Tyr Ser
305 310

(2) INFORMATION FOR SEQ ID NO:535:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 308 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..308

(D) OTHER INFORMATION: / Ceres Seq. ID 1498602

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:

Met Glu Gly Ser His Val Ile Gln Asn Asp Tyr Asp Ser Leu Asp Val
1 5 10 15
His Val Gly Gln Cys Phe Ser Val Leu Val Thr Ala Asn Gln Ala Ala

20										25										30													
Lys	Asp	Tyr	Tyr	Met	Val	Ala	Ser	Thr	Arg	Phe	Leu	Lys	Lys	Glu	Leu	Lys	Asn	Val	Gln	Ala	Ser	Lys	Asn	Val	Gln	Ala	Ser	Lys	Asn	Val	Gln	Ala	Ser
35										40										45													
Ser	Thr	Val	Gly	Val	Ile	Arg	Tyr	Glu	Gly	Ser	Asn	Val	Gln	Ala	Ser	Ser	Thr	Val	Gly	Val	Ile	Arg	Tyr	Glu	Gly	Ser	Asn	Val	Gln	Ala	Ser		
50										55										60													
Thr	Glu	Leu	Pro	Lys	Ala	Pro	Val	Gly	Trp	Ala	Trp	Ser	Leu	Asn	Gln	Thr	Glu	Leu	Pro	Lys	Ala	Pro	Val	Gly	Trp	Ala	Trp	Ser	Leu	Asn	Gln		
65										70										75													
Phe	Arg	Ser	Phe	Arg	Trp	Asn	Leu	Thr	Ser	Asn	Ala	Ala	Arg	Pro	Asn	Phe	Arg	Ser	Phe	Arg	Trp	Asn	Leu	Thr	Ser	Asn	Ala	Ala	Arg	Pro	Asn		
85										90										95													
Pro	Gln	Gly	Ser	Tyr	His	Tyr	Gly	Lys	Ile	Asn	Ile	Thr	Arg	Ser	Ile	Pro	Gln	Gly	Ser	Tyr	His	Tyr	Gly	Lys	Ile	Asn	Ile	Thr	Arg	Ser	Ile		
100										105										110													
Lys	Leu	Val	Asn	Ser	Lys	Ser	Val	Val	Asp	Gly	Lys	Val	Arg	Phe	Gly	Lys	Leu	Val	Asn	Ser	Lys	Ser	Val	Val	Asp	Gly	Lys	Val	Arg	Phe	Gly		
115										120										125													
Phe	Asn	Gly	Val	Ser	His	Val	Asp	Thr	Glu	Thr	Pro	Leu	Lys	Leu	Ala	Phe	Asn	Gly	Val	Ser	His	Val	Asp	Thr	Glu	Thr	Pro	Leu	Lys	Leu	Ala		
130										135										140													
Glu	Tyr	Phe	Gln	Met	Ser	Glu	Lys	Val	Phe	Lys	Tyr	Asn	Val	Ile	Lys	Glu	Tyr	Phe	Gln	Met	Ser	Glu	Lys	Val	Phe	Lys	Tyr	Asn	Val	Ile	Lys		
145										150										155													
Asp	Glu	Pro	Ala	Ala	Lys	Ile	Thr	Ala	Leu	Thr	Val	Gln	Pro	Asn	Val	Asp	Glu	Pro	Ala	Ala	Lys	Ile	Thr	Ala	Leu	Thr	Val	Gln	Pro	Asn	Val		
165										170										175													
Leu	Asn	Ile	Thr	Phe	Arg	Thr	Phe	Val	Glu	Ile	Ile	Phe	Glu	Asn	His	Leu	Asn	Ile	Thr	Phe	Arg	Thr	Phe	Val	Glu	Ile	Ile	Phe	Glu	Asn	His		
180										185										190													
Glu	Lys	Thr	Met	Gln	Ser	Phe	His	Leu	Asp	Gly	Tyr	Ser	Phe	Phe	Ala	Glu	Lys	Thr	Met	Gln	Ser	Phe	His	Leu	Asp	Gly	Tyr	Ser	Phe	Phe	Ala		
195										200										205													
Val	Ala	Ser	Glu	Pro	Gly	Arg	Trp	Thr	Pro	Glu	Lys	Arg	Glu	Asn	Tyr	Val	Ala	Ser	Glu	Pro	Gly	Arg	Trp	Thr	Pro	Glu	Lys	Arg	Glu	Asn	Tyr		
210										215										220													
Asn	Leu	Leu	Asp	Ala	Val	Ser	Arg	His	Thr	Val	Gln	Val	Tyr	Pro	Lys	Asn	Leu	Leu	Asp	Ala	Val	Ser	Arg	His	Thr	Val	Gln	Val	Tyr	Pro	Lys		
225										230										235													
Ser	Trp	Ser	Ala	Ile	Leu	Leu	Thr	Phe	Asp	Asn	Ala	Gly	Met	Trp	Asn	Ser	Trp	Ser	Ala	Ile	Leu	Leu	Thr	Phe	Asp	Asn	Ala	Gly	Met	Trp	Asn		
245										250										255													
Ile	Arg	Ser	Glu	Asn	Leu	Glu	Arg	Lys	Tyr	Leu	Gly	Glu	Gln	Leu	Tyr	Ile	Arg	Ser	Glu	Asn	Leu	Glu	Arg	Lys	Tyr	Leu	Gly	Glu	Gln	Leu	Tyr		
260										265										270													
Val	Ser	Val	Leu	Ser	Pro	Glu	Lys	Ser	Leu	Arg	Asp	Glu	Tyr	Asn	Ile	Val	Ser	Val	Leu	Ser	Pro	Glu	Lys	Ser	Leu	Arg	Asp	Glu	Tyr	Asn	Ile		
275										280										285													
Pro	Leu	Asn	Thr	Asn	Leu	Cys	Gly	Ile	Val	Lys	Gly	Leu	Pro	Leu	Pro	Pro	Leu	Asn	Thr	Asn	Leu	Cys	Gly	Ile	Val	Lys	Gly	Leu	Pro	Leu	Pro		
290										295										300													
Ala	His	Tyr	Ser													Ala	His	Tyr	Ser														

(2) INFORMATION FOR SEQ ID NO:536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1444
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:

aaaatatcaa	aacacgagac	agatttgatt	ccatttttat	tactgttact	atcatccaaa	60
acottgggat	ttgtagccat	gagctctgtt	tcagatctca	tcaaccttaa	ccctctagac	120
tcactgaca	aaatcattgc	tgaatacata	tgggttggtg	gttctggaat	ggacatgaga	180
agcaaaacca	ggactctacc	tggaccagtg	actgacctt	cgcagctacc	aaagtggaa	240
tatgatgggt	caagcacagg	acaagctcct	ggtgaagaca	gtgaagtcat	cttatagtta	300
ataaattctt	tttcttgatc	tttaataaag	tttcttctca	ttgtgttttt	tttcgattct	360
tgtttactaa	tccttttgtg	gtttgtatat	ctttgtttag	ccctcaagcc	atattcaaa	420
ctctcttccg	tagaggaaac	aacattcttg	tcattgtcga	tgcgtacact	ccgcgsggtg	480
aaaccaatcc	gactaacaaa	agacacgctg	cggctaaggt	cttttagcaac	cctgatgttg	540
cagctgaagt	gccatgggat	ggtattgagc	aagaatacac	tttactccag	aaagatgtga	600
ggtggcctgt	tggttggcct	attggcggtt	atcccgcccc	tcaggggacc	tactattgag	660
gtattgggag	agacaaatct	tttggcagag	atgttgttga	ttctcactac	aaggcctggt	720

tatacgtctgg	aatcaacatt	agtggcatca	atggagaagt	catgccgggt	cagtgggagt	780
tcacaggtcgg	tcacagctggt	ggtatctcgg	ctgctgatga	aatgttgggtc	gctcgtttaca	840
tttttgagag	gatcacagag	attgctggtg	tagtggatc	ttttgaccog	aaaccgattc	900
ccgggtgactg	gaacggtgct	ggtgctcact	gcaactacag	taccaagtca	atgaggggaag	960
aaggcgggtta	cgagatcatc	aagaaagcaa	tcgataaatt	gggactgaga	cacaaagarc	1020
rcattgctgc	ttacsgtgaa	ggcaatgagc	gtcgtctcac	aggacaccac	gagactgctg	1080
acatacaacac	tttctcttgg	ggtgttgaga	accgtggagc	atcgatccga	gtaggactgt	1140
atacgggagaa	agaaggga	ggatactttg	aggacaggag	gccagctctg	atacgtggatc	1200
cttacattgt	tacttccatg	attgcagaga	ccaccatcct	ctggaatcct	tgatgatcat	1260
cgatgaaga	aaaaatcttg	aatgtcactc	aaatttgggt	ttcttgcaag	attcaaaagt	1320
tgtgttctct	atcaagcaat	gtcttaggat	aagtcaaaga	tttgcctgc	ttattctgct	1380
ttttatttac	ttcacatcct	attgaaaaca	tttctgtgta	ttatttatga	ataaacatta	1440
tctt						

(2) INFORMATION FOR SEQ ID NO:537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..266
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498611

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:

```

Met Cys Asp Ala Tyr Thr Pro Ala Gly Glu Pro Ile Pro Thr Asn Lys
1           5           10           15
Arg His Ala Ala Ala Lys Val Phe Ser Asn Pro Asp Val Ala Ala Glu
20           25           30           35
Val Pro Trp Tyr Tyr Gly Ile Glu Gln Glu Tyr Thr Leu Leu Gln Lys Asp
35           40           45           50
Val Arg Trp Pro Val Gly Trp Pro Ile Gly Gly Tyr Pro Gly Pro Gln
50           55           60           65
Gly Pro Tyr Tyr Cys Gly Ile Gly Ala Asp Lys Ser Phe Gly Arg Asp
65           70           75           80
Val Val Asp Ser His Tyr Lys Ala Cys Leu Tyr Ala Gly Ile Asn Ile
85           90           95           100
Ser Gly Ile Asn Gly Glu Val Met Pro Gly Gln Trp Glu Phe Gln Val
100          105          110          115
Gly Pro Ala Val Gly Ile Ser Ala Ala Asp Glu Ile Trp Val Ala Arg
115          120          125          130
Tyr Ile Leu Glu Arg Ile Thr Glu Ile Ala Gly Val Val Val Ser Phe
130          135          140          145
Asp Pro Lys Pro Ile Pro Gly Asp Trp Asn Gly Ala Gly Ala His Cys
145          150          155          160
Asn Tyr Ser Thr Lys Ser Met Arg Glu Glu Gly Gly Tyr Glu Ile Ile
165          170          175          180
Lys Lys Ala Ile Asp Lys Leu Gly Leu Arg His Lys Xaa Xaa Ile Ala
180          185          190          195
Ala Tyr Xaa Glu Gly Asn Glu Arg Arg Leu Thr Gly His His Glu Thr
195          200          205          210
Ala Asp Ile Asn Thr Phe Leu Trp Gly Val Ala Asn Arg Gly Ala Ser
210          215          220          225
Ile Arg Val Gly Arg Asp Thr Glu Lys Glu Gly Lys Gly Tyr Phe Glu
225          230          235          240
Asp Arg Arg Pro Ala Ser Asn Met Asp Pro Tyr Ile Val Thr Ser Met
245          250          255          260
Ile Ala Glu Thr Thr Ile Leu Trp Asn Pro
260          265

```

(2) INFORMATION FOR SEQ ID NO:538:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..163
(D) OTHER INFORMATION: / Ceres Seq. ID 1498612
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:
Met Pro Gly Gln Trp Glu Phe Gln Val Gly Pro Ala Val Gly Ile Ser
1 5 10 15
Ala Ala Asp Glu Ile Trp Val Ala Arg Tyr Ile Leu Glu Arg Ile Thr
20 25 30
Glu Ile Ala Gly Val Val Val Ser Phe Asp Pro Lys Pro Ile Pro Gly
35 40 45
Asp Trp Asn Gly Ala Gly Ala His Cys Asn Tyr Ser Thr Lys Ser Met
50 55 60
Arg Glu Glu Gly Gly Tyr Glu Ile Ile Lys Lys Ala Ile Asp Lys Leu
65 70 75 80
Gly Leu Arg His Lys Xaa Xaa Ile Ala Ala Tyr Xaa Glu Gly Asn Glu
85 90 95
Arg Arg Leu Thr Gly His His Glu Thr Ala Asp Ile Asn Thr Phe Leu
100 105 110
Trp Gly Val Ala Asn Arg Gly Ala Ser Ile Arg Val Gly Arg Asp Thr
115 120 125
Glu Lys Glu Gly Lys Gly Tyr Phe Glu Asp Arg Arg Pro Ala Ser Asn
130 135 140
Met Asp Pro Tyr Ile Val Thr Ser Met Ile Ala Glu Thr Thr Ile Leu
145 150 155 160
Trp Asn Pro

(2) INFORMATION FOR SEQ ID NO:539:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1772 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..1772

(D) OTHER INFORMATION: / Ceres Seq. ID 1498616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

agcacatgac	cgagtcgcgc	tcagaaaaag	gggccaaactg	ctccgtagcc	gccaaagaatc	60
tcgcagatcc	cgattcctct	tgatcatcgt	cttcttctac	caaaaattgtt	gcgcgacaaat	120
ggagaaatcc	aacagtttat	cagatatttt	caaggaggttc	tacatcccta	cgtaactcct	180
ctcgccgaaa	acagaaagag	aggaggagga	ggagagtcgt	cctacacctg	cgagccccgt	240
ccctgtcttc	atcaactcca	aaagcgggtg	tcagttgggt	ggcgaaactca	ttctcaccta	300
ccgatctctt	ctcaatcaca	atcaggtctt	tgatctcgac	caggagactc	cagataaaagt	360
gctccgcaga	atctatctta	acctggagag	gctcaaaagt	gatgatccg	ctcgatcagat	420
tggggagaaa	ttaaaaatca	ttgttgacag	aggtgatggc	actgctgggt	ggctccttgg	480
agttgtatgt	gaccttaaat	tgctacatcc	tcctccaatt	gccactgtac	ctttgggtac	540
aggaaacaac	cttccctttg	cttttggatg	gggaaagaag	aatccagga	cagataggac	600
tgcatgtgag	tcgttttttg	aacaagtgtt	gaaggcaaaa	gtgatgaaga	ttgacaattg	660
gctcatactt	atgaggatga	aaactcccaa	agaaggtggt	tcttgtgatc	ctgtgtcttc	720
ctttgagtta	ccacattctc	tacatgcatt	tcacccgtgt	tctccaactg	atgaactaaa	780
caaggaaagg	tgccacactt	ttcgaggagg	gttctggaat	tactttagcc	tcggaatgga	840
tgctcagatt	tccttatcgt	tcattcttga	gaggaaagctt	caccctgaaa	agtttaagaa	900
tcagctggtt	aatcagagta	cgtatgtaaa	gcttgggttc	acgcaaggat	ggttttgtgc	960
ctctcttttc	cacctgcctt	cacggaatat	agctcagctt	gccaaagtta	agattgcaac	1020

tagaataatggc	cagtggtcagg	acctccacat	accacatagc	atcagggtcca	ttgtatgtct	1080
gaatctgccc	agcttttcgg	gaggattaaa	tccttggggc	acaccaaatac	ccaggaaaaca	1140
acgtgataga	ggcttgactc	caccatttgt	agatgatggc	ctcattgagg	ttgttgggtt	1200
tagaataatgt	tggcatggtc	ttgtttctgt	cgctcccaat	ggacatggga	cacgacttgc	1260
ccaggcaaat	cgtatttcgt	tcgaatttca	caaagggtgca	accgaccata	cattcatgag	1320
gatggatggg	gagccctgga	aacagccaat	gccactggat	gatgaaactg	tgatggtaga	1380
gatttcacac	cttggtccaa	tgaacatgt	tgcaactcat	gactgcccgt	ccagaagtgt	1440
gtttgacctt	tcaacacccc	gccatcagga	tggtgcagaa	gattatgatg	ataatgaaga	1500
cgactcaantg	gctgaaggcg	aagaatttag	aaagtgttgg	gctgcggata	ccttcaagat	1560
tcctgatgag	gttgatatatt	ctcaacttag	ttagacaatt	aaccattttc	attgttgatt	1620
ctatgcattc	ttcctccgga	ctccaatttt	tttattcact	ctttcataaa	ggagacaacta	1680
gcagcaactg	gttttagattg	gtaaccatct	tttttctttg	cttttgtttg	gttggttcacg	1740
tttaatggcc	gagataatgt	atctggattt	at			

(2) INFORMATION FOR SEQ ID NO:540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 530 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..530
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498617

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

Ala	His	Asp	Arg	Val	Arg	Val	Arg	Lys	Arg	Gly	Gln	Leu	Leu	Arg	Ser
1				5					10					15	
Arg	Gln	Glu	Ser	Arg	Arg	Ser	Arg	Phe	Leu	Leu	Ile	Ile	Val	Phe	Phe
			20					25					30		
Tyr	Gln	Asn	Cys	Cys	Ala	Thr	Met	Glu	Lys	Tyr	Asn	Ser	Leu	Ser	Asp
		35					40				45				
Phe	Leu	Lys	Glu	Phe	Tyr	Ile	Pro	Thr	Tyr	Val	Leu	Ser	Ala	Glu	Thr
		50				55				60					
Glu	Glu	Glu	Glu	Glu	Glu	Ser	Arg	Pro	Thr	Pro	Ala	Ser	Pro	Val	
					70					75				80	
Leu	Val	Phe	Ile	Asn	Ser	Lys	Ser	Gly	Gly	Gln	Leu	Gly	Gly	Glu	Leu
				85				90						95	
Ile	Leu	Thr	Tyr	Arg	Ser	Leu	Leu	Asn	His	Asn	Gln	Val	Phe	Asp	Leu
				100				105					110		
Asp	Gln	Glu	Thr	Pro	Asp	Lys	Val	Leu	Arg	Arg	Ile	Tyr	Leu	Asn	Leu
				115			120					125			
Glu	Arg	Leu	Lys	Asp	Asp	Asp	Ser	Ala	Arg	Gln	Ile	Gly	Glu	Lys	Leu
				130			135					140			
Lys	Ile	Ile	Val	Ala	Gly	Gly	Asp	Gly	Thr	Ala	Gly	Trp	Leu	Leu	Gly
				145			150			155					160
Val	Val	Cys	Asp	Leu	Lys	Leu	Ser	His	Pro	Pro	Pro	Ile	Ala	Thr	Val
				165					170					175	
Pro	Leu	Gly	Thr	Gly	Asn	Asn	Leu	Pro	Phe	Ala	Phe	Gly	Trp	Gly	Lys
				180				185					190		
Lys	Asn	Pro	Gly	Thr	Asp	Arg	Thr	Ala	Val	Glu	Ser	Phe	Leu	Glu	Gln
				195			200					205			
Val	Leu	Lys	Ala	Lys	Val	Met	Lys	Ile	Asp	Asn	Trp	His	Ile	Leu	Met
				210			215				220				
Arg	Met	Lys	Thr	Pro	Lys	Glu	Gly	Gly	Ser	Cys	Asp	Pro	Val	Ala	Pro
				225			230			235				240	
Leu	Glu	Leu	Pro	His	Ser	Leu	His	Ala	Phe	His	Arg	Val	Ser	Pro	Thr
				245				250					255		
Asp	Glu	Leu	Asn	Lys	Glu	Gly	Cys	His	Thr	Phe	Arg	Gly	Gly	Phe	Trp
				260			265						270		
Asn	Tyr	Phe	Ser	Leu	Gly	Met	Asp	Ala	Gln	Ile	Ser	Tyr	Ala	Phe	His
				275			280					285			

Ser Glu Arg Lys Leu His Pro Glu Lys Phe Lys Asn Gln Leu Val Asn
290 295 300
Gln Ser Thr Tyr Val Lys Leu Gly Cys Thr Gln Gly Trp Phe Cys Ala
305 310 315 320
Ser Leu Phe His Pro Ala Ser Arg Asn Ile Ala Gln Leu Ala Lys Val
325 330 335
Lys Ile Ala Thr Arg Asn Gly Gln Trp Gln Asp Leu His Ile Pro His
340 345 350
Ser Ile Arg Ser Ile Val Cys Leu Asn Leu Pro Ser Phe Ser Gly Gly
355 360 365
Leu Asn Pro Trp Gly Thr Pro Asn Pro Arg Lys Gln Arg Asp Arg Gly
370 375 380
Leu Thr Pro Pro Phe Val Asp Asp Gly Leu Ile Glu Val Val Gly Phe
385 390 395 400
Arg Asn Ala Trp His Gly Leu Val Leu Leu Ala Pro Asn Gly His Gly
405 410 415
Thr Arg Leu Ala Gln Ala Asn Arg Ile Arg Phe Glu Phe His Lys Gly
420 425 430
Ala Thr Asp His Thr Phe Met Arg Met Asp Gly Glu Pro Trp Lys Gln
435 440 445
Pro Leu Pro Leu Asp Asp Glu Thr Val Met Val Glu Ile Ser His Leu
450 455 460
Gly Gln Val Asn Met Leu Ala Thr His Asp Cys Arg Ser Arg Ser Val
465 470 475 480
Phe Asp Pro Ser Thr Pro Arg His Gln Asp Gly Ala Glu Asp Tyr Asp
485 490 495
Asp Asn Glu Asp Asp Ser Xaa Ala Glu Gly Glu Glu Phe Arg Lys Phe
500 505 510
Gly Ala Ala Asp Thr Phe Lys Ile Pro Asp Glu Val Asp Ile Ser Gln
515 520 525
Leu Ser
530

(2) INFORMATION FOR SEQ ID NO:541:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 491 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..491

(D) OTHER INFORMATION: / Ceres Seq. ID 1498618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:

Met Glu Lys Tyr Asn Ser Leu Ser Asp Phe Leu Lys Glu Phe Tyr Ile
1 5 10 15
Pro Thr Tyr Val Leu Ser Ala Glu Thr Glu Glu Glu Glu Glu Glu
20 25 30
Ser Arg Pro Thr Pro Ala Ser Pro Val Leu Val Phe Ile Asn Ser Lys
35 40 45
Ser Gly Gly Gln Leu Gly Gly Glu Leu Ile Leu Thr Tyr Arg Ser Leu
50 55 60
Leu Asn His Asn Gln Val Phe Asp Leu Asp Gln Glu Thr Pro Asp Lys
65 70 75 80
Val Leu Arg Arg Ile Tyr Leu Asn Leu Glu Arg Leu Lys Asp Asp Asp
85 90 95
Ser Ala Arg Gln Ile Gly Glu Lys Leu Lys Ile Ile Val Ala Gly Gly
100 105 110
Asp Gly Thr Ala Gly Trp Leu Leu Gly Val Val Cys Asp Leu Lys Leu
115 120 125
Ser His Pro Pro Pro Ile Ala Thr Val Pro Leu Gly Thr Gly Asn Asn

130	135	140
Leu Pro Phe Ala Phe Gly Trp Gly Lys Lys Asn Pro Gly Thr Asp Arg		
145	150	155
Thr Ala Val Glu Ser Phe Leu Glu Gln Val Leu Lys Ala Lys Val Met		160
	165	170
Lys Ile Asp Asn Trp His Ile Leu Met Arg Met Lys Thr Pro Lys Glu		175
	180	185
Gly Gly Ser Cys Asp Pro Val Ala Pro Leu Glu Leu Pro His Ser Leu		190
	195	200
His Ala Phe His Arg Val Ser Pro Thr Asp Glu Leu Asn Lys Glu Gly		205
	210	215
Cys His Thr Phe Arg Gly Gly Phe Trp Asn Tyr Phe Ser Leu Gly Met		220
	225	230
Asp Ala Gln Ile Ser Tyr Ala Phe His Ser Glu Arg Lys Leu His Pro		235
	245	250
Glu Lys Phe Lys Asn Gln Leu Val Asn Gln Ser Thr Tyr Val Lys Leu		255
	260	265
Gly Cys Thr Gln Gly Trp Phe Cys Ala Ser Leu Phe His Pro Ala Ser		270
	275	280
Arg Asn Ile Ala Gln Leu Ala Lys Val Lys Ile Ala Thr Arg Asn Gly		285
	290	295
Gln Trp Gln Asp Leu His Ile Pro His Ser Ile Arg Ser Ile Val Cys		300
	305	310
Leu Asn Leu Pro Ser Phe Ser Gly Gly Leu Asn Pro Trp Gly Thr Pro		315
	325	330
Asn Pro Arg Lys Gln Arg Asp Arg Gly Leu Thr Pro Pro Phe Val Asp		335
	340	345
Asp Gly Leu Ile Glu Val Val Gly Phe Arg Asn Ala Trp His Gly Leu		350
	355	360
Val Leu Leu Ala Pro Asn Gly His Gly Thr Arg Leu Ala Gln Ala Asn		365
	370	375
Arg Ile Arg Phe Glu Phe His Lys Gly Ala Thr Asp His Thr Phe Met		380
	385	390
Arg Met Asp Gly Glu Pro Trp Lys Gln Pro Leu Pro Leu Asp Asp Glu		395
	405	410
Thr Val Met Val Glu Ile Ser His Leu Gly Gln Val Asn Met Leu Ala		415
	420	425
Thr His Asp Cys Arg Ser Arg Ser Val Phe Asp Pro Ser Thr Pro Arg		430
	435	440
His Gln Asp Gly Ala Glu Asp Tyr Asp Asp Asn Glu Asp Asp Ser Xaa		445
	450	455
Ala Glu Gly Glu Glu Phe Arg Lys Phe Gly Ala Ala Asp Thr Phe Lys		460
	465	470
Ile Pro Asp Glu Val Asp Ile Ser Gln Leu Ser		475
	485	490

(2) INFORMATION FOR SEQ ID NO:542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..316

(D) OTHER INFORMATION: / Ceres Seq. ID 1498619

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:

Met Lys Ile Asp Asn Trp His Ile Leu Met Arg Met Lys Thr Pro Lys		
1	5	10
Glu Gly Gly Ser Cys Asp Pro Val Ala Pro Leu Glu Leu Pro His Ser		15
	20	25
		30

Leu His Ala Phe His Arg Val Ser Pro Thr Asp Glu Leu Asn Lys Glu
35 40 45
Gly Cys His Thr Phe Arg Gly Gly Phe Trp Asn Tyr Phe Ser Leu Gly
50 55 60
Met Asp Ala Gln Ile Ser Tyr Ala Phe His Ser Glu Arg Lys Leu His
65 70 75 80
Pro Glu Lys Phe Lys Asn Gln Leu Val Asn Gln Ser Thr Tyr Val Lys
85 90 95
Leu Gly Cys Thr Gln Gly Trp Phe Cys Ala Ser Leu Phe His Pro Ala
100 105 110
Ser Arg Asn Ile Ala Gln Leu Ala Lys Val Lys Ile Ala Thr Arg Asn
115 120 125
Gly Gln Trp Gln Asp Leu His Ile Pro His Ser Ile Arg Ser Ile Val
130 135 140
Cys Leu Asn Leu Pro Ser Phe Ser Gly Gly Leu Asn Pro Trp Gly Thr
145 150 155 160
Pro Asn Pro Arg Lys Gln Arg Asp Arg Gly Leu Thr Pro Pro Phe Val
165 170 175
Asp Asp Gly Leu Ile Glu Val Val Gly Phe Arg Asn Ala Trp His Gly
180 185 190
Leu Val Leu Leu Ala Pro Asn Gly His Gly Thr Arg Leu Ala Gln Ala
195 200 205
Asn Arg Ile Arg Phe Glu Phe His Lys Gly Ala Thr Asp His Thr Phe
210 215 220
Met Arg Met Asp Gly Glu Pro Trp Lys Gln Pro Leu Pro Leu Asp Asp
225 230 235 240
Glu Thr Val Met Val Glu Ile Ser His Leu Gly Gln Val Asn Met Leu
245 250 255
Ala Thr His Asp Cys Arg Ser Arg Ser Val Phe Asp Pro Ser Thr Pro
260 265 270
Arg His Gln Asp Gly Ala Glu Asp Tyr Asp Asp Asn Glu Asp Asp Ser
275 280 285
Xaa Ala Glu Gly Glu Glu Phe Arg Lys Phe Gly Ala Ala Asp Thr Phe
290 295 300
Lys Ile Pro Asp Glu Val Asp Ile Ser Gln Leu Ser
305 310 315

(2) INFORMATION FOR SEQ ID NO:543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 855 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..855
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498628

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:

aaacaaaac	agagcaaaagt	ttttcaaaaa	aaaaaaaaac	agagccacga	agaaattttac	60
agaaaaattca	aaaccatcga	taaagatggg	agatgtgatt	ttgttcattg	atgatacagaa	120
atcgaaagtgt	agaatcacgc	gttgccagaat	ttgccatgaa	gaagaagaag	aaagtgttctt	180
cgaagtccca	tgtgcttgtt	caggcacgcgt	taagttcgca	cacagaaaact	gcatacaacg	240
ttggtgtaat	gaaaaaggaa	acacaaacttg	tgaaatctgt	cttcagggtgt	ataaagatgg	300
atatacagca	gtttcaaaac	aatcgaaatt	gattgaacaa	gaagtcacaa	tcagagtaaa	360
tgagcagaaga	agaagaagaa	gtagaagatt	agtgctctata	gctgaatccg	atattttctca	420
gtgtaattct	gttgcgtgata	gaggagcttc	gtttgcaga	tcattaactt	ttactctttc	480
agtatttttg	ctgatgaaac	atatactcga	tgtgatttac	ggaaccogaag	aataatccatt	540
ctctgtattt	acggtactaa	cattaaaggc	cattgggata	ctattgcccac	tgtccattat	600
aattcgaaaca	atctcaacta	ttcagaaaac	tcttcgtcgt	cgctaatcaat	atcctgaatc	660
tgaagaagaa	gataggttga	gctctgacga	cgacgatgac	ttggaagatg	aagatgaaga	720
gcaacaacaa	catttggctt	aaactctcca	attaacgaac	ttaacgaaat	ttttttcttc	780

ttcttttcta attcttttctt ttttaaaacg aaaagcatct atttgatgct catggtcatt 840
tttactcgca aagtc

(2) INFORMATION FOR SEQ ID NO:544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..246
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498629

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:

Asn	Lys	Asn	Arg	Ala	Lys	Phe	Phe	Lys	Lys	Lys	Lys	Asn	Arg	Ala	Thr
1				5					10					15	
Lys	Lys	Phe	Thr	Glu	Asn	Ser	Lys	Pro	Ser	Ile	Lys	Met	Gly	Asp	Val
			20					25					30		
Ile	Leu	Phe	Ile	Asp	Asp	Thr	Lys	Ser	Lys	Val	Arg	Ile	Thr	Arg	Cys
		35				40					45				
Arg	Ile	Cys	His	Glu	Glu	Glu	Glu	Ser	Phe	Phe	Glu	Val	Pro	Cys	
		50				55				60					
Ala	Cys	Ser	Gly	Thr	Val	Lys	Phe	Ala	His	Arg	Asn	Cys	Ile	Gln	Arg
65					70					75				80	
Trp	Cys	Asn	Glu	Lys	Gly	Asn	Thr	Thr	Cys	Glu	Ile	Cys	Leu	Gln	Val
					85				90					95	
Tyr	Lys	Asp	Gly	Tyr	Thr	Ala	Val	Ser	Lys	Gln	Ser	Lys	Leu	Ile	Glu
			100					105					110		
Gln	Glu	Val	Thr	Ile	Arg	Val	Asn	Gly	Arg	Arg	Arg	Arg	Ser	Arg	
			115				120					125			
Arg	Leu	Val	Ser	Ile	Ala	Glu	Ser	Asp	Ile	Ser	Gln	Cys	Asn	Ser	Val
			130				135					140			
Ala	Asp	Arg	Gly	Ala	Ser	Phe	Cys	Arg	Ser	Leu	Thr	Phe	Thr	Leu	Ser
145					150					155				160	
Val	Phe	Leu	Leu	Met	Lys	His	Thr	Phe	Asp	Val	Ile	Tyr	Gly	Thr	Glu
				165					170					175	
Glu	Tyr	Pro	Phe	Ser	Val	Phe	Thr	Val	Leu	Thr	Leu	Lys	Ala	Ile	Gly
				180				185					190		
Ile	Leu	Leu	Pro	Met	Ser	Ile	Ile	Arg	Thr	Ile	Ser	Thr	Ile	Gln	
				195				200				205			
Lys	Thr	Leu	Arg	Arg	Arg	His	Gln	Tyr	Pro	Glu	Ser	Glu	Glu	Alu	Asp
						215					220				
Arg	Leu	Ser	Ser	Asp	Asp	Asp	Asp	Asp	Leu	Glu	Asp	Glu	Asp	Glu	Glu
225					230					235				240	
Gln	Gln	Gln	His	Leu	Ala										
				245											

(2) INFORMATION FOR SEQ ID NO:545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..218
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:

Met	Gly	Asp	Val	Ile	Leu	Phe	Ile	Asp	Asp	Thr	Lys	Ser	Lys	Val	Arg
1				5						10				15	
Ile	Thr	Arg	Cys	Arg	Ile	Cys	His	Glu	Glu	Glu	Glu	Ser	Phe	Phe	

(2) INFORMATION FOR SEQ ID NO:546:

(A) LENGTH: 1589 base pairs

(B) TYPE: nucleic acid

```
(C) STRANDEDNESS: single
```

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (g

(A) NAME/KEY: -

(B) LOCATION: 1..1589

(D) OTHER INFORMATION: / Ceres Seq. ID 1498631

attgaagdt	aacagtgaat	atcgcttttgc	tgtcgttttgc	gtttctctacc	aacctctcc	60
atggctgtgt	cgctccaatt	cagcggtata	tgcgtctcag	cggataactt	cgtgcggag	120
atgctatctc	ctggatccgg	atctctccgc	cgccggaaag	ctttatcatt	ccggtctcgt	180
tttcggcgat	agAACGctcc	ttgcgcattc	gttgtagtgg	actccgagt	cgagcccca	240
gtgttcqcta	agaaacttgac	gagaaacgat	aattacaact	ctaaaggggt	cgtctataag	300
gaggagacac	tcaagctcat	gaatccagag	taccacagt	atatattga	gacactgaa	360
acaatatggt	atgcttattc	ttggggagat	tattctgtga	aactcgttaa	agcatatggt	420
ttttctgtgg	gtgttgagac	tgctgttcag	atgtcatatg	aagcagctaa	cgaggtttca	480
gaggagagag	tttggtattc	taacgaacct	attcataacc	acacggctaa	taagagttgt	540
gaagatagat	atgttataat	tattccgggt	gaggattaca	agaaacagt	tgatgtagta	600
gaaagaaagt	atgtggttat	ctctctcgtg	tttgtagctg	gtgttgacga	gtgtgatgt	660
cttaactgata	aaagaggtgca	aattgtgtgc	acgacttgtc	ttcgtgtgac	aaaggtgtgtg	720
acaacagttg	agaaagcacaa	gaagggggaa	tacacatcag	taactcgatg	taataataat	780
catgagagga	cgaattgcaac	tgcgtctttt	cgaggaaagt	aatcatatgt	aaagaacatc	840
aaagaggcaa	attacgtttg	tgattctatt	ctcgtgtggc	ataacgatgt	atctagcttc	900
acaaaagagg	agttctagg	gaattctaaa	taCGcaatt	cgaaaggtt	cgatcccgac	960
aatgaccttc	tcaaaagttg	tattgcaaac	caaacaca	tgctaaaggg	agaaacagag	1020
gagatagaaa	gattactgca	gacacaaact	atgcgcaagt	atgagatgga	aaatgtaagc	1080
ggacattttca	tcaagcttaa	cacaaatcga	gacgctaact	aagacgcaga	agacgcaact	1140
tatgagctat	tggaaagaaa	gattgatctc	atgtcatgtg	tttgcggatg	gaattcagtc	1200
acaacacctc	accttcagga	aatctcaag	cgacggggaa	tccatcatac	cttgatcgat	1260
agtgaagaac	ggtatgagac	ttggaaatac	atagctcata	tgctccacta	tggaaagact	1320
ctgcagagAAC	gaaaactttc	tcccaaaagg	accaataaca	atcgggttga	catcaggtgc	1380
atcagccccg	gataaqqctc	tgcaagatgc	tttgttgaag	gtgttcgaca	ttaaacgtga	1440

agagtatttg cagctggcgtt gattcgccat tgtgatcgta ttcaaaatact atttgtcatg 1500
tcaagagtgt actaaatat atgtagttgt atgatttgct tttataactt ttgtaagagg 1560
ttttgtaatt caaagtaaac atctcgtt

(2) INFORMATION FOR SEQ ID NO:547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..444

- (D) OTHER INFORMATION: / Ceres Seq. ID 1498632

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:

Met	Ala	Val	Ala	Leu	Gln	Phe	Ser	Arg	Leu	Cys	Val	Arg	Pro	Asp	Thr	
1			5					10					15			
Phe	Val	Arg	Glu	Asn	His	Leu	Ser	Gly	Ser	Gly	Ser	Leu	Arg	Arg	Arg	
			20				25					30				
Lys	Ala	Leu	Ser	Val	Arg	Cys	Ser	Ser	Gly	Asp	Glu	Asn	Ala	Pro	Ser	
		35				40					45					
Pro	Ser	Val	Val	Met	Asp	Ser	Asp	Phe	Asp	Ala	Lys	Val	Phe	Arg	Lys	
		50				55				60						
Asn	Leu	Thr	Arg	Ser	Asp	Asn	Tyr	Asn	Arg	Lys	Gly	Phe	Gly	His	Lys	
		65				70				75				80		
Glu	Glu	Thr	Leu	Lys	Leu	Met	Asn	Arg	Glu	Tyr	Thr	Ser	Asp	Ile	Leu	
			85						90					95		
Glu	Thr	Leu	Lys	Thr	Asn	Gly	Tyr	Thr	Ser	Trp	Gly	Asp	Val	Thr		
		100						105					110			
Val	Lys	Leu	Ala	Lys	Ala	Tyr	Gly	Phe	Cys	Trp	Gly	Val	Glu	Arg	Ala	
		115					120				125					
Val	Gln	Ile	Ala	Tyr	Glu	Ala	Arg	Lys	Gln	Phe	Pro	Glu	Glu	Arg	Leu	
		130				135					140					
Trp	Ile	Thr	Asn	Glu	Ile	Ile	His	Asn	Pro	Thr	Val	Asn	Lys	Arg	Leu	
		145				150				155				160		
Glu	Asp	Met	Asp	Val	Lys	Ile	Ile	Pro	Val	Glu	Asp	Ser	Lys	Lys	Gln	
			165					170					175			
Phe	Asp	Val	Val	Glu	Lys	Asp	Asp	Val	Val	Ile	Leu	Pro	Ala	Phe	Gly	
		180						185					190			
Ala	Gly	Val	Asp	Glu	Met	Tyr	Val	Leu	Asn	Asp	Lys	Lys	Val	Gln	Ile	
		195					200					205				
Val	Asp	Thr	Thr	Cys	Pro	Trp	Val	Thr	Lys	Val	Trp	Asn	Thr	Val	Glu	
		210				215					220					
Lys	His	Lys	Lys	Gly	Glu	Tyr	Thr	Ser	Val	Ile	His	Gly	Lys	Tyr	Asn	
		225				230				235				240		
His	Glu	Glu	Thr	Ile	Ala	Thr	Ala	Ser	Phe	Ala	Gly	Lys	Tyr	Ile	Ile	
			245						250					255		
Val	Lys	Asn	Met	Lys	Glu	Ala	Asn	Tyr	Val	Cys	Asp	Tyr	Ile	Leu	Gly	
		260						265					270			
Gly	Gln	Tyr	Asp	Gly	Ser	Ser	Ser	Thr	Lys	Glu	Glu	Phe	Met	Glu	Lys	
		275					280					285				
Phe	Lys	Tyr	Ala	Ile	Ser	Lys	Gly	Phe	Asp	Pro	Asp	Asn	Asp	Leu	Val	
		290				295				300						
Lys	Val	Gly	Ile	Ala	Asn	Gln	Thr	Thr	Met	Leu	Lys	Gly	Glu	Thr	Glu	
		305				310				315				320		
Glu	Ile	Gly	Arg	Leu	Glu	Thr	Thr	Met	Met	Arg	Lys	Tyr	Gly	Val		
			325					330					335			
Glu	Asn	Val	Ser	Gly	His	Phe	Ile	Ser	Phe	Asn	Thr	Ile	Cys	Asp	Ala	
		340						345					350			
Thr	Gln	Glu	Arg	Gln	Asp	Ala	Ile	Tyr	Glu	Leu	Val	Glu	Glu	Lys	Ile	
		355				360						365				

Asp Leu Met Leu Val Val Gly Gly Trp Asn Ser Ser Asn Thr Ser His
370 375 380
Leu Gln Glu Ile Ser Glu Ala Arg Gly Ile Pro Ser Tyr Trp Ile Asp
385 390 395 400
Ser Glu Lys Arg Ile Gly Pro Gly Asn Lys Ile Ala Tyr Lys Leu His
405 410 415
Tyr Gly Glu Leu Val Glu Xaa Gly Lys Leu Ser Pro Lys Gly Thr Asn
420 425 430
Asn Asn Arg Cys Asp Ile Arg Cys Ile Asn Pro Gly
435 440

(2) INFORMATION FOR SEQ ID NO:548:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 392 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..392

(D) OTHER INFORMATION: / Ceres Seq. ID 1498633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:

Met Asp Ser Asp Phe Asp Ala Lys Val Phe Arg Lys Asn Leu Thr Arg
1 5 10 15
Ser Asp Asn Tyr Asn Arg Lys Gly Phe Gly His Lys Glu Thr Leu
20 25 30
Lys Leu Met Asn Arg Glu Tyr Thr Ser Asp Ile Leu Glu Thr Leu Lys
35 40 45
Thr Asn Gly Tyr Thr Tyr Ser Trp Gly Asp Val Thr Val Lys Leu Ala
50 55 60
Lys Ala Tyr Gly Phe Cys Trp Gly Val Glu Arg Ala Val Gln Ile Ala
65 70 75 80
Tyr Glu Ala Arg Lys Gln Phe Pro Glu Glu Arg Leu Trp Ile Thr Asn
85 90 95
Glu Ile Ile His Asn Pro Thr Val Asn Lys Arg Leu Glu Asp Met Asp
100 105 110
Val Lys Ile Ile Pro Val Glu Asp Ser Lys Lys Gln Phe Asp Val Val
115 120 125
Glu Lys Asp Asp Val Val Ile Leu Pro Ala Phe Gly Ala Gly Val Asp
130 135 140
Glu Met Tyr Val Leu Asn Asp Lys Lys Val Gln Ile Val Asp Thr Thr
145 150 155 160
Cys Pro Trp Val Thr Lys Val Trp Asn Thr Val Glu Lys His Lys Lys
165 170 175
Gly Glu Tyr Thr Ser Val Ile His Gly Lys Tyr Asn His Glu Glu Thr
180 185 190
Ile Ala Thr Ala Ser Phe Ala Gly Lys Tyr Ile Ile Val Lys Asn Met
195 200 205
Lys Glu Ala Asn Tyr Val Cys Asp Tyr Ile Leu Gly Gly Gln Tyr Asp
210 215 220
Gly Ser Ser Ser Thr Lys Glu Glu Phe Met Glu Lys Phe Lys Tyr Ala
225 230 235 240
Ile Ser Lys Gly Phe Asp Pro Asp Asn Asp Leu Val Lys Val Gly Ile
245 250 255
Ala Asn Gln Thr Thr Met Leu Lys Gly Glu Thr Glu Glu Ile Gly Arg
260 265 270
Leu Leu Glu Thr Thr Met Met Arg Lys Tyr Gly Val Glu Asn Val Ser
275 280 285
Gly His Phe Ile Ser Phe Asn Thr Ile Cys Asp Ala Thr Gln Glu Arg
290 295 300
Gln Asp Ala Ile Tyr Glu Leu Val Glu Glu Lys Ile Asp Leu Met Leu

(2) INFORMATION FOR SEQ ID NO:549:

(A) LENGTH: 358 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(1X) FEATURE.

(A) NAME/KEY: peptide
(B) LOCATION: 1 358

(B) LOCATION: 1..35

(D) OTHER INFORMATION: / Ceres Seq. ID 1498634
SEQUENCE DESCRIPTION: SEQ ID NO: 540:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:
 Ser Ser Gly Thr Thr Ser Asp Ile Leu Gly T

1	Met	Asn	Arg	Glu	Tyr	Trp	Ser	Asp	Ile	Leu	Glu	Trp	Leu	Lys	Trp	Asn
Gly	Tyr	Thr	Thr	5	Ser	Trp	Gly	Asp	Val	Thr	Val	Lys	Leu	Ala	Lys	Ala
				20					25					30		
Tyr	Gly	Phe	Cys	Trp	Gly	Val	Glu	Arg	Ala	Val	Gln	Ile	Ala	Tyr	Glu	
				35				40				45				
Ala	Arg	Lys	Gln	Phe	Pro	Glu	Glu	Arg	Leu	Trp	Ile	Thr	Asn	Glu	Ile	
				50				55				60				
Ile	His	Asn	Pro	Thr	Val	Asn	Lys	Arg	Leu	Glu	Asp	Met	Asp	Val	Lys	
					70						75				80	
Ile	Ile	Pro	Val	Glu	Asp	Ser	Lys	Lys	Gln	Phe	Asp	Val	Val	Glu	Lys	
					85				90					95		
Asp	Asp	Val	Val	Ile	Leu	Pro	Ala	Phe	Gly	Ala	Gly	Val	Asp	Glu	Met	
				100				105					110			
Tyr	Val	Leu	Asn	Asp	Lys	Lys	Val	Gln	Ile	Val	Asp	Thr	Thr	Cys	Pro	
				115				120				125				
Trp	Val	Thr	Lys	Val	Trp	Asn	Thr	Val	Glu	Lys	His	Lys	Lys	Gly	Glu	
						135					140					
Tyr	Thr	Ser	Val	Ile	His	Gly	Lys	Tyr	Asn	His	Glu	Glu	Thr	Ile	Ala	
					150					155					160	
Thr	Ala	Ser	Phe	Ala	Gly	Lys	Tyr	Ile	Ile	Val	Lys	Asn	Met	Lys	Glu	
				165					170					175		
Ala	Asn	Tyr	Val	Cys	Asp	Tyr	Ile	Leu	Gly	Gly	Gln	Tyr	Asp	Gly	Ser	
				180				185					190			
Ser	Ser	Thr	Lys	Glu	Glu	Phe	Met	Glu	Lys	Phe	Lys	Tyr	Ala	Ile	Ser	
				195				200				205				
Lys	Gly	Phe	Asp	Pro	Asp	Asn	Asp	Leu	Val	Lys	Val	Gly	Ile	Ala	Asn	
				210			215				220					
Gln	Thr	Thr	Met	Leu	Lys	Gly	Glu	Thr	Glu	Glu	Ile	Gly	Arg	Glu	Leu	
					230					235					240	
Glu	Thr	Thr	Met	Met	Arg	Lys	Tyr	Gly	Val	Glu	Asn	Val	Ser	Gly	His	
				245					250					255		
Phe	Ile	Ser	Phe	Asn	Thr	Ile	Cys	Asp	Ala	Thr	Gln	Glu	Arg	Gln	Asp	
			260					265					270			
Ala	Ile	Tyr	Glu	Leu	Val	Glu	Glu	Lys	Ile	Asp	Leu	Met	Leu	Val	Val	
				275				280				285				
Gly	Gly	Trp	Asn	Ser	Ser	Asn	Thr	Ser	His	Leu	Gln	Glu	Ile	Ser	Glu	
						295					300					

Ala Arg Gly Ile Pro Ser Tyr Trp Ile Asp Ser Glu Lys Arg Ile Gly
305 310 315 320
Pro Gly Asn Lys Ile Ala Tyr Lys Leu His Tyr Gly Glu Leu Val Glu
325 330 335
Xaa Gly Lys Leu Ser Pro Lys Gly Thr Asn Asn Asn Arg Cys Asp Ile
340 345 350
Arg Cys Ile Asn Pro Gly
355

(2) INFORMATION FOR SEQ ID NO:550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1213

(D) OTHER INFORMATION: / Ceres Seq. ID 1498635

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:

acatcaaacg	aattacaaca	tacacaactt	gtaacttcaa	atagattact	ttcaaagaag	60
agagagagaa	agaaagatgg	agaagaacat	gaagtttcca	gtagtagact	tgccaagct	120
caatggggaa	gagagagacc	aaacccatggc	tctaatacaat	gaagcttggtg	agaattggggg	180
cttctttgag	atagtgaacc	atggattacc	acatgactta	atggacaaga	tcgagaagat	240
gacaaaaggac	cattacaaga	catgccaaaga	acaaaagtgc	aatgacatgc	tcaagtccaa	300
agggtttgat	aactttgaga	cagaagtgcga	agatgtcgat	tgggaaaagca	ctttctacgt	360
tcgtcacctc	cctcaatcca	atctcaatga	catttcagat	gtgtctgatg	aatacgacgg	420
ccatgaaaga	ctttggttaag	agactggaga	atcttctga	ggattgtttg	gtactactgt	480
gtgagaatct	aggggttagag	aaaggggtatt	tgaagaaagt	gtttcatgga	acaaaaggcc	540
caacctttgg	gacaaaaggtg	agcaattatc	caccatgtcc	taaacacagag	atgatcaaa	600
gtcttagagg	ccacactgtg	gcaggaggcca	tcactctgtt	gtttcaagac	gacaaagtca	660
gtggctccca	gcttcttaaa	gatggtgact	ggattgatgt	tcctcctctc	aacactcta	720
ttgtcatcaa	tcttgggtgac	caacttgagg	tgataaccac	cgaggagat	aagagtgtgc	780
tgccacgtgt	ggtgactcaa	caagaaggaa	acaggatgtc	gggtgcatcg	tttacaacc	840
cggggaagcg	tgccgagatc	tcaccagcta	cttcgcttgt	cgagaaagat	tcagagatcc	900
cgagtttctg	ctttgatgac	tacatgaagc	tttatgcagg	gggtcaagttt	cagcccaagg	960
agccacggtt	cgcagcaatg	aagaatgctt	ctgcagttac	agaactgaat	ctcacagcag	1020
ccgtagagac	tttctaaaaa	tggatttgag	attcaagtga	gcagagagaa	gaamsmtgag	1080
ttgtgttgtg	gtgttatggc	aataagttaa	aacctgtatt	agtggttgatt	aattgttggt	1140
caattgtgtg	gttttaaaagt	gtgggggtgt	tatgtttatg	gaagatgata	ataattataa	1200
aaatcctaat	tct					

(2) INFORMATION FOR SEQ ID NO:551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..251

(D) OTHER INFORMATION: / Ceres Seq. ID 1498636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:

Met	Thr	Cys	Ser	Ser	Pro	Lys	Val	Trp	Ile	Ile	Leu	Arg	Gln	Lys	Ser
1					5				10					15	
Lys	Met	Ser	Ile	Gly	Lys	Ala	Leu	Ser	Thr	Phe	Val	Thr	Ser	Leu	Asn
			20				25							30	
Pro	Ile	Ser	Met	Thr	Phe	Gln	Met	Cys	Leu	Met	Asn	Thr	Thr	Ala	Met
		35				40					45				
Lys	Asp	Phe	Gly	Lys	Arg	Leu	Glu	Asn	Leu	Ala	Glu	Asp	Leu	Leu	Asp
	50					55					60				

Leu Leu Cys Glu Asn Leu Gly Leu Glu Lys Gly Tyr Leu Lys Lys Val
65 70 75 80
Phe His Gly Thr Lys Gly Pro Thr Phe Gly Thr Lys Val Ser Asn Tyr
85 90 95
Pro Pro Cys Pro Lys Pro Glu Met Ile Lys Gly Leu Arg Ala His Thr
100 105 110
Asp Ala Gly Gly Ile Ile Leu Leu Phe Gln Asp Asp Lys Val Ser Gly
115 120 125
Leu Gln Leu Leu Lys Asp Gly Asp Trp Ile Asp Val Pro Pro Leu Asn
130 135 140
His Ser Ile Val Ile Asn Leu Gly Asp Gln Leu Glu Val Ile Thr Asn
145 150 155 160
Gly Lys Tyr Lys Ser Val Leu His Arg Val Val Thr Gln Gln Glu Gly
165 170 175
Asn Arg Met Ser Val Ala Ser Phe Tyr Asn Pro Gly Ser Asp Ala Glu
180 185 190
Ile Ser Pro Ala Thr Ser Leu Val Glu Lys Asp Ser Glu Tyr Pro Ser
195 200 205
Phe Val Phe Asp Asp Tyr Met Lys Leu Tyr Ala Gly Val Lys Phe Gln
210 215 220
Pro Lys Glu Pro Arg Phe Ala Ala Met Lys Asn Ala Ser Ala Val Thr
225 230 235 240
Glu Leu Asn Pro Thr Ala Ala Val Glu Thr Phe
245 250

(2) INFORMATION FOR SEQ ID NO:552:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..234

(D) OTHER INFORMATION: / Ceres Seq. ID 1498637

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:

Met Ser Ile Gly Lys Ala Leu Ser Thr Phe Val Thr Ser Leu Asn Pro
1 5 10 15
Ile Ser Met Thr Phe Gln Met Cys Leu Met Asn Thr Thr Ala Met Lys
20 25 30
Asp Phe Gly Lys Arg Leu Glu Asn Leu Ala Glu Asp Leu Leu Asp Leu
35 40 45
Leu Cys Glu Asn Leu Gly Leu Glu Lys Gly Tyr Leu Lys Lys Val Phe
50 55 60
His Gly Thr Lys Gly Pro Thr Phe Gly Thr Lys Val Ser Asn Tyr Pro
65 70 75 80
Pro Cys Pro Lys Pro Glu Met Ile Lys Gly Leu Arg Ala His Thr Asp
85 90 95
Ala Gly Gly Ile Ile Leu Leu Phe Gln Asp Asp Lys Val Ser Gly Leu
100 105 110
Gln Leu Leu Lys Asp Gly Asp Trp Ile Asp Val Pro Pro Leu Asn His
115 120 125
Ser Ile Val Ile Asn Leu Gly Asp Gln Leu Glu Val Ile Thr Asn Gly
130 135 140
Lys Tyr Lys Ser Val Leu His Arg Val Val Thr Gln Gln Glu Gly Asn
145 150 155 160
Arg Met Ser Val Ala Ser Phe Tyr Asn Pro Gly Ser Asp Ala Glu Ile
165 170 175
Ser Pro Ala Thr Ser Leu Val Glu Lys Asp Ser Glu Tyr Pro Ser Phe
180 185 190
Val Phe Asp Asp Tyr Met Lys Leu Tyr Ala Gly Val Lys Phe Gln Pro

195 200 205
Lys Glu Pro Arg Phe Ala Ala Met Lys Asn Ala Ser Ala Val Thr Glu
210 215 220
Leu Asn Pro Thr Ala Ala Val Glu Thr Phe
225 230

(2) INFORMATION FOR SEQ ID NO:553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..216
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498638

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:

Met	Thr	Phe	Gln	Met	Cys	Leu	Met	Asn	Thr	Thr	Ala	Met	Lys	Asp	Phe
1			5					10					15		
Gly	Lys	Arg	Leu	Glu	Asn	Leu	Ala	Glu	Asp	Leu	Leu	Asp	Leu	Leu	Cys
			20				25					30			
Glu	Asn	Leu	Gly	Leu	Glu	Lys	Gly	Tyr	Leu	Lys	Lys	Val	Phe	His	Gly
		35					40				45				
Thr	Lys	Gly	Pro	Thr	Phe	Gly	Thr	Lys	Val	Ser	Asn	Tyr	Pro	Pro	Cys
		50				55				60					
Pro	Lys	Pro	Glu	Met	Ile	Lys	Gly	Leu	Arg	Ala	His	Thr	Asp	Ala	Gly
		65			70				75				80		
Gly	Ile	Ile	Leu	Leu	Phe	Gln	Asp	Asp	Lys	Val	Ser	Gly	Leu	Gln	Leu
			85						90				95		
Leu	Lys	Asp	Gly	Asp	Trp	Ile	Asp	Val	Pro	Pro	Leu	Asn	His	Ser	Ile
			100				105					110			
Val	Ile	Asn	Leu	Gly	Asp	Gln	Leu	Glu	Val	Ile	Thr	Asn	Gly	Lys	Tyr
		115				120					125				
Lys	Ser	Val	Leu	His	Arg	Val	Val	Thr	Gln	Gln	Glu	Gly	Asn	Arg	Met
		130				135					140				
Ser	Val	Ala	Ser	Phe	Tyr	Asn	Pro	Gly	Ser	Asp	Ala	Glu	Ile	Ser	Pro
		145			150					155				160	
Ala	Thr	Ser	Leu	Val	Glu	Lys	Asp	Ser	Glu	Tyr	Pro	Ser	Phe	Val	Phe
			165						170				175		
Asp	Asp	Tyr	Met	Lys	Leu	Tyr	Ala	Gly	Val	Lys	Phe	Gln	Pro	Lys	Glu
		180					185						190		
Pro	Arg	Phe	Ala	Ala	Met	Lys	Asn	Ala	Ser	Ala	Val	Thr	Glu	Leu	Asn
		195				200					205				
Pro	Thr	Ala	Ala	Val	Glu	Thr	Phe								
		210				215									

(2) INFORMATION FOR SEQ ID NO:554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1065 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1065
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

acttaaccca	raagcaaaaa	gagaagaaga	agaaggaatc	gaaaaaatgaa	gactccgatac	60
cacgcgggtt	cgacatgggt	gaggaggcag	cctccaaagg	tgaaagcttt	ccttgccgctc	120
gtatctggca	tgcgggctct	tggtctctct	aaactcatcg	ttcacgatac	cgacaatctc	180
ttcgttgccg	ccgaagctgt	tcattctatt	ggaatctctg	ttcttatsta	taaactcatg	240

aaggagaaga	cttgtgctgg	attgtcattg	aaatctcagg	agcttacggc	gatatattcta	300
gctgtgaggc	tttattgcag	ttttgtaatg	gaatatgata	tacataccat	tctggacttg	360
gctactttgg	gaacaactct	ctgggttata	tatatgatcc	gttttaacct	caaagctact	420
tacatggagg	aaaaagacaa	cttcgcctct	tattatgtgc	tggcgccctg	tggtgtgcta	480
gctgtatgga	ttcatccatc	aacgtcacac	aatatattga	atagaatatt	ctggggattc	540
tggttttacc	tcgaagctgt	ttcagtagtg	ccacagttga	gagtgatgca	gaacacaaag	600
attgtcgaac	ccttcacggc	tcattatggt	tttgcaactg	gagtagcaag	atttttttagc	660
tggtgcacct	gggtttttaca	gatgatggac	acgcacggac	gactgcttgt	agtgctgggt	720
tatggactat	ggccatcgat	ggttataatc	tcagaaatag	tccaagcatt	catattggca	780
gatttctggt	actactacgt	taaaagtgtt	ttcgggtggc	agcttgttct	aaggtctcca	840
tctgggggtg	tgtaagttaa	aaaggaaaaa	agataagaca	cattatgacg	aaatttgtta	900
cacgaagata	gacttcagct	tggtgtaact	tgagtagcct	ctggttactc	tcaagttact	960
ccttcaggcc	aagtccta	tctattaact	gtgttgata	ttttgtgtg	ggcatcatc	1020
atagacagtc	ccttgatat	tattgacatg	atttttyca	ctgcc		

(2) INFORMATION FOR SEQ ID NO:555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..269
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498640

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:

Met	Lys	Thr	Pro	Ile	His	Ala	Val	Ser	Thr	Trp	Val	Arg	Arg	Gln	Pro
1			5					10						15	
Pro	Lys	Val	Lys	Ala	Phe	Leu	Ala	Val	Val	Ser	Gly	Met	Ala	Ala	Leu
			20					25					30		
Val	Leu	Leu	Lys	Leu	Ile	Val	His	Asp	His	Asp	Asn	Leu	Phe	Val	Ala
			35				40				45				
Ala	Glu	Ala	Val	His	Ser	Ile	Gly	Ile	Ser	Val	Leu	Xaa	Tyr	Lys	Leu
			50				55				60				
Met	Lys	Glu	Lys	Thr	Cys	Ala	Gly	Leu	Ser	Leu	Lys	Ser	Gln	Glu	Leu
65					70					75				80	
Thr	Ala	Ile	Phe	Leu	Ala	Val	Arg	Leu	Tyr	Cys	Ser	Phe	Val	Met	Glu
				85					90				95		
Tyr	Asp	Ile	His	Thr	Ile	Leu	Asp	Leu	Ala	Thr	Leu	Gly	Thr	Thr	Leu
				100				105					110		
Trp	Val	Ile	Tyr	Met	Ile	Arg	Phe	Asn	Leu	Lys	Ala	Thr	Tyr	Met	Glu
				115			120				125				
Glu	Lys	Asp	Asn	Phe	Ala	Leu	Tyr	Val	Leu	Ala	Pro	Cys	Val	Val	
						135				140					
Leu	Ala	Val	Trp	Ile	His	Pro	Ser	Thr	His	Asn	Ile	Leu	Asn	Arg	
145					150				155					160	
Ile	Ser	Trp	Gly	Phe	Cys	Val	Tyr	Leu	Glu	Ala	Val	Ser	Val	Leu	Pro
				165					170					175	
Gln	Leu	Arg	Val	Met	Gln	Asn	Thr	Lys	Ile	Val	Glu	Pro	Phe	Thr	Ala
				180				185					190		
His	Tyr	Val	Phe	Ala	Leu	Gly	Val	Ala	Arg	Phe	Phe	Ser	Cys	Ala	His
				195				200				205			
Trp	Val	Leu	Gln	Met	Met	Asp	Thr	His	Gly	Arg	Leu	Leu	Val	Val	Leu
				210			215				220				
Gly	Tyr	Gly	Leu	Trp	Pro	Ser	Met	Val	Ile	Ile	Ser	Glu	Ile	Val	Gln
225					230				235					240	
Ala	Phe	Ile	Leu	Ala	Asp	Phe	Cys	Tyr	Tyr	Tyr	Val	Lys	Ser	Val	Phe
				245					250					255	
Gly	Gly	Gln	Leu	Val	Leu	Arg	Leu	Pro	Ser	Gly	Val	Val			
				260				265							

(2) INFORMATION FOR SEQ ID NO:556:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 241 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..241
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498641
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:

Met	Ala	Ala	Leu	Val	Leu	Leu	Lys	Leu	Ile	Val	His	Asp	His	Asp	Asn	
1			5					10						15		
Leu	Phe	Val	Ala	Ala	Glu	Ala	Val	His	Ser	Ile	Gly	Ile	Ser	Val	Leu	
			20					25					30			
Xaa	Tyr	Lys	Leu	Met	Lys	Glu	Lys	Thr	Cys	Ala	Gly	Leu	Ser	Leu	Lys	
			35				40					45				
Ser	Gln	Glu	Leu	Thr	Ala	Ile	Phe	Leu	Ala	Val	Arg	Leu	Tyr	Cys	Ser	
			50				55				60					
Phe	Val	Met	Glu	Tyr	Asp	Ile	His	Thr	Ile	Leu	Asp	Leu	Ala	Thr	Leu	
65					70					75					80	
Gly	Thr	Thr	Leu	Trp	Val	Ile	Tyr	Met	Ile	Arg	Phe	Asn	Leu	Lys	Ala	
					85					90				95		
Thr	Tyr	Met	Glu	Glu	Lys	Asp	Asn	Phe	Ala	Leu	Tyr	Tyr	Val	Leu	Ala	
					100			105						110		
Pro	Cys	Val	Val	Leu	Ala	Val	Trp	Ile	His	Pro	Ser	Thr	Ser	His	Asn	
					115			120				125				
Ile	Leu	Asn	Arg	Ile	Ser	Trp	Gly	Phe	Cys	Val	Tyr	Leu	Glu	Ala	Val	
					130			135				140				
Ser	Val	Leu	Pro	Gln	Leu	Arg	Val	Met	Gln	Asn	Thr	Lys	Ile	Val	Glu	
145					150					155					160	
Pro	Phe	Thr	Ala	His	Tyr	Val	Phe	Ala	Leu	Gly	Val	Ala	Arg	Phe	Phe	
					165					170				175		
Ser	Cys	Ala	His	Trp	Val	Leu	Gln	Met	Asp	Thr	His	Gly	Arg	Leu		
					180			185				190				
Leu	Val	Val	Leu	Gly	Tyr	Gly	Leu	Trp	Pro	Ser	Met	Val	Ile	Ile	Ser	
					195			200				205				
Glu	Ile	Val	Gln	Ala	Phe	Ile	Leu	Ala	Asp	Phe	Cys	Tyr	Tyr	Tyr	Val	
					210			215				220				
Lys	Ser	Val	Phe	Gly	Gly	Gln	Leu	Val	Leu	Arg	Leu	Pro	Ser	Gly	Val	
225					230					235				240		
Val																

(2) INFORMATION FOR SEQ ID NO:557:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 205 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..205
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498642
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:

Met	Lys	Glu	Lys	Thr	Cys	Ala	Gly	Leu	Ser	Leu	Lys	Ser	Gln	Glu	Leu	
1			5					10					15			
Thr	Ala	Ile	Phe	Leu	Ala	Val	Arg	Leu	Tyr	Cys	Ser	Phe	Val	Met	Glu	
					20			25					30			
Tyr	Asp	Ile	His	Thr	Ile	Leu	Asp	Leu	Ala	Thr	Leu	Gly	Thr	Thr	Leu	
					35			40				45				

Trp Val Ile Tyr Met Ile Arg Phe Asn Leu Lys Ala Thr Tyr Met Glu
50 55 60
Glu Lys Asp Asn Phe Ala Leu Tyr Tyr Val Leu Ala Pro Cys Val Val
65 70 75 80
Leu Ala Val Trp Ile His Pro Ser Thr Ser His Asn Ile Leu Asn Arg
85 90 95
Ile Ser Trp Gly Phe Cys Val Tyr Leu Glu Ala Val Ser Val Leu Pro
100 105 110
Gln Leu Arg Val Met Gln Asn Thr Lys Ile Val Glu Pro Phe Thr Ala
115 120 125
His Tyr Val Phe Ala Leu Gly Val Ala Arg Phe Phe Ser Cys Ala His
130 135 140
Trp Val Leu Gln Met Met Asp Thr His Gly Arg Leu Leu Val Val Leu
145 150 155 160
Gly Tyr Gly Leu Trp Pro Ser Met Val Ile Ile Ser Glu Ile Val Gln
165 170 175
Ala Phe Ile Leu Ala Asp Phe Cys Tyr Tyr Tyr Val Lys Ser Val Phe
180 185 190
Gly Gly Gln Leu Val Leu Arg Leu Pro Ser Gly Val Val
195 200 205

(2) INFORMATION FOR SEQ ID NO:558:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 772 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..772
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498643

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:

agcgaaaatc ccaaacaaaa aaataaaaaga atggcgctctc tgtgcctttc tctccaccaa 60
accctaacta atccccctgtc ggctcccaga tgcagaccac tcagcctctc ctcccccgga 120
tctcaacact tctcgatccg cccctctagc agacgcgcga ccgccttgac gaccgcgcc 180
tcttacacc cgcgcgcggc gactgagcgc gtgatttcga tagcgctgta cgcgctgccc 240
ttcttcaatt ctctgcagta cgggcgggttc ctgttcgcgc agtacccaag gctgggattg 300
ctgttcgagc caatcttccc aatcctgaac ctgtacagat cggtgcccga cgcgagcttc 360
gtggcattct tcgggctgta cctgggagtg gtgaggaaca cgagtttcag taggtacgtg 420
aggttcaacg cgatgcaggc ggtgacgctg gatgtgtctc tggcggttcc ggtgctgctg 480
accgcaatc tgcgtccggg tcaaggaggg gggtttgaa tgaaggcgat gatgtggggg 540
cacacggggg ttttctgtt cagctttatg tgttttgtgt atggagtcgt cagctcctta 600
ctcggcaaaa ctccatacat tccattttgc gctgatgcgc cggtagaca actetaattc 660
cggccaatat ctacctcact cagtgttcgg gttttcgatt ctagaatcgg ttatttctgg 720
tttataagag agaccaaaac aatcagtggt gttaattaac cattaccggt tc

(2) INFORMATION FOR SEQ ID NO:559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..218
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498644

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:

Ser Glu Asn Pro Lys Gln Lys Asn Lys Arg Met Ala Ser Leu Cys Leu
1 5 10 15
Ser Leu His Gln Thr Leu Thr Asn Pro Leu Ser Ala Pro Arg Cys Arg
20 25 30

Pro Leu Ser Leu Ser Phe Pro Gly Ser Ser Thr Phe Ser Ile Arg Pro
35 40 45
Ser Ser Arg Arg Ala Thr Ala Leu Thr Thr Arg Ala Ser Tyr Thr Pro
50 55 60
Thr Pro Ala Thr Glu Arg Val Ile Ser Ile Ala Ser Tyr Ala Leu Pro
65 70 75 80
Phe Phe Asn Ser Leu Gln Tyr Gly Arg Phe Leu Phe Ala Gln Tyr Pro
85 90 95
Arg Leu Gly Leu Leu Phe Glu Pro Ile Phe Pro Ile Leu Asn Leu Tyr
100 105 110
Arg Ser Val Pro Tyr Ala Ser Phe Val Ala Phe Phe Gly Leu Tyr Leu
115 120 125
Gly Val Val Arg Asn Thr Ser Phe Ser Arg Tyr Val Arg Phe Asn Ala
130 135 140
Met Gln Ala Val Thr Leu Asp Val Leu Leu Ala Val Pro Val Leu Leu
145 150 155 160
Thr Arg Ile Leu Asp Pro Gly Gln Gly Gly Gly Phe Gly Met Lys Ala
165 170 175
Met Met Trp Gly His Thr Gly Val Phe Val Phe Ser Phe Met Cys Phe
180 185 190
Val Tyr Gly Val Val Ser Ser Leu Leu Gly Lys Thr Pro Tyr Ile Pro
195 200 205
Phe Val Ala Asp Ala Ala Gly Arg Gln Leu
210 215

(2) INFORMATION FOR SEQ ID NO:560:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..208

(D) OTHER INFORMATION: / Ceres Seq. ID 1498645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:

Met Ala Ser Leu Cys Leu Ser Leu His Gln Thr Leu Thr Asn Pro Leu
1 5 10 15
Ser Ala Pro Arg Cys Arg Pro Leu Ser Leu Ser Phe Pro Gly Ser Ser
20 25 30
Thr Phe Ser Ile Arg Pro Ser Ser Arg Arg Ala Thr Ala Leu Thr Thr
35 40 45
Arg Ala Ser Tyr Thr Pro Thr Pro Ala Thr Glu Arg Val Ile Ser Ile
50 55 60
Ala Ser Tyr Ala Leu Pro Phe Phe Asn Ser Leu Gln Tyr Gly Arg Phe
65 70 75 80
Leu Phe Ala Gln Tyr Pro Arg Leu Gly Leu Leu Phe Glu Pro Ile Phe
85 90 95
Pro Ile Leu Asn Leu Tyr Arg Ser Val Pro Tyr Ala Ser Phe Val Ala
100 105 110
Phe Phe Gly Leu Tyr Leu Gly Val Val Arg Asn Thr Ser Phe Ser Arg
115 120 125
Tyr Val Arg Phe Asn Ala Met Gln Ala Val Thr Leu Asp Val Leu Leu
130 135 140
Ala Val Pro Val Leu Leu Thr Arg Ile Leu Asp Pro Gly Gln Gly Gly
145 150 155 160
Gly Phe Gly Met Lys Ala Met Met Trp Gly His Thr Gly Val Phe Val
165 170 175
Phe Ser Phe Met Cys Phe Val Tyr Gly Val Val Ser Ser Leu Leu Gly
180 185 190
Lys Thr Pro Tyr Ile Pro Phe Val Ala Asp Ala Ala Gly Arg Gln Leu

195

200

205

(2) INFORMATION FOR SEQ ID NO:561:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1645 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1645

(D) OTHER INFORMATION: / Ceres Seq. ID 1498646

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:

```
amcaaaaaaa aaaaagaaaa aaggagataa taatcacaaa ctacaaaaagt agaagaaga      60
aaaaagaaca aagtatcagt tcttgaatat ttgcatcaat ggaggaaatcc aaacacacct      120
acgtgtcgat cataccaagt ccgggaatgg gtcatctcat accactcgtc gagtttgcta      180
aacgactcgt ccatcttcac ggccctaccg ttaccttcgt catcgccggc gaaggtccac      240
catcaaaagc tcagagaacc gtctctcgact ctctcccttc ttcattctcc tccgtctctc      300
tccctctcgt tgatctcacc gatctctctt cgtccactcg catcgaatct cggatctccc      360
tcacccgtgac tegtctaaac ccggagctcc ggaaagtctt cgaactgttc gtggaggagg      420
gtcgtttgcc aacggcgctc gtctctgata tcttcgggtac ggacgcttc gacgtggccc      480
tagaatttca cgtgccaccg tatattttct acccaacaac ggccaacgct ttgtcgtttt      540
ttctccattt gcttaacta kacgaaacgg tgtcgtgtga gttcagggaag ttaacggaaac      600
cgcttatcgt tcttgagatg tactccggtg ccgggaaaga ttcccttgac ccggcccaag      660
accggaaaag cgaatgcata aatggcgctc tcataaacac caagagggtac aaagaagccg      720
aaggtattct tgtgaatacc ttctttgagc tagagccaaa tgctataaag gccctgcaag      780
aaccgggtct tgataaacc cccggtttatc ccggttggaac gttgggttaac attggtgaac      840
aagaggctaa gcaaacggaa gactotgaat gtttaaaagt gttggataac cagccgctcg      900
gttcggtttt atatgtgtcc tttggtagtg ggggtaccct cacatgtgag cagctcaatg      960
agctgtctct tggctttgca gatagtgagc aacggtttct ttgggtcata cgaagtctta      1020
gtgggtagtc taatctgtcg tattttgatt cacatagcca aacagatcca ttgacatttt      1080
taccaccggg atttttagag cggactaaaa aaagagggtt tgtgatccct tttgggctc      1140
cacaagccca agtcttgagg catccatcca cgggaggatt tttaactcat tgggatgga      1200
attcgactct agagagtgtg gtaagcggtg ttccacttat agcatggcca ttatacgca      1260
aacagaagat gaatcggtt ttgttgagt aagatatctg tgcggcaact aggcccgctg      1320
ccggggacga tgggttagtt agaagagaag aggtggctag agtggtataaa ggatgatgg      1380
aaggtgaaga aggcaaaagg gtgaggaaca agatgaagga gttgaaggaa gcagcttga      1440
gggtgttgaa ggaatgatgg acttcgacaa aagcacttag tcttggtgcc ttaagatgga      1500
aagcccaaaa aaaaagagta gagcaaaatg gcaaccata aatatttgat tctctaata      1560
gatttgata atcaacggtg ggaattgtgc aaatgtggtt ctgtatgtat atgtatgttc      1620
tactttttt tgcctcgttt gtctc
```

(2) INFORMATION FOR SEQ ID NO:562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..480

(D) OTHER INFORMATION: / Ceres Seq. ID 1498647

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:

```
Met Glu Glu Ser Lys Thr Pro His Val Ala Ile Ile Pro Ser Pro Gly
1          5          10          15
Met Gly His Leu Ile Pro Leu Val Glu Phe Ala Lys Arg Leu Val His
20          25          30
Leu His Gly Leu Thr Val Thr Phe Val Ile Ala Gly Glu Gly Pro Pro
35          40          45
```


Ser Lys Ala Gln Arg Thr Val Leu Asp Ser Leu Pro Ser Ser Ile Ser
50 55 60
Ser Val Phe Leu Pro Pro Val Asp Leu Thr Asp Leu Ser Ser Ser Thr
65 70 75 80
Arg Ile Glu Ser Arg Ile Ser Leu Thr Val Thr Arg Ser Asn Pro Glu
85 90 95
Leu Arg Lys Val Phe Asp Ser Phe Val Glu Gly Gly Arg Leu Pro Thr
100 105 110
Ala Leu Val Val Asp Leu Phe Gly Thr Asp Ala Phe Asp Val Ala Val
115 120 125
Glu Phe His Val Pro Pro Tyr Ile Phe Tyr Pro Thr Thr Ala Asn Val
130 135 140
Leu Ser Phe Phe Leu His Leu Pro Lys Leu Xaa Glu Thr Val Ser Cys
145 150 155 160
Glu Phe Arg Glu Leu Thr Glu Pro Leu Met Leu Pro Gly Cys Val Pro
165 170 175
Val Ala Gly Lys Asp Phe Leu Asp Pro Ala Gln Asp Arg Lys Asp Asp
180 185 190
Ala Tyr Lys Trp Leu Leu His Asn Thr Lys Arg Tyr Lys Glu Ala Glu
195 200 205
Gly Ile Leu Val Asn Thr Phe Phe Glu Leu Glu Pro Asn Ala Ile Lys
210 215 220
Ala Leu Gln Glu Pro Gly Leu Asp Lys Pro Pro Val Tyr Pro Val Gly
225 230 235 240
Pro Leu Val Asn Ile Gly Lys Gln Glu Ala Lys Gln Thr Glu Glu Ser
245 250 255
Glu Cys Leu Lys Trp Leu Asp Asn Gln Pro Leu Gly Ser Val Leu Tyr
260 265 270
Val Ser Phe Gly Ser Gly Gly Thr Leu Thr Cys Glu Gln Leu Asn Glu
275 280 285
Leu Ala Leu Gly Leu Ala Asp Ser Glu Gln Arg Phe Leu Trp Val Ile
290 295 300
Arg Ser Pro Ser Gly Ile Ala Asn Ser Ser Tyr Phe Asp Ser His Ser
305 310 315 320
Gln Thr Asp Pro Leu Thr Phe Leu Pro Pro Gly Phe Leu Glu Arg Thr
325 330 335
Lys Lys Arg Gly Phe Val Ile Pro Phe Trp Ala Pro Gln Ala Gln Val
340 345 350
Leu Ala His Pro Ser Thr Gly Gly Phe Leu Thr His Cys Gly Trp Asn
355 360 365
Ser Thr Leu Glu Ser Val Val Ser Gly Ile Pro Leu Ile Ala Trp Pro
370 375 380
Leu Tyr Ala Glu Gln Lys Met Asn Ala Val Leu Leu Ser Glu Asp Ile
385 390 395 400
Arg Ala Ala Leu Arg Pro Arg Ala Gly Asp Asp Gly Leu Val Arg Arg
405 410 415
Glu Glu Val Ala Arg Val Val Lys Gly Leu Met Glu Gly Glu Glu Gly
420 425 430
Lys Gly Val Arg Asn Lys Met Lys Glu Leu Lys Glu Ala Ala Cys Arg
435 440 445
Val Leu Lys Asp Asp Gly Thr Ser Thr Lys Ala Leu Ser Leu Val Ala
450 455 460
Leu Lys Trp Lys Ala His Lys Lys Glu Leu Glu Gln Asn Gly Asn His
465 470 475 480

(2) INFORMATION FOR SEQ ID NO:563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..464

(D) OTHER INFORMATION: / Ceres Seq. ID 1498648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:

Met	Gly	His	Leu	Ile	Pro	Leu	Val	Glu	Phe	Ala	Lys	Arg	Leu	Val	His
1				5				10					15		
Leu	His	Gly	Leu	Thr	Val	Thr	Phe	Val	Ile	Ala	Gly	Glu	Gly	Pro	Pro
			20					25					30		
Ser	Lys	Ala	Gln	Arg	Thr	Val	Leu	Asp	Ser	Leu	Pro	Ser	Ser	Ile	Ser
		35					40					45			
Ser	Val	Phe	Leu	Pro	Pro	Val	Asp	Leu	Thr	Asp	Leu	Ser	Ser	Thr	
		50					55				60				
Arg	Ile	Glu	Ser	Arg	Ile	Ser	Leu	Thr	Val	Thr	Arg	Ser	Asn	Pro	Glu
65				70					75					80	
Leu	Arg	Lys	Val	Phe	Asp	Ser	Phe	Val	Glu	Gly	Gly	Arg	Leu	Pro	Thr
			85						90				95		
Ala	Leu	Val	Val	Asp	Leu	Phe	Gly	Thr	Asp	Ala	Phe	Asp	Val	Ala	Val
			100					105					110		
Glu	Phe	His	Val	Pro	Pro	Tyr	Ile	Phe	Tyr	Pro	Thr	Thr	Ala	Asn	Val
		115					120					125			
Leu	Ser	Phe	Phe	Leu	His	Leu	Pro	Lys	Leu	Xaa	Glu	Thr	Val	Ser	Cys
		130				135					140				
Glu	Phe	Arg	Glu	Leu	Thr	Glu	Pro	Leu	Met	Leu	Pro	Gly	Cys	Val	Pro
145				150						155				160	
Val	Ala	Gly	Lys	Asp	Phe	Leu	Asp	Pro	Ala	Gln	Asp	Arg	Lys	Asp	Asp
			165					170					175		
Ala	Tyr	Lys	Trp	Leu	Leu	His	Asn	Thr	Lys	Arg	Tyr	Lys	Glu	Ala	Glu
			180					185					190		
Gly	Ile	Leu	Val	Asn	Thr	Phe	Phe	Glu	Leu	Glu	Pro	Asn	Ala	Ile	Lys
		195					200					205			
Ala	Leu	Gln	Glu	Pro	Gly	Leu	Asp	Lys	Pro	Pro	Val	Tyr	Pro	Val	Gly
		210				215					220				
Pro	Leu	Val	Asn	Ile	Gly	Lys	Gln	Glu	Ala	Lys	Gln	Thr	Glu	Glu	Ser
225				230						235				240	
Glu	Cys	Leu	Lys	Trp	Leu	Asp	Asn	Gln	Pro	Leu	Gly	Ser	Val	Leu	Tyr
			245						250					255	
Val	Ser	Phe	Gly	Ser	Gly	Gly	Thr	Leu	Thr	Cys	Glu	Gln	Leu	Asn	Glu
			260				265						270		
Leu	Ala	Leu	Gly	Leu	Ala	Asp	Ser	Glu	Gln	Arg	Phe	Leu	Trp	Val	Ile
		275					280					285			
Arg	Ser	Pro	Ser	Gly	Ile	Ala	Asn	Ser	Ser	Tyr	Phe	Asp	Ser	His	Ser
		290				295					300				
Gln	Thr	Asp	Pro	Leu	Thr	Phe	Leu	Pro	Pro	Gly	Phe	Leu	Glu	Arg	Thr
				310						315				320	
Lys	Lys	Arg	Gly	Phe	Val	Ile	Pro	Phe	Trp	Ala	Pro	Gln	Ala	Gln	Val
				325					330					335	
Leu	Ala	His	Pro	Ser	Thr	Gly	Gly	Phe	Leu	Thr	His	Cys	Gly	Trp	Asn
			340					345					350		
Ser	Thr	Leu	Glu	Ser	Val	Val	Ser	Gly	Ile	Pro	Leu	Ile	Ala	Trp	Pro
		355					360					365			
Leu	Tyr	Ala	Glu	Gln	Lys	Met	Asn	Ala	Val	Leu	Leu	Ser	Glu	Asp	Ile
		370				375					380				
Arg	Ala	Ala	Leu	Arg	Pro	Arg	Ala	Gly	Asp	Asp	Gly	Leu	Val	Arg	Arg
385				390						395				400	
Glu	Glu	Val	Ala	Arg	Val	Val	Lys	Gly	Leu	Met	Glu	Gly	Glu	Gly	Gly
			405					410					415		
Lys	Gly	Val	Arg	Asn	Lys	Met	Lys	Glu	Leu	Lys	Glu	Ala	Ala	Cys	Arg
			420					425					430		

Val	Leu	Lys	Asp	Asp	Gly	Thr	Ser	Thr	Lys	Ala	Leu	Ser	Leu	Val	Ala
	435						440					445			
Leu	Lys	Trp	Lys	Ala	His	Lys	Lys	Glu	Leu	Glu	Gln	Asn	Gly	Asn	His
	450					455					460				

(2) INFORMATION FOR SEQ ID NO:564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..311
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:

Met	Leu	Pro	Gly	Cys	Val	Pro	Val	Ala	Gly	Lys	Asp	Phe	Leu	Asp	Pro
1				5					10					15	
Ala	Gln	Asp	Arg	Lys	Asp	Asp	Ala	Tyr	Lys	Trp	Leu	Leu	His	Asn	Thr
		20					25						30		
Lys	Arg	Tyr	Lys	Glu	Ala	Glu	Gly	Ile	Leu	Val	Asn	Thr	Phe	Phe	Glu
		35					40				45				
Leu	Glu	Pro	Asn	Ala	Ile	Lys	Ala	Leu	Gln	Glu	Pro	Gly	Leu	Asp	Lys
		50				55					60				
Pro	Pro	Val	Tyr	Pro	Val	Gly	Pro	Leu	Val	Asn	Ile	Gly	Lys	Gln	Glu
65				70					75					80	
Ala	Lys	Gln	Thr	Glu	Glu	Ser	Glu	Cys	Leu	Lys	Trp	Leu	Asp	Asn	Gln
			85						90				95		
Pro	Leu	Gly	Ser	Val	Leu	Tyr	Val	Ser	Phe	Gly	Ser	Gly	Gly	Thr	Leu
		100					105						110		
Thr	Cys	Glu	Gln	Leu	Asn	Glu	Leu	Ala	Leu	Gly	Leu	Ala	Asp	Ser	Glu
		115					120					125			
Gln	Arg	Phe	Leu	Trp	Val	Ile	Arg	Ser	Pro	Ser	Gly	Ile	Ala	Asn	Ser
		130				135					140				
Ser	Tyr	Phe	Asp	Ser	His	Ser	Gln	Thr	Asp	Pro	Leu	Thr	Phe	Leu	Pro
			150						155					160	
Pro	Gly	Phe	Leu	Glu	Arg	Thr	Lys	Lys	Arg	Gly	Phe	Val	Ile	Pro	Phe
			165						170				175		
Trp	Ala	Pro	Gln	Ala	Gln	Val	Leu	Ala	His	Pro	Ser	Thr	Gly	Gly	Phe
			180				185						190		
Leu	Thr	His	Cys	Gly	Trp	Asn	Ser	Thr	Leu	Glu	Ser	Val	Val	Ser	Gly
		195				200						205			
Ile	Pro	Leu	Ile	Ala	Trp	Pro	Leu	Tyr	Ala	Glu	Gln	Lys	Met	Asn	Ala
		210				215					220				
Val	Leu	Leu	Ser	Glu	Asp	Ile	Arg	Ala	Ala	Leu	Arg	Pro	Arg	Ala	Gly
225				230					235					240	
Asp	Asp	Gly	Leu	Val	Arg	Arg	Glu	Glu	Val	Ala	Arg	Val	Val	Lys	Gly
			245						250				255		
Leu	Met	Glu	Gly	Glu	Glu	Gly	Lys	Gly	Val	Arg	Asn	Lys	Met	Lys	Glu
		260				265						270			
Leu	Lys	Glu	Ala	Ala	Cys	Arg	Val	Leu	Lys	Asp	Asp	Gly	Thr	Ser	Thr
		275				280					285				
Lys	Ala	Leu	Ser	Leu	Val	Ala	Leu	Lys	Trp	Lys	Ala	His	Lys	Lys	Glu
		290				295					300				
Leu	Glu	Gln	Asn	Gly	Asn	His									
305						310									

(2) INFORMATION FOR SEQ ID NO:565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1499 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1499
(D) OTHER INFORMATION: / Ceres Seq. ID 1498650
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565:

atctcttgg	ctctccgcc	atctctgctc	tcttttattt	tcccagaaag	tttttttttt	60
tttcccgat	tcggttaatc	tcattgggg	ttccattgat	agcaatggcg	acggctttcg	120
ctcccacata	gctcaactgc	acggttccct	tgcatggatc	ccatgagaat	cgctcttcgc	180
ctccgatccg	attggtccct	ccttcttctt	tcctcggtac	cacccgttcc	ctctcccttc	240
gcagactcaa	tcactccaac	gccaccgcgc	gatctcccg	cgctctgtgc	caggaagtgt	300
tcaaggagaa	gcaatccaac	acaataacca	gcctgttgat	aaccaaagag	gaaggattgg	360
agttgtatga	agatatgata	ctaggtagat	ctttcgaaag	catgtgtgct	caaatgtatt	420
accgaggcaa	gatgtttgg	tttgttca	tgtacaatgg	ccaagaggct	gtttctactg	480
gctttatcaa	gctccttacc	aagtctgact	ctgtcgtag	tacctaccgt	gaacatgtcc	540
atgccctcag	caaaaggtgc	tctgctcg	ctgttatgag	cgagctcttc	ggcaagggtta	600
ctggatgctg	cagagggcaa	ggtggatcca	tgacatgtt	ctccaaagaa	cacaacatgc	660
ttggtggc	tgttttatt	ggtgaaggca	tctctgtcgc	cactggtgct	gcctttagct	720
ccaagtacag	gagggaaagt	tgaaacagg	attgtgatga	tgctactgtc	gccttttctg	780
gagatggaac	ttgtaacaac	ggacagttct	tcgagtgtct	caacatggct	gctctctata	840
aactgcctat	tatcttgg	gtcgagaata	actgtggg	cattgggatg	tctcacttga	900
gagcactct	tgaccccgag	atttggaa	aaggtcctgc	atttgggatg	ctcgtgttct	960
atgttgacgg	tatggatg	tgaaaggtca	gggaagtcgc	taaaagggtc	gtcactagag	1020
ctagaagagg	agaaggtcca	acctgtgtg	aatgtgagac	ttatagattt	agaggacact	1080
cttggctgga	tcctcgatgc	tcctgtgatg	ctgtcgagaa	agccaaatcac	ggcgctagag	1140
accacaatgc	agcattgaag	aagtatttga	tagagaacaa	gcttgcaaa	gaagcagagc	1200
taaaagtcaat	agagaaaaag	atagacgagt	tggtggagga	agcggttgag	tttgcagacg	1260
ctagtccaca	gcccggctgc	agtcagttgc	tagagaatgt	gtttgtgat	ccaaaaggat	1320
ttggaaattg	acctgatgga	cggtaacagat	gtgaggaccc	caagtttacc	gaaggcacag	1380
ctcaagtctg	agaagacaag	tttaaccata	agctgtctac	tgtctcttcg	atgtttctat	1440
atactcttatt	aagttaaatg	ctacagagaa	tcagtttgaa	tcatttgcac	tttttgctg	

(2) INFORMATION FOR SEQ ID NO:566:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 462 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..462
(D) OTHER INFORMATION: / Ceres Seq. ID 1498651
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:

Leu	Leu	Phe	Ser	Pro	Pro	Ile	Ser	Ala	Leu	Phe	Tyr	Phe	Pro	Arg	Lys
1				5					10					15	
Phe	Phe	Phe	Phe	Ser	Arg	Ile	Pro	Leu	Ile	Ser	Leu	Gly	Phe	Pro	Leu
				20				25					30		
Ile	Ala	Met	Ala	Thr	Ala	Phe	Ala	Pro	Thr	Lys	Leu	Thr	Ala	Thr	Val
		35				40						45			
Pro	Leu	His	Gly	Ser	His	Glu	Asn	Arg	Leu	Leu	Leu	Pro	Ile	Arg	Leu
	50					55				60					
Ala	Pro	Pro	Ser	Ser	Phe	Leu	Gly	Ser	Thr	Arg	Ser	Leu	Ser	Leu	Arg
65					70					75				80	
Arg	Leu	Asn	His	Ser	Asn	Ala	Thr	Arg	Arg	Ser	Pro	Val	Val	Ser	Val
				85						90				95	
Gln	Glu	Val	Val	Lys	Glu	Lys	Gln	Ser	Thr	Asn	Asn	Thr	Ser	Leu	Leu
				100				105					110		
Ile	Thr	Lys	Glu	Glu	Gly	Leu	Glu	Leu	Tyr	Glu	Asp	Met	Ile	Leu	Gly

Pro Ser Ser Phe Leu Gly Ser Thr Arg Ser Leu Ser Leu Arg Arg Leu

Asn His Ser Asn Ala Thr Arg Arg Ser Pro Val Val Ser Val Gln Gln
50 55 60
Val Val Lys Glu Lys Gln Ser Thr Asn Asn Thr Ser Leu Leu Ile Thr
65 70 75 80
Lys Glu Glu Gly Leu Glu Leu Tyr Glu Asp Met Ile Leu Gly Arg Ser
85 90 95
Phe Glu Asp Met Cys Ala Gln Met Tyr Arg Gly Lys Met Phe Gly
100 105 110
Phe Val His Leu Tyr Asn Gly Gln Glu Ala Val Ser Thr Gly Phe Ile
115 120 125
Lys Leu Leu Thr Lys Ser Asp Ser Val Val Ser Thr Tyr Arg Asp His
130 135 140
Val His Ala Leu Ser Lys Gly Val Ser Ala Arg Ala Val Met Ser Glu
145 150 155 160
Leu Phe Gly Lys Val Thr Gly Cys Cys Arg Gly Gln Gly Gly Ser Met
165 170 175
His Met Phe Ser Lys Glu His Asn Met Leu Gly Gly Phe Ala Phe Ile
180 185 190
Gly Glu Gly Ile Pro Val Ala Thr Gly Ala Ala Phe Ser Ser Lys Tyr
195 200 205
Arg Arg Glu Val Leu Lys Gln Asp Cys Asp Asp Val Thr Val Ala Phe
210 215 220
Phe Gly Asp Gly Thr Cys Asn Asn Gly Gln Phe Glu Cys Leu Asn
225 230 235 240
Met Ala Ala Leu Tyr Lys Leu Pro Ile Ile Phe Val Val Glu Asn Asn
245 250 255
Leu Trp Ala Ile Gly Met Ser His Leu Arg Ala Thr Ser Asp Pro Glu
260 265 270
Ile Trp Lys Lys Gly Pro Ala Phe Gly Met Pro Gly Val His Val Asp
275 280 285
Gly Met Asp Val Leu Lys Val Arg Glu Val Ala Lys Glu Ala Val Thr
290 295 300
Arg Ala Arg Arg Gly Glu Gly Pro Thr Leu Val Glu Cys Glu Thr Tyr
305 310 315 320
Arg Phe Arg Gly His Ser Leu Ala Asp Pro Asp Glu Leu Arg Asp Ala
325 330 335
Ala Glu Lys Ala Lys Tyr Ala Ala Arg Asp Pro Ile Ala Ala Leu Lys
340 345 350
Lys Tyr Leu Ile Glu Asn Lys Leu Ala Lys Glu Ala Glu Leu Lys Ser
355 360 365
Ile Glu Lys Lys Ile Asp Glu Leu Val Glu Glu Ala Val Glu Phe Ala
370 375 380
Asp Ala Ser Pro Gln Pro Gly Arg Ser Gln Leu Leu Glu Asn Val Phe
385 390 395 400
Ala Asp Pro Lys Gly Phe Gly Ile Gly Pro Asp Gly Arg Tyr Arg Cys
405 410 415
Glu Asp Pro Lys Phe Thr Glu Gly Thr Ala Gln Val
420 425

(2) INFORMATION FOR SEQ ID NO:568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..338
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498653

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:

Met Ile Leu Gly Arg Ser Phe Glu Asp Met Cys Ala Gln Met Tyr Tyr

```

1           5           10           15
Arg Gly Lys Met Phe Gly Phe Val His Leu Tyr Asn Gly Gln Glu Ala
20           25           30
Val Ser Thr Gly Phe Ile Lys Leu Leu Thr Lys Ser Asp Ser Val Val
35           40           45
Ser Thr Tyr Arg Asp His Val His Ala Leu Ser Lys Gly Val Ser Ala
50           55           60
Arg Ala Val Met Ser Glu Leu Phe Gly Lys Val Thr Gly Cys Cys Arg
65           70           75           80
Gly Gln Gly Gly Ser Met His Met Phe Ser Lys Glu His Asn Met Leu
85           90           95
Gly Gly Phe Ala Phe Ile Gly Glu Gly Ile Pro Val Ala Thr Gly Ala
100          105          110
Ala Phe Ser Ser Lys Tyr Arg Arg Glu Val Leu Lys Gln Asp Cys Asp
115          120          125
Asp Val Thr Val Ala Phe Phe Gly Asp Gly Thr Cys Asn Asn Gly Gln
130          135          140
Phe Phe Glu Cys Leu Asn Met Ala Ala Leu Tyr Lys Leu Pro Ile Ile
145          150          155          160
Phe Val Val Glu Asn Asn Leu Trp Ala Ile Gly Met Ser His Leu Arg
165          170          175
Ala Thr Ser Asp Pro Glu Ile Trp Lys Lys Gly Pro Ala Phe Gly Met
180          185          190
Pro Gly Val His Val Asp Gly Met Asp Val Leu Lys Val Arg Glu Val
195          200          205
Ala Lys Glu Ala Val Thr Arg Ala Arg Arg Gly Glu Gly Pro Thr Leu
210          215          220
Val Glu Cys Glu Thr Tyr Arg Phe Arg Gly His Ser Leu Ala Asp Pro
225          230          235          240
Asp Glu Leu Arg Asp Ala Ala Glu Lys Ala Lys Tyr Ala Ala Arg Asp
245          250          255
Pro Ile Ala Ala Leu Lys Lys Tyr Leu Ile Glu Asn Lys Leu Ala Lys
260          265          270
Glu Ala Glu Leu Lys Ser Ile Glu Lys Lys Ile Asp Glu Leu Val Glu
275          280          285
Glu Ala Val Glu Phe Ala Asp Ala Ser Pro Gln Pro Gly Arg Ser Gln
290          295          300
Leu Leu Glu Asn Val Phe Ala Asp Pro Lys Gly Phe Gly Ile Gly Pro
305          310          315          320
Asp Gly Arg Tyr Arg Cys Glu Asp Pro Lys Phe Thr Glu Gly Thr Ala
325          330          335
Gln Val

```

(2) INFORMATION FOR SEQ ID NO:569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1278

(D) OTHER INFORMATION: / Ceres Seq. ID 1498654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:

```

atccttcttc tctgtatctc tgtgtattct tctctcatgg agcctgctca tatcgattgg      60
aagagaatcg attctcgttt tgttgaagac gttttttacg aacacatcag agctcctaaa      120
tggttcgatt tcttggccccc taccattttt gactccattg acgacgatcg ttggtctcgc      180
aaacctgaat gtaatcatcc caagagacct gaggactttt tctcaacgcc gactctttcc      240
aagcatccaa gtctagggga tacgaatgag actctaacag agcagaatca gaggaggagg      300
ggatatgtct tctacacctt tactccaaac aaccaagaaa gtgaaaatca gaacccgaac      360

```

ttagccacac	ctccaagcta	ccaagcaaaa	tcattggagag	cagcaaat	atcaacttct	420
gtcaagaaga	tgaataaaga	agttccaaga	ctaaagagca	cacaatcagc	tagaatactg	480
ttttcaggga	gagacatat	tggtcatatc	tcagatttbt	gctatgaatt	gaagagatta	540
gccacaaggg	ttactgagag	agaagatact	gggaaatctg	aagtgaagga	gagtcataca	600
gtgggtggaa	tagtaaatca	gccttactct	gttcattgact	tggaattgaa	aaaggaataa	660
aagccactgc	ttgaagtaag	caaagataag	ctccctgagt	ccacggatgt	taaaggaagc	720
acatttaaag	agaaccgtag	aagaaagaaa	agagtggatg	atgcagagaa	cattctctgc	780
tcacttaatg	tgagactgt	aaaaaacaaa	ggagaggagg	gtagaagaaa	gaagagatta	840
gatgatcgag	agaacatccc	agttctctta	aaactggaga	ctataaagaa	caaaggacac	900
gaacgattcc	tgacagcaat	caggacaaac	ccaccatctc	ctcaatgctt	ctctgagaac	960
cggagacgcta	cattgaaacc	cttgaggacc	aaacctacgg	aagtgttgaa	gagaaaggaa	1020
gtggaagctg	aagaagaaaa	gaacagaaa	agtggagaaa	gcaaaagaa	aacaaggagg	1080
ttggagcttc	tctgtgttct	aaagccttgc	actttagcca	actagaaaac	cttcacaaaa	1140
ttctttctat	attgattcat	tcttttgtaa	atttcatttt	attcaactgt	aactaacgag	1200
atgattatct	tgctcagata	tataattctg	ggcaaatgtg	attcaatctc	ttacttttac	1260
acatacaacg	atttgttt					

(2) INFORMATION FOR SEQ ID NO:570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..374
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498655

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:

Ile	Leu	Ser	Leu	Cys	Ile	Ser	Val	Tyr	Ser	Ser	Leu	Met	Glu	Pro	Ala	
1			5					10			15					
His	Ile	Asp	Trp	Lys	Arg	Ile	Asp	Ser	Arg	Phe	Val	Glu	Asp	Val	Phe	
			20					25					30			
Tyr	Glu	His	Ile	Arg	Ala	Pro	Lys	Trp	Phe	Asp	Phe	Leu	Ala	Pro	Thr	
			35				40					45				
His	Phe	Asp	Ser	Ile	Asp	Asp	Asp	Ala	Trp	Phe	Cys	Lys	Pro	Glu	Cys	
			50			55					60					
Asn	His	Pro	Lys	Arg	Pro	Glu	Asp	Phe	Phe	Ser	Thr	Pro	Thr	Ser	Ser	
65					70					75					80	
Lys	His	Pro	Ser	Leu	Arg	Asp	Thr	Asn	Glu	Thr	Leu	Thr	Glu	Gln	Asn	
				85				90						95		
Gln	Arg	Arg	Arg	Gly	Tyr	Ala	Leu	Ser	Pro	Ser	Thr	Pro	Asn	Asn	Gln	
			100					105					110			
Glu	Ser	Glu	Asn	Gln	Asn	Pro	Asn	Leu	Ala	Thr	Pro	Pro	Ser	Tyr	Gln	
			115				120						125			
Ala	Lys	Ser	Trp	Arg	Ala	Ala	Ile	Lys	Ser	Thr	Ser	Val	Lys	Lys	Met	
			130			135						140				
Asn	Lys	Glu	Val	Pro	Arg	Leu	Lys	Ser	Thr	Gln	Ser	Ala	Arg	Asn	Leu	
145					150					155				160		
Phe	Ser	Gly	Arg	Asp	Ile	Phe	Gly	His	Ile	Ser	Asp	Xaa	Cys	Tyr	Glu	
				165				170						175		
Leu	Lys	Arg	Leu	Ala	Thr	Arg	Val	Thr	Glu	Arg	Glu	Asp	Thr	Gly	Lys	
			180					185					190			
Ser	Glu	Val	Lys	Glu	Ser	His	Gln	Val	Gly	Gly	Ile	Val	Asn	Gln	Pro	
			195				200					205				
Tyr	Ser	Val	His	Asp	Leu	Glu	Leu	Lys	Lys	Glu	Ile	Lys	Pro	Leu	Leu	
			210			215						220				
Glu	Val	Ser	Lys	Asp	Lys	Leu	Pro	Glu	Ser	Thr	Asp	Val	Lys	Gly	Ser	
225					230					235				240		
Thr	Phe	Lys	Glu	Asn	Arg	Arg	Arg	Lys	Lys	Arg	Val	Asp	Asp	Ala	Glu	
				245					250					255		
Asn	Ile	Pro	Val	Ser	Leu	Asn	Val	Glu	Thr	Val	Lys	Asn	Lys	Gly	Glu	

Met	Glu	Pro	Ala	His	Ile	Asp	Trp	Lys	Arg	Ile	Asp	Ser	Arg	Phe	Val
1				5					10					15	
Glu	Asp	Val	Phe	Tyr	Glu	His	Ile	Arg	Ala	Pro	Lys	Trp	Phe	Asp	Phe
		20						25					30		
Leu	Ala	Pro	Thr	His	Phe	Asp	Ser	Ile	Asp	Asp	Asp	Ala	Trp	Phe	Cys
		35					40					45			
Lys	Pro	Glu	Cys	Asn	His	Pro	Lys	Arg	Pro	Glu	Asp	Phe	Phe	Ser	Thr
	50					55					60				
Pro	Thr	Ser	Ser	Lys	His	Pro	Ser	Leu	Arg	Asp	Thr	Asn	Glu	Thr	Leu
65				70						75				80	
Thr	Glu	Gln	Asn	Gln	Arg	Arg	Arg	Gly	Tyr	Ala	Leu	Ser	Pro	Ser	Thr
			85					90						95	
Pro	Asn	Asn	Gln	Glu	Ser	Glu	Asn	Gln	Asn	Pro	Asn	Leu	Ala	Thr	Pro
			100					105					110		
Pro	Ser	Tyr	Gln	Ala	Lys	Ser	Trp	Arg	Ala	Ala	Ile	Lys	Ser	Thr	Ser
		115					120					125			
Val	Lys	Lys	Met	Asn	Lys	Glu	Val	Pro	Arg	Leu	Lys	Ser	Thr	Gln	Ser
130						135				140					
Ala	Arg	Asn	Leu	Phe	Ser	Gly	Arg	Asp	Ile	Phe	Gly	His	Ile	Ser	Asp
145				150						155				160	
Xaa	Cys	Tyr	Glu	Leu	Lys	Arg	Leu	Ala	Thr	Arg	Val	Thr	Glu	Arg	Glu
			165					170					175		
Asp	Thr	Gly	Lys	Ser	Glu	Val	Lys	Glu	Ser	His	Gln	Val	Gly	Gly	Ile
		180						185					190		
Val	Asn	Gln	Pro	Tyr	Ser	Val	His	Asp	Leu	Glu	Leu	Lys	Lys	Glu	Ile
		195				200						205			
Lys	Pro	Leu	Leu	Glu	Val	Ser	Lys	Asp	Lys	Leu	Pro	Glu	Ser	Thr	Asp
210						215					220				
Val	Lys	Gly	Ser	Thr	Phe	Lys	Glu	Asn	Arg	Arg	Arg	Lys	Lys	Arg	Val
225				230						235				240	
Asp	Asp	Ala	Glu	Asn	Ile	Pro	Val	Ser	Leu	Asn	Val	Glu	Thr	Val	Lys
			245						250					255	
Asn	Lys	Gly	Glu	Glu	Gly	Arg	Arg	Lys	Lys	Arg	Met	Asp	Asp	Ala	Glu
		260						265					270		

Asn Ile Pro Val Pro Leu Lys Leu Glu Thr Ile Lys Asn Lys Gly His
275 280 285
Glu Arg Phe Leu Gln Gln Ile Arg Thr Asn Pro Pro Ser Pro Gln Cys
290 295 300
Phe Ser Glu Asn Arg Thr Ala Thr Leu Lys Pro Leu Arg Thr Lys Pro
305 310 315 320
Thr Glu Val Leu Lys Arg Lys Glu Asp Glu Ala Glu Glu Glu Lys Asn
325 330 335
Arg Lys Ser Gly Glu Ser Lys Glu Ala Thr Arg Gly Leu Asp Val Leu
340 345 350
Trp Phe Leu Lys Pro Cys Thr Leu Ala Asn
355 360

(2) INFORMATION FOR SEQ ID NO:572:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..231

(D) OTHER INFORMATION: / Ceres Seq. ID 1498657

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:

Met Asn Lys Glu Val Pro Arg Leu Lys Ser Thr Gln Ser Ala Arg Asn
1 5 10 15
Leu Phe Ser Gly Arg Asp Ile Phe Gly His Ile Ser Asp Xaa Cys Tyr
20 25 30
Glu Leu Lys Arg Leu Ala Thr Arg Val Thr Glu Arg Glu Asp Thr Gly
35 40 45
Lys Ser Glu Val Lys Glu Ser His Gln Val Gly Gly Ile Val Asn Gln
50 55 60
Pro Tyr Ser Val His Asp Leu Glu Leu Lys Lys Glu Ile Lys Pro Leu
65 70 75 80
Leu Glu Val Ser Lys Asp Lys Leu Pro Glu Ser Thr Asp Val Lys Gly
85 90 95
Ser Thr Phe Lys Glu Asn Arg Arg Arg Lys Lys Arg Val Asp Asp Ala
100 105 110
Glu Asn Ile Pro Val Ser Leu Asn Val Glu Thr Val Lys Asn Lys Gly
115 120 125
Glu Glu Gly Arg Arg Lys Lys Arg Met Asp Asp Ala Glu Asn Ile Pro
130 135 140
Val Pro Leu Lys Leu Glu Thr Ile Lys Asn Lys Gly His Glu Arg Phe
145 150 155 160
Leu Gln Gln Ile Arg Thr Asn Pro Pro Ser Pro Gln Cys Phe Ser Glu
165 170 175
Asn Arg Thr Ala Thr Leu Lys Pro Leu Arg Thr Lys Pro Thr Glu Val
180 185 190
Leu Lys Arg Lys Glu Asp Glu Ala Glu Glu Lys Asn Arg Lys Ser
195 200 205
Gly Glu Ser Lys Glu Ala Thr Arg Gly Leu Asp Val Leu Trp Phe Leu
210 215 220
Lys Pro Cys Thr Leu Ala Asn
225 230

(2) INFORMATION FOR SEQ ID NO:573:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1135

(D) OTHER INFORMATION: / Ceres Seq. ID 1498658

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:

acaaaactcat	catcataagc	aacaatgggt	gtgtcactct	tctcttccag	aaatgttttc	60
tatacgttaa	gcttatgctt	atttgcagca	ttataccagc	cggttatgag	tagaccggct	120
aagtttgaag	atgactttag	gatcgcatgg	tccgatactc	atatcaactca	aattgacgga	180
ggcatagcca	ttcagctcaa	attggaccct	agctcaggat	gtggatttgc	ttcgaagaag	240
caataacttt	tggcccggtg	gagcatgaaa	atcaaaactg	tccccgggtg	ttctgccggg	300
actgtcactg	cctctacat	gaattcagat	accgattcgg	tacgagacga	gcttgatttt	360
gagttcttag	gaaatcgaag	tggacaacct	tacacagtgc	aaaccaatgt	gtttgctctg	420
ggtaaaaggc	atagagagca	aagagttaac	ctttggttcg	acccttctcg	tgattttccac	480
gaatatgcc	tctcatgaaa	ccatctccgt	attgtcttct	acgtagacaa	tgtgcccatc	540
agggtttaca	agaacaatga	ggcaaggaaa	gtaccatacc	caagattcca	accaatgggt	600
gtatatccca	cgttatggga	agccgatgat	tgggcgacac	gtggaggaa	agagaaaatc	660
aaattggtcga	gagcgccatt	ttatgcttat	tacaaagatt	ttgatataga	aggatgtccg	720
gttccaggag	ccgcagattg	tcccgcgtat	tcaagaat	gggtgggaagg	cagtgcgtac	780
caccagttga	gtccggtgga	agctcgaaat	tatagatggg	tccgagtgaa	ccatatgttc	840
tacgattatt	gcactgacaa	atctcgtttt	cctgttccac	ctccagaatg	ctcgctgtga	900
atctgatcca	aacattattg	tcttaaaagc	aaaacaagtg	cgaagtgtgt	ccataagcaa	960
cggtgcaatg	tattgtgaagt	gattaatgag	tcttgtggta	tgtgtggaat	tgctcataat	1020
cgatctgatt	gtggctcaat	gttcatatat	atatgtatat	ctttgaattt	tactttgttt	1080
tcatgatgtc	ttatgttttt	ttgatctatt	gaagagaacc	atgtttgttt	gttgc	

(2) INFORMATION FOR SEQ ID NO:574:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 293 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..293

(D) OTHER INFORMATION: / Ceres Seq. ID 1498659

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:

Met	Val	Val	Ser	Leu	Phe	Ser	Ser	Arg	Asn	Val	Phe	Tyr	Thr	Leu	Ser
1			5					10						15	
Leu	Cys	Leu	Phe	Ala	Ala	Leu	Tyr	Gln	Pro	Val	Met	Ser	Arg	Pro	Ala
			20					25					30		
Lys	Phe	Glu	Asp	Asp	Phe	Arg	Ile	Ala	Trp	Ser	Asp	Thr	His	Ile	Thr
			35				40					45			
Gln	Ile	Asp	Gly	Gly	Ile	Ala	Ile	Gln	Leu	Lys	Leu	Asp	Pro	Ser	Ser
			50			55					60				
Gly	Cys	Gly	Phe	Ala	Ser	Lys	Lys	Gln	Tyr	Leu	Phe	Gly	Arg	Val	Ser
65				70					75				80		
Met	Lys	Ile	Lys	Leu	Ile	Pro	Gly	Asp	Ser	Ala	Gly	Thr	Val	Thr	Ala
			85					90					95		
Phe	Tyr	Met	Asn	Ser	Asp	Thr	Asp	Ser	Val	Arg	Asp	Glu	Leu	Asp	Phe
			100				105					110			
Glu	Phe	Leu	Gly	Asn	Arg	Ser	Gly	Gln	Pro	Tyr	Thr	Val	Gln	Thr	Asn
			115			120					125				
Val	Phe	Ala	His	Gly	Lys	Gly	Asp	Arg	Glu	Gln	Arg	Val	Asn	Leu	Trp
			130			135					140				
Phe	Asp	Pro	Ser	Arg	Asp	Phe	His	Glu	Tyr	Ala	Ile	Ser	Trp	Asn	His
145				150					155				160		
Leu	Arg	Ile	Val	Phe	Tyr	Val	Asp	Asn	Val	Pro	Ile	Arg	Val	Tyr	Lys
			165						170				175		
Asn	Asn	Glu	Ala	Arg	Lys	Val	Pro	Tyr	Pro	Arg	Phe	Gln	Pro	Met	Gly
			180				185					190			
Val	Tyr	Ser	Thr	Leu	Trp	Glu	Ala	Asp	Asp	Trp	Ala	Thr	Gly	Gly	

```

      195                200                205
Ile Glu Lys Ile Asn Trp Ser Arg Ala Pro Phe Tyr Ala Tyr Tyr Lys
 210                215                220
Asp Phe Asp Ile Glu Gly Cys Pro Val Pro Gly Pro Ala Asp Cys Pro
 225                230                235                240
Ala Asn Ser Lys Asn Trp Trp Glu Gly Ser Ala Tyr His Gln Leu Ser
      245                250                255
Pro Val Glu Ala Arg Ser Tyr Arg Trp Val Arg Val Asn His Met Val
      260                265                270
Tyr Asp Tyr Cys Thr Asp Lys Ser Arg Phe Pro Val Pro Pro Pro Glu
      275                280                285
Cys Ser Ala Gly Ile
 290

```

(2) INFORMATION FOR SEQ ID NO:575:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..266
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:

```

Met Ser Arg Pro Ala Lys Phe Glu Asp Asp Phe Arg Ile Ala Trp Ser
 1      5      10      15
Asp Thr His Ile Thr Gln Ile Asp Gly Gly Ile Ala Ile Gln Leu Lys
      20      25      30
Leu Asp Pro Ser Ser Gly Cys Gly Phe Ala Ser Lys Lys Gln Tyr Leu
      35      40      45
Phe Gly Arg Val Ser Met Lys Ile Lys Leu Ile Pro Gly Asp Ser Ala
      50      55      60
Gly Thr Val Thr Ala Phe Tyr Met Asn Ser Asp Thr Asp Ser Val Arg
      65      70      75      80
Asp Glu Leu Asp Phe Glu Phe Leu Gly Asn Arg Ser Gly Gln Pro Tyr
      85      90      95
Thr Val Gln Thr Asn Val Phe Ala His Gly Lys Gly Asp Arg Glu Gln
      100      105      110
Arg Val Asn Leu Trp Phe Asp Pro Ser Arg Asp Phe His Glu Tyr Ala
      115      120      125
Ile Ser Trp Asn His Leu Arg Ile Val Phe Tyr Val Asp Asn Val Pro
      130      135      140
Ile Arg Val Tyr Lys Asn Asn Glu Ala Arg Lys Val Pro Tyr Pro Arg
      145      150      155      160
Phe Gln Pro Met Gly Val Tyr Ser Thr Leu Trp Glu Ala Asp Asp Trp
      165      170      175
Ala Thr Arg Gly Gly Ile Glu Lys Ile Asn Trp Ser Arg Ala Pro Phe
      180      185      190
Tyr Ala Tyr Tyr Lys Asp Phe Asp Ile Glu Gly Cys Pro Val Pro Gly
      195      200      205
Pro Ala Asp Cys Pro Ala Asn Ser Lys Asn Trp Trp Glu Gly Ser Ala
      210      215      220
Tyr His Gln Leu Ser Pro Val Glu Ala Arg Ser Tyr Arg Trp Val Arg
      225      230      235      240
Val Asn His Met Val Tyr Asp Tyr Cys Thr Asp Lys Ser Arg Phe Pro
      245      250      255
Val Pro Pro Pro Glu Cys Ser Ala Gly Ile
      260      265

```

(2) INFORMATION FOR SEQ ID NO:576:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..213
(D) OTHER INFORMATION: / Ceres Seq. ID 1498661
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:
Met Lys Ile Lys Leu Ile Pro Gly Asp Ser Ala Gly Thr Val Thr Ala
1 5 10 15
Phe Tyr Met Asn Ser Asp Thr Asp Ser Val Arg Asp Glu Leu Asp Phe
20 25 30
Glu Phe Leu Gly Asn Arg Ser Gly Gln Pro Tyr Thr Val Gln Thr Asn
35 40 45
Val Phe Ala His Gly Lys Gly Asp Arg Glu Gln Arg Val Asn Leu Trp
50 55 60
Phe Asp Pro Ser Arg Asp Phe His Glu Tyr Ala Ile Ser Trp Asn His
65 70 75 80
Leu Arg Ile Val Phe Tyr Val Asp Asn Val Pro Ile Arg Val Tyr Lys
85 90 95
Asn Asn Glu Ala Arg Lys Val Pro Tyr Pro Arg Phe Gln Pro Met Gly
100 105 110
Val Tyr Ser Thr Leu Trp Glu Ala Asp Asp Trp Ala Thr Arg Gly Gly
115 120 125
Ile Glu Lys Ile Asn Trp Ser Arg Ala Pro Phe Tyr Ala Tyr Tyr Lys
130 135 140
Asp Phe Asp Ile Glu Gly Cys Pro Val Pro Gly Pro Ala Asp Cys Pro
145 150 155 160
Ala Asn Ser Lys Asn Trp Trp Glu Gly Ser Ala Tyr His Gln Leu Ser
165 170 175
Pro Val Glu Ala Arg Ser Tyr Arg Trp Val Arg Val Asn His Met Val
180 185 190
Tyr Asp Tyr Cys Thr Asp Lys Ser Arg Phe Pro Val Pro Pro Glu
195 200 205
Cys Ser Ala Gly Ile
210

(2) INFORMATION FOR SEQ ID NO:577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1519 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1519
(D) OTHER INFORMATION: / Ceres Seq. ID 1498662

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:

aaaaataact taatcacaca caaggagaga agagagaaag agagaaagag agacagagat 60
aatggcgctac agtgcgtggt tcttacacca gagcgcatcg gcttcatcag ccgcacgatac 120
atcatctctcc tctctatccc agcgtcacgt gtcgctctcc aaacctgttc agatcatctg 180
taaaagctcaa cagctctcatg aagacgataa ctccgcgcgtc tcccgccgtc ttgctctcac 240
tctctctctgc ggcgcgcgtc ctgttggttc caaagtatct cctgctgtag ccgcctacgg 300
tgaagctgca aacgtgtgttg ggaagccaaa gacgaacaca gactctttgc catacaatgg 360
agatgggttc aaagtgcagg ttccagcaaa atggaaccca agcaaaagaga ttgagtatcc 420
aggacaagtc cttaggtttcg aagacaactt cgatgctact agcaatctca atgtcatggt 480
cactcttacc gacaagaagt ccatcaactga ttacgggttct cccgaagagt tctctctca 540
ggttaattac ctctagggga aacaagctta ctctgggtgag actgctctcg agggaggtct 600
tgacaacaat gcagtgggcaa cagcaaacat tctggagtca tcactctcagg aagttgggtg 660

gaaaccctac	tattactgt	ctgtgttgac	aagaacggct	gatggagacg	aaggtgggaa	720
gcatacagctg	atcacagcaa	ccgtgaagga	gggaagcktt	acatctgcaa	agcacaagct	780
ggagacaaga	ggtggttcaa	gggagccagg	aaatttgcg	agagcgacg	cacttctttc	840
agtggttgc	gmrgtgaag	caacacacg	taacaatgct	ctgcttgc	tcttcttgc	900
tctcttggtaa	aaaatggaaa	atgaaactga	gcttttgaga	actatcaaga	tgatgttacc	960
ttttcgccat	cacttgtgta	cctatgatac	cagactcgtt	tccaagtttt	cttaaaaaaa	1020
aactatattc	aatatagatt	ttctcaaat	aaaaaataaa	aaaaaataaa	aaaaaataaa	1080
aaaaaamcaa	aaaaaataaa	aaaaaagctt	ctcgkgccgt	tttttttttt	tttttttgga	1140
gtttttgtgt	ggagcgttga	gattggagaa	gctagaagga	ttgacgggtg	agggccaacg	1200
tgacacaggag	tttgtgtgtg	ggttagctca	gagggattaga	cgccctcaag	agcgtgcaga	1260
cgagagagct	aagaagctta	agaagaccga	tgaggtttgc	tttatgttga	tcttcgataa	1320
gcagattagct	gtgtaaactc	ttgaaaatat	caaatctttc	ctttctccgt	ctttctgttt	1380
tttactctaa	tgaggccctac	tcattggtgt	gtgagtggtt	cctcaagtat	cattgtccaa	1440
taaggagcga	attttattat	ggctggctgt	tttattacaa	attatgtgta	tggtgtaata	1500
attaaagatt	gaattatct					

(2) INFORMATION FOR SEQ ID NO:578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..282
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:

Met	Ala	Tyr	Ser	Ala	Cys	Phe	Leu	His	Gln	Ser	Ala	Leu	Ala	Ser	Ser
1			5					10						15	
Ala	Ala	Arg	Ser	Ser	Ser	Ser	Ser	Ser	Gln	Arg	His	Val	Ser	Leu	
			20					25				30			
Ser	Lys	Pro	Val	Gln	Ile	Ile	Cys	Lys	Ala	Gln	Gln	Ser	His	Glu	Asp
			35				40				45				
Asp	Asn	Ser	Ala	Val	Ser	Arg	Arg	Leu	Ala	Leu	Thr	Leu	Leu	Gly	
			50				55				60				
Ala	Ala	Ala	Val	Gly	Ser	Lys	Val	Ser	Pro	Ala	Asp	Ala	Ala	Tyr	Gly
			65				70				75			80	
Glu	Ala	Ala	Asn	Val	Phe	Gly	Lys	Pro	Lys	Thr	Asn	Thr	Asp	Phe	Leu
			85					90						95	
Pro	Tyr	Asn	Gly	Asp	Gly	Phe	Lys	Val	Gln	Val	Pro	Ala	Lys	Trp	Asn
			100				105						110		
Pro	Ser	Lys	Glu	Ile	Glu	Tyr	Pro	Gly	Gln	Val	Leu	Arg	Phe	Glu	Asp
			115				120						125		
Asn	Phe	Asp	Ala	Thr	Ser	Asn	Leu	Asn	Val	Met	Val	Thr	Pro	Thr	Asp
			130				135				140				
Lys	Lys	Ser	Ile	Thr	Asp	Tyr	Gly	Ser	Pro	Glu	Glu	Phe	Leu	Ser	Gln
			145				150				155			160	
Val	Asn	Tyr	Leu	Leu	Gly	Lys	Gln	Ala	Tyr	Phe	Gly	Glu	Thr	Ala	Ser
			165					170						175	
Glu	Gly	Gly	Phe	Asp	Asn	Asn	Ala	Val	Ala	Thr	Ala	Asn	Ile	Leu	Glu
			180					185					190		
Ser	Ser	Ser	Gln	Glu	Val	Gly	Gly	Lys	Pro	Tyr	Tyr	Tyr	Leu	Ser	Val
			195					200					205		
Leu	Thr	Arg	Thr	Ala	Asp	Gly	Asp	Glu	Gly	Gly	Lys	His	Gln	Leu	Ile
			210				215						220		
Thr	Ala	Thr	Val	Lys	Glu	Gly	Ser	Xaa	Thr	Ser	Ala	Lys	His	Lys	Leu
			225				230				235			240	
Glu	Thr	Arg	Gly	Gly	Ser	Arg	Glu	Pro	Gly	Asn	Leu	Ser	Arg	Gln	
			245					250						255	
Pro	Leu	Leu	Ser	Val	Leu	Leu	Xaa	Lys	Ala	Thr	Gln	Arg	Asn	Asn	
			260				265						270		

Ala Leu Leu Ala Phe Phe Ile Cys Leu Leu
275 280

(2) INFORMATION FOR SEQ ID NO:579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498664

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

Met	Val	Thr	Pro	Thr	Asp	Lys	Lys	Ser	Ile	Thr	Asp	Tyr	Gly	Ser	Pro
1			5					10					15		
Glu	Glu	Phe	Leu	Ser	Gln	Val	Asn	Tyr	Leu	Leu	Gly	Lys	Gln	Ala	Tyr
			20					25					30		
Phe	Gly	Glu	Thr	Ala	Ser	Glu	Gly	Gly	Phe	Asp	Asn	Asn	Ala	Val	Ala
			35				40					45			
Thr	Ala	Asn	Ile	Leu	Glu	Ser	Ser	Ser	Gln	Glu	Val	Gly	Gly	Lys	Pro
			50			55					60				
Tyr	Tyr	Tyr	Leu	Ser	Val	Leu	Thr	Arg	Thr	Ala	Asp	Gly	Asp	Glu	Gly
65					70				75					80	
Gly	Lys	His	Gln	Leu	Ile	Thr	Ala	Thr	Val	Lys	Glu	Gly	Ser	Xaa	Thr
			85						90				95		
Ser	Ala	Lys	His	Lys	Leu	Glu	Thr	Arg	Gly	Gly	Ser	Arg	Glu	Pro	Gly
			100					105					110		
Asn	Leu	Ser	Arg	Ala	Gln	Pro	Leu	Leu	Ser	Val	Leu	Leu	Xaa	Xaa	Lys
			115				120					125			
Ala	Thr	Gln	Arg	Asn	Asn	Ala	Leu	Leu	Ala	Phe	Phe	Ile	Cys	Leu	Leu
			130			135						140			

(2) INFORMATION FOR SEQ ID NO:580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..476
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498665

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:

tctctctctc	tcctctctctc	tggtctcttaa	tttagagaga	aaaaataaagc	attctctcctt	60
ctctgttttc	gagcgggaaa	ttctggagat	ggctatacaa	gcgcagttga	attacaacgc	120
tcggaatgcg	aatcaaatcg	gttttggtgg	gtccgagttt	tccttgatca	acaacaatgg	180
cgttattgga	atcgcatcat	caacaacaac	agtcctcttc	tcaaaagcttt	ttagctgtctc	240
agatggagaa	acagaagcaa	gagatcgatc	agttcatcaa	aatacagaac	gagaggttga	300
gatatgtgtt	gcaagaacag	aggaagcgag	aaatggagat	gattttaagg	aaaatggaga	360
gtaaagcttt	gcttttgatg	agtcagaagg	aagaagaaat	gtcgaaagca	ttgaacaaga	420
acatggaact	cgaagatctg	ttgagaaaaa	tggaaatgga	gaatcagacg	tggcag	

(2) INFORMATION FOR SEQ ID NO:581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1498666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:

Leu Ser Leu Ser Leu Ser Leu Phe Phe Asn Leu Glu Arg Lys Asn Lys
1 5 10 15
His Ser Ser Phe Ser Val Phe Glu Arg Glu Ile Leu Glu Met Ala Ile
20 25 30
Gln Ala Gln Leu Asn Tyr Asn Ala Pro Asn Ala Asn Gln Ile Gly Phe
35 40 45
Gly Gly Ser Glu Phe Ser Leu Ile Asn Asn Asn Gly Val Ile Gly Ile
50 55 60
Ala Ser Ser Thr Thr Thr Val Ser Phe Ser Lys Leu Phe Ser Cys Ser
65 70 75 80
Asp Gly Glu Thr Glu Ala Arg Asp Arg Ser Val His Gln Asn Thr Glu
85 90 95
Arg Glu Val Glu Ile Cys Val Ala Arg Thr Glu Glu Ala Arg Asn Gly
100 105 110
Asp Asp Phe Lys Glu Asn Gly Glu
115 120

(2) INFORMATION FOR SEQ ID NO:582:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..91

(D) OTHER INFORMATION: / Ceres Seq. ID 1498667

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:

Met Ala Ile Gln Ala Gln Leu Asn Tyr Asn Ala Pro Asn Ala Asn Gln
1 5 10 15
Ile Gly Phe Gly Gly Ser Glu Phe Ser Leu Ile Asn Asn Asn Gly Val
20 25 30
Ile Gly Ile Ala Ser Ser Thr Thr Thr Val Ser Phe Ser Lys Leu Phe
35 40 45
Ser Cys Ser Asp Gly Glu Thr Glu Ala Arg Asp Arg Ser Val His Gln
50 55 60
Asn Thr Glu Arg Glu Val Glu Ile Cys Val Ala Arg Thr Glu Glu Ala
65 70 75 80
Arg Asn Gly Asp Asp Phe Lys Glu Asn Gly Glu
85 90

(2) INFORMATION FOR SEQ ID NO:583:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..100

(D) OTHER INFORMATION: / Ceres Seq. ID 1498668

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:

Met Ala Leu Leu Glu Ser His His Gln Gln Gln Ser Pro Ser Gln
1 5 10 15
Ser Phe Leu Ala Ala Gln Met Glu Lys Gln Lys Gln Glu Ile Asp Gln
20 25 30

(2) INFORMATION FOR SEQ ID NO:584:

(A) LENGTH: 777 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:

(2) INFORMATION FOR SEQ ID NO:585:

(A) LENGTH: 188 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..18

(xi) SEQUENCE DESCRIPTION: SEO ID NO:585:

Ile	Gly	Thr	Lys	Tyr	Phe	Leu	Arg	Lys	Lys	Ile	Met	Gly	Phe	Cys	Phe
1				5					10					15	
Ser	Lys	Phe	Gly	Lys	Ser	Gln	Thr	His	Glu	Ile	Pro	Ile	Ser	Ser	Ser
			20					25					30		
Ser	Asp	Ser	Ser	Pro	Pro	His	His	Tyr	Gln	Pro	Leu	Pro	Lys	Pro	Thr
		35					40					45			
Val	Ser	Gln	Gly	Gln	Thr	Ser	Asn	Pro	Thr	Ser	Asn	Pro	Gln	Pro	Lys
						55					60				
Pro	Lys	Pro	Ala	Pro	Pro	Pro	Pro	Ser	Thr	Ser	Ser	Ser	Gly	Ser	Gln
65					70				75						80
Ile	Gly	Pro	Ile	Leu	Asn	Arg	Pro	Met	Ile	Asp	Leu	Ser	Ala	Leu	Tyr
				85					90					95	
Asp	Leu	His	Lys	Glu	Leu	Gly	Arg	Gly	Gln	Phe	Gly	Ile	Thr	Tyr	Lys
			100					105					110		

Cys Thr Asp Lys Ser Asn Gly Arg Glu Tyr Ala Cys Lys Ser Ile Ser
115 120 125
Lys Arg Lys Leu Ile Arg Arg Lys Asp Ile Glu Asp Val Arg Arg Glu
130 135 140
Val Met Ile Leu Gln His Leu Thr Gly Gln Pro Asn Ile Val Glu Phe
145 150 155 160
Arg Gly Ala Tyr Glu Asp Lys Asp Asn Leu His Leu Val Met Glu Leu
165 170 175
Cys Ser Gly Gly Asp Tyr Val Gly Gly His His
180 185

(2) INFORMATION FOR SEQ ID NO:586:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..177

(D) OTHER INFORMATION: / Ceres Seq. ID 1498673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:

Met Gly Phe Cys Phe Ser Lys Phe Gly Lys Ser Gln Thr His Glu Ile
1 5 10 15
Pro Ile Ser Ser Ser Ser Asp Ser Ser Pro Pro His His Tyr Gln Pro
20 25 30
Leu Pro Lys Pro Thr Val Ser Gln Gly Gln Thr Ser Asn Pro Thr Ser
35 40 45
Asn Pro Gln Pro Lys Pro Lys Pro Ala Pro Pro Pro Pro Ser Thr
50 55 60
Ser Ser Gly Ser Gln Ile Gly Pro Ile Leu Asn Arg Pro Met Ile Asp
65 70 75 80
Leu Ser Ala Leu Tyr Asp Leu His Lys Glu Leu Gly Arg Gly Gln Phe
85 90 95
Gly Ile Thr Tyr Lys Cys Thr Asp Lys Ser Asn Gly Arg Glu Tyr Ala
100 105 110
Cys Lys Ser Ile Ser Lys Arg Lys Leu Ile Arg Arg Lys Asp Ile Glu
115 120 125
Asp Val Arg Arg Glu Val Met Ile Leu Gln His Leu Thr Gly Gln Pro
130 135 140
Asn Ile Val Glu Phe Arg Gly Ala Tyr Glu Asp Lys Asp Asn Leu His
145 150 155 160
Leu Val Met Glu Leu Cys Ser Gly Gly Asp Tyr Val Gly Gly Gly His
165 170 175
His

(2) INFORMATION FOR SEQ ID NO:587:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..100

(D) OTHER INFORMATION: / Ceres Seq. ID 1498674

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:

Met Ile Asp Leu Ser Ala Leu Tyr Asp Leu His Lys Glu Leu Gly Arg
1 5 10 15
Gly Gln Phe Gly Ile Thr Tyr Lys Cys Thr Asp Lys Ser Asn Gly Arg

20	25	30
Glu Tyr Ala Cys Lys Ser Ile Ser Lys Arg Lys Leu Ile Arg Arg Lys		
35	40	45
Asp Ile Glu Asp Val Arg Arg Glu Val Met Ile Leu Gln His Leu Thr		
50	55	60
Gly Gln Pro Asn Ile Val Glu Phe Arg Gly Ala Tyr Glu Asp Lys Asp		
65	70	75
Asn Leu His Leu Val Met Glu Leu Cys Ser Gly Gly Asp Tyr Val Gly		
85	90	95
Gly Gly His His		
100		

(2) INFORMATION FOR SEQ ID NO:588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 489 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..489
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498679

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

aatacaagtg atttccatta ttctctgtct acgtatacaa ttgatcttcc cccatctcca	60
attcagatttt ggacagaggt attttttgat ccgattctta cgaatcctga atcttctctg	120
tagattaatc gatcgatcgg ttcttaattc gcggaaaatt gtttcagtaa cctgtgatcg	180
tgctgggttg ggtagaagag atcgaagtgg gagcaaaatc atgatgaatc ggctattcgg	240
gaaacccaag caggaggcta atgctctcca aactttagac aagcttaacg agacgcttgg	300
agatgctaga gaaaaaggag aaagtactct tgaagaaagc tggtgcagag ttgagaagg	360
caaaagaata ctcccggtct aagaacaaac gagcggctat acagtstttg aaaaggaaga	420
ggtyatatga gggacaagtc gaacagcttg ggaatttctt ttgccttctc acctctatca	480
tcactctac	

(2) INFORMATION FOR SEQ ID NO:589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..117
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498680

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

Ile Gln Val Ile Ser Ile Ile Ser Arg Leu Arg Ile Gln Leu Phe	
1	15
Pro His Leu Gln Phe Arg Phe Gly Gln Arg Tyr Phe Leu Ile Arg Phe	
20	30
Leu Arg Ile Leu Asn Leu Pro Arg Arg Leu Ile Asp Arg Ser Val Leu	
35	45
Asn Ser Arg Lys Ile Val Ser Val Thr Cys Asp Arg Val Gly Trp Gly	
50	60
Arg Arg Asp Arg Ser Gly Ser Lys Ile Met Met Asn Arg Leu Phe Gly	
65	80
Lys Pro Lys Gln Glu Ala Asn Ala Leu Gln Thr Leu Asp Lys Leu Asn	
85	95
Glu Thr Leu Gly Asp Ala Arg Glu Lys Gly Glu Ser Thr Leu Glu Glu	
100	110
Ser Trp Cys Arg Gly	
115	

(2) INFORMATION FOR SEQ ID NO:590:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 62 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..62
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498681
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:
Met Leu Glu Lys Lys Glu Lys Val Leu Leu Lys Lys Ala Gly Ala Glu
1 5 10 15
Val Glu Lys Ala Lys Glu Tyr Ser Arg Ala Lys Asn Lys Arg Ala Ala
 20 25 30
Ile Gln Xaa Leu Lys Arg Lys Arg Xaa Tyr Glu Gly Gln Val Glu Gln
 35 40 45
Leu Gly Asn Phe Phe Cys Leu Leu Thr Ser Ile Ile Tyr
 50 55 60
(2) INFORMATION FOR SEQ ID NO:591:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2409 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..2409
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498682
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:
aaaaaaaagaa ttcttagtag aaagagagaa ggcgtgaaat tccgtagcga gagattcttc 60
gccggagtaa ttcttttgcg tgatcttacc ggcgtgcttaa ttcgtcttcg cctgattcgt 120
tggtttcaaa atctgtctct ctctttcaat cggaggttaa ttgtttttct gtgtgggggt 180
caaaagcgaag atggtgaacg ctatggtgga gagagcgacg agcgangatg ctgactggcg 240
ctgattggcg tatgaacctc gagactctgt atatgctcaa tagcgatcca gcgcaasaaa 300
agatgttgtg aaaggcatta aaaaacggat tggtagcagg aatccaaaag ctgacttctc 360
tgcccttaact ctgcttgaga caatagttaa gaactgtggt gacatggttc atatgcatgt 420
ggctgagaaa ggtgttatct atgagatggt ccggaatggt aagaagaagc cggacttcca 480
tgtcaaaagaa aagattctgg tccttatcga tacatggcaa gaggcccttg gtggccctag 540
ggcaagatat ccacaatact atgcaggata ccaggaattg ttgcgtgctg gtgcgttttt 600
ccctcagaga tcagagagat cagctcctgt gttcacacct cctcaaacac agcctttgac 660
atcttaacct ccaaatcttc gtaacgctgg acctggtaat gatgtgcctg aacctcaagc 720
agagccagaa ttccgcgact taagtttgtc ggagattcaa aatgcaaaa gtatcatgga 780
tgtgtctgcg gagatctgag gtgcattaga gcccgaaaac aaggaggatc tcaaaaaga 840
ggttatggtc gatctggtgg agcagtgctg tacatacaaa caaagagtgg tgcacctcgt 900
caactcgact tcggacaggt cttgtttatg tcaaggctgt gctttgaatt atgacttga 960
cggtgtctta accaattatg aagcaattgc ttctggatta cctgaactt cttctcagat 1020
cgagaagccc aagtcgcaga cagggaaaac cctgtttgat gttgatggtc cactttatga 1080
tacaggggag agcagtaaat agcggaacgg agctacatcg agctatcctc acgggggtct 1140
aaatcaggtg gccctccctg caccacctgt aactaatggt tcagccaatt ccaaaataga 1200
cctctcagat ggcatgatac tttgccctgt tctgtttgg agaatctcca gccaatcagt 1260
ccggttgcat cagatcaaaa tgcactggcc cttatcgaca tgttctcaga taatactaata 1320
aatccaagtc ctgcaactgc aagaagtggc aatccagctc agaatatccc ttggaatcct 1380
caagggcacc aacaaccaa tagtcaagct ggagaagctg gattacaaca atccaatgga 1440
tttggccctc aagtggggta ttccgagttt gagcagccat catacgggca aggactctct 1500
ttctcctgga gcagtcagcc tgcacagcaa ccagtcacgc tccaagacta tagtccctct 1560
gacagtcagg catttccacc tccccatgg gaagctcagg tccaagacta tagtccctct 1620
ggcgagtcag gaagtcggtt ttctcctgga atgcatacaa ctcagactgc ctccacacat 1680
gctcaaccag ttaacaacaa caatccatat cctcaaatct cccaaaccgg gccaccagtc 1740
aacaataaca gtccatatgc tcaaatgccc caaacagctc aagcagtgc caacatcagt 1800

```
ccatatactc aaattccaca aaacggcggt tacatgccar actttcaacc aaatcaggct 1860
cttgggtcag gctatcaacc acagcaacaa cagcagcagc agatgatgat ggctcagtag 1920
tatgcccac agcaacagct acagcaacaa caacagcaac aggcgtatgg aaaccagatg 1980
ggaggatacg gatatggcta ntamtcaaca gcaacaagga agcagcccat atctggacca 2040
gcaaatgtac ggtttatcca tgagagacca gacatcgcat caggtagcat catcatcatc 2100
taccacatct tatctgcctc caatgaaacc taagaataaa ccagaggaga agctatttgg 2160
ggatcttgtg gacatctcca aattcaagcc tacaaaacog acttcgggaa gagctgggtac 2220
catgtgaaa ttctcccatc cattcatcat ttaccagtat tcatctcttc tatctctctc 2280
agctaacctt cttctctctc tttgttaagc ttttttcatc attgatttta ttaccctett 2340
gggagataca tagatataca tatgtgttat gtcttctctt ataatttacc gttgggttatg 2400
ggtttgttc
```

(2) INFORMATION FOR SEQ ID NO:592:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 323 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..323

(D) OTHER INFORMATION: / Ceres Seq. ID 1498683

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:

```
Met Val His Met His Val Ala Glu Lys Gly Val Ile His Glu Met Val
1 5 10 15
Arg Ile Val Lys Lys Lys Pro Asp Phe His Val Lys Glu Lys Ile Leu
20 25 30
Val Leu Ile Asp Thr Trp Gln Glu Ala Phe Gly Gly Pro Arg Ala Arg
35 40 45
Tyr Pro Gln Tyr Tyr Ala Gly Tyr Gln Glu Leu Leu Arg Ala Gly Ala
50 55 60
Val Phe Pro Gln Arg Ser Glu Arg Ser Ala Pro Val Phe Thr Pro Pro
65 70 75 80
Gln Thr Gln Pro Leu Thr Ser Tyr Pro Pro Asn Leu Arg Asn Ala Gly
85 90 95
Pro Gly Asn Asp Val Pro Glu Pro Ser Ala Glu Pro Glu Phe Pro Thr
100 105 110
Leu Ser Leu Ser Glu Ile Gln Asn Ala Lys Gly Ile Met Asp Val Leu
115 120 125
Ala Glu Met Leu Ser Ala Leu Glu Pro Gly Asn Lys Glu Asp Leu Lys
130 135 140
Gln Glu Val Met Val Asp Leu Val Glu Gln Cys Arg Thr Tyr Lys Gln
145 150 155 160
Arg Val Val His Leu Val Asn Ser Thr Ser Asp Glu Ser Leu Leu Cys
165 170 175
Gln Gly Leu Ala Leu Asn Asp Asp Leu Gln Arg Val Leu Thr Asn Tyr
180 185 190
Glu Ala Ile Ala Ser Gly Leu Pro Gly Thr Ser Ser Gln Ile Glu Lys
195 200 205
Pro Lys Ser Glu Thr Gly Lys Ser Leu Val Asp Val Asp Gly Pro Leu
210 215 220
Ile Asp Thr Gly Asp Ser Ser Asn Gln Ala Asn Gly Ala Thr Ser Ser
225 230 235 240
Ser Gly Asn Gly Val Leu Asn Gln Leu Ala Leu Pro Ala Pro Pro Val
245 250 255
Thr Asn Gly Ser Ala Asn Ser Lys Ile Asp Leu Leu Ser Gly Asp Asp
260 265 270
Leu Ala Leu Val Pro Val Gly Thr Phe Leu Ser Gln Gln Val Arg Leu
275 280 285
His Gln Ile Lys Met His Ser Pro Leu Ser Thr Cys Ser Gln Ile Ile
290 295 300
```

Leu Ile Ile Gln Val Leu Gln Leu His Gln Val Ala Ile Gln Leu Arg
305 310 315 320
Ile Phe Leu

(2) INFORMATION FOR SEQ ID NO:593:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..320

(D) OTHER INFORMATION: / Ceres Seq. ID 1498684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

Met His Val Ala Glu Lys Gly Val Ile His Glu Met Val Arg Ile Val
1 5 10 15
Lys Lys Lys Pro Asp Phe His Val Lys Glu Lys Ile Leu Val Leu Ile
20 25 30
Asp Thr Trp Gln Glu Ala Phe Gly Gly Pro Arg Ala Arg Tyr Pro Gln
35 40 45
Tyr Tyr Ala Gly Tyr Gln Glu Leu Leu Arg Ala Gly Ala Val Phe Pro
50 55 60
Gln Arg Ser Glu Arg Ser Ala Pro Val Phe Thr Pro Pro Gln Thr Gln
65 70 75 80
Pro Leu Thr Ser Tyr Pro Pro Asn Leu Arg Asn Ala Gly Pro Gly Asn
85 90 95
Asp Val Pro Glu Pro Ser Ala Glu Pro Glu Phe Pro Thr Leu Ser Leu
100 105 110
Ser Glu Ile Gln Asn Ala Lys Gly Ile Met Asp Val Leu Ala Glu Met
115 120 125
Leu Ser Ala Leu Glu Pro Gly Asn Lys Glu Asp Leu Lys Gln Glu Val
130 135 140
Met Val Asp Leu Val Glu Gln Cys Arg Thr Tyr Lys Gln Arg Val Val
145 150 155 160
His Leu Val Asn Ser Thr Ser Asp Glu Ser Leu Leu Cys Gln Gly Leu
165 170 175
Ala Leu Asn Asp Asp Leu Gln Arg Val Leu Thr Asn Tyr Glu Ala Ile
180 185 190
Ala Ser Gly Leu Pro Gly Thr Ser Ser Gln Ile Glu Lys Pro Lys Ser
195 200 205
Glu Thr Gly Lys Ser Leu Val Asp Val Asp Gly Pro Leu Ile Asp Thr
210 215 220
Gly Asp Ser Ser Asn Gln Ala Asn Gly Ala Thr Ser Ser Ser Gly Asn
225 230 235 240
Gly Val Leu Asn Gln Leu Ala Leu Pro Ala Pro Pro Val Thr Asn Gly
245 250 255
Ser Ala Asn Ser Lys Ile Asp Leu Leu Ser Gly Asp Asp Leu Ala Leu
260 265 270
Val Pro Val Gly Thr Phe Leu Ser Gln Gln Val Arg Leu His Gln Ile
275 280 285
Lys Met His Ser Pro Leu Ser Thr Cys Ser Gln Ile Ile Leu Ile Ile
290 295 300
Gln Val Leu Gln Leu His Gln Val Ala Ile Gln Leu Arg Ile Phe Leu
305 310 315 320

(2) INFORMATION FOR SEQ ID NO:594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..309
(D) OTHER INFORMATION: / Ceres Seq. ID 1498685
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:
Met Val Arg Ile Val Lys Lys Lys Pro Asp Phe His Val Lys Glu Lys
1 5 10 15
Ile Leu Val Leu Ile Asp Thr Trp Gln Glu Ala Phe Gly Gly Pro Arg
20 25 30
Ala Arg Tyr Pro Gln Tyr Tyr Ala Gly Tyr Gln Glu Leu Arg Ala
35 40 45
Gly Ala Val Phe Pro Gln Arg Ser Glu Arg Ser Ala Pro Val Phe Thr
50 55 60
Pro Pro Gln Thr Gln Pro Leu Thr Ser Tyr Pro Pro Asn Leu Arg Asn
65 70 75 80
Ala Gly Pro Gly Asn Asp Val Pro Glu Pro Ser Ala Glu Pro Glu Phe
85 90 95
Pro Thr Leu Ser Leu Ser Glu Ile Gln Asn Ala Lys Gly Ile Met Asp
100 105 110
Val Leu Ala Glu Met Leu Ser Ala Leu Glu Pro Gly Asn Lys Glu Asp
115 120 125
Leu Lys Gln Glu Val Met Val Asp Leu Val Glu Gln Cys Arg Thr Tyr
130 135 140
Lys Gln Arg Val Val His Leu Val Asn Ser Thr Ser Asp Glu Ser Leu
145 150 155 160
Leu Cys Gln Gly Leu Ala Leu Asn Asp Asp Leu Gln Arg Val Leu Thr
165 170 175
Asn Tyr Glu Ala Ile Ala Ser Gly Leu Pro Gly Thr Ser Ser Gln Ile
180 185 190
Glu Lys Pro Lys Ser Glu Thr Gly Lys Ser Leu Val Asp Val Asp Gly
195 200 205
Pro Leu Ile Asp Thr Gly Asp Ser Ser Asn Gln Ala Asn Gly Ala Thr
210 215 220
Ser Ser Ser Gly Asn Gly Val Leu Asn Gln Leu Ala Leu Pro Ala Pro
225 230 235 240
Pro Val Thr Asn Gly Ser Ala Asn Ser Lys Ile Asp Leu Leu Ser Gly
245 250 255
Asp Asp Leu Ala Leu Val Pro Val Gly Thr Phe Leu Ser Gln Gln Val
260 265 270
Arg Leu His Gln Ile Lys Met His Ser Pro Leu Ser Thr Cys Ser Gln
275 280 285
Ile Ile Leu Ile Ile Gln Val Leu Gln Leu His Gln Val Ala Ile Gln
290 295 300
Leu Arg Ile Phe Leu
305

(2) INFORMATION FOR SEQ ID NO:595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 860 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..860
(D) OTHER INFORMATION: / Ceres Seq. ID 1498686

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:

aaacacaaaa	aaaaaaactt	aagaaaattt	gaaatcctca	gaattgcaga	gcaagaacaa	60
accatggcga	atcctatttc	agagattctg	gagaaccaag	ttctaaccgt	ggctaagaag	120
atggaagata	agatagacaa	cgagatcgcc	tccttagaaa	agcttgacga	ggacgatcta	180
gaggttttga	gagagagaag	gttaaagcaa	atgaagaaaa	tgccagagaa	gaagaaacgt	240
tggtattagc	ttggacatgg	tgaatactct	gagatccatt	ctgagaaga	cttcttctcc	300
gtcgtaaaag	ccagcgaaag	cgctgtctgc	catttctacc	ggcagaattg	gccatgtaaa	360
gtgatggata	mscacatgag	tatatggca	aagcaacaca	ttgagacacg	ttttgtgaag	420
atccaaagct	agaaaaagtc	gttcttggct	gagaggtcca	agattgttgt	tctaactact	480
cttgacacta	ttaaagaacac	taaagtgcag	gattatgtgg	ttgggttcaa	tgagcttgga	540
gggaaagatg	atttcagcac	tgaggatttg	gaagagagaa	tagctagagc	gcaagtgtatt	600
cattacgatg	gagagtcac	gtcgcttaaa	ccaaagtcca	caacacaagt	tagaaggaa	660
gtgaggcaga	gtgctcgttc	agattcagac	tccgaataga	ctctcggttt	tttcagcaaa	720
cgtttgtgtg	tatgttcacg	atcttcactc	tatcttcagc	ccttttttgg	tgtaggtttg	780
tattgtgcga	attcagttgt	gatgtgtaat	acaaagtagg	agatgatctt	atatgcata	840
ttgatgagtt	tttaaccttg					

(2) INFORMATION FOR SEQ ID NO:596:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..232
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:

Lys	Pro	Lys	Lys	Lys	Asn	Leu	Arg	Lys	Phe	Glu	Ile	Leu	Arg	Ile	Ala
1				5					10					15	
Glu	Gln	Arg	Thr	Thr	Met	Ala	Asn	Pro	Ile	Gln	Glu	Ile	Leu	Glu	Asn
				20				25					30		
Gln	Val	Leu	Thr	Val	Ala	Lys	Ala	Met	Glu	Asp	Lys	Ile	Asp	Asn	Glu
				35			40					45			
Ile	Ala	Ser	Leu	Glu	Lys	Leu	Asp	Glu	Asp	Asp	Leu	Glu	Val	Leu	Arg
				50			55				60				
Glu	Arg	Arg	Leu	Lys	Gln	Met	Lys	Lys	Met	Ala	Glu	Lys	Lys	Lys	Arg
				65			70				75				80
Trp	Ile	Ser	Leu	Gly	His	Gly	Glu	Tyr	Ser	Glu	Ile	His	Ser	Glu	Lys
				85				90						95	
Asp	Phe	Phe	Ser	Val	Val	Lys	Ala	Ser	Glu	Arg	Val	Val	Cys	His	Phe
				100				105					110		
Tyr	Arg	Glu	Asn	Trp	Pro	Cys	Lys	Val	Met	Asp	Xaa	His	Met	Ser	Ile
				115			120					125			
Leu	Ala	Lys	Gln	His	Ile	Glu	Thr	Arg	Phe	Val	Lys	Ile	Gln	Ala	Glu
				130			135				140				
Lys	Ser	Pro	Phe	Leu	Ala	Glu	Arg	Leu	Lys	Ile	Val	Val	Leu	Pro	Thr
				145			150			155					160
Leu	Ala	Leu	Ile	Lys	Asn	Thr	Lys	Val	Asp	Asp	Tyr	Val	Val	Gly	Phe
				165				170						175	
Asn	Glu	Leu	Gly	Gly	Lys	Asp	Asp	Phe	Ser	Thr	Glu	Asp	Leu	Glu	Glu
				180				185					190		
Arg	Ile	Ala	Arg	Ala	Gln	Val	Ile	His	Tyr	Asp	Gly	Glu	Ser	Ser	Ser
				195			200					205			
Leu	Lys	Pro	Lys	Ser	Thr	Gln	Val	Arg	Arg	Asn	Val	Arg	Gln	Ser	
				210			215				220				
Ala	Arg	Ser	Asp	Ser	Asp	Ser	Glu								
				225			230								

(2) INFORMATION FOR SEQ ID NO:597:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..211
(D) OTHER INFORMATION: / Ceres Seq. ID 1498688
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:
Met Ala Asn Pro Ile Gln Glu Ile Leu Glu Asn Gln Val Leu Thr Val
1 5 10 15
Ala Lys Ala Met Glu Asp Lys Ile Asp Asn Glu Ile Ala Ser Leu Glu
20 25 30
Lys Leu Asp Glu Asp Asp Leu Glu Val Leu Arg Glu Arg Arg Leu Lys
35 40 45
Gln Met Lys Lys Met Ala Glu Lys Lys Lys Arg Trp Ile Ser Leu Gly
50 55 60
His Gly Glu Tyr Ser Glu Ile His Ser Glu Lys Asp Phe Phe Ser Val
65 70 75 80
Val Lys Ala Ser Glu Arg Val Val Cys His Phe Tyr Arg Glu Asn Trp
85 90 95
Pro Cys Lys Val Met Asp Xaa His Met Ser Ile Leu Ala Lys Gln His
100 105 110
Ile Glu Thr Arg Phe Val Lys Ile Gln Ala Glu Lys Ser Pro Phe Leu
115 120 125
Ala Glu Arg Leu Lys Ile Val Val Leu Pro Thr Leu Ala Leu Ile Lys
130 135 140
Asn Thr Lys Val Asp Asp Tyr Val Val Gly Phe Asn Glu Leu Gly Gly
145 150 155 160
Lys Asp Asp Phe Ser Thr Glu Asp Leu Glu Glu Arg Ile Ala Arg Ala
165 170 175
Gln Val Ile His Tyr Asp Gly Glu Ser Ser Ser Leu Lys Pro Lys Ser
180 185 190
Thr Thr Gln Val Arg Arg Asn Val Arg Gln Ser Ala Arg Ser Asp Ser
195 200 205
Asp Ser Glu
210

(2) INFORMATION FOR SEQ ID NO:598:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..192
(D) OTHER INFORMATION: / Ceres Seq. ID 1498689
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:
Met Glu Asp Lys Ile Asp Asn Glu Ile Ala Ser Leu Glu Lys Leu Asp
1 5 10 15
Glu Asp Asp Leu Glu Val Leu Arg Glu Arg Arg Leu Lys Gln Met Lys
20 25 30
Lys Met Ala Glu Lys Lys Lys Arg Trp Ile Ser Leu Gly His Gly Glu
35 40 45
Tyr Ser Glu Ile His Ser Glu Lys Asp Phe Phe Ser Val Val Lys Ala
50 55 60
Ser Glu Arg Val Val Cys His Phe Tyr Arg Glu Asn Trp Pro Cys Lys
65 70 75 80
Val Met Asp Xaa His Met Ser Ile Leu Ala Lys Gln His Ile Glu Thr
85 90 95
Arg Phe Val Lys Ile Gln Ala Glu Lys Ser Pro Phe Leu Ala Glu Arg

100	105	110
Leu Lys Ile Val Val Leu Pro Thr Leu Ala Leu Ile Lys Asn Thr Lys		
115	120	125
Val Asp Asp Tyr Val Val Gly Phe Asn Glu Leu Gly Gly Lys Asp Asp		
130	135	140
Phe Ser Thr Glu Asp Leu Glu Glu Arg Ile Ala Arg Ala Gln Val Ile		
145	150	155
His Tyr Asp Gly Glu Ser Ser Ser Leu Lys Pro Lys Ser Thr Thr Gln		
165	170	175
Val Arg Arg Asn Val Arg Gln Ser Ala Arg Ser Asp Ser Asp Ser Glu		
180	185	190

(2) INFORMATION FOR SEQ ID NO:599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1418
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:

aacttagcct	tggtctctct	cttcacgcgc	atatctccgc	tgctctcttc	gtctccatca	60
gaagaagaag	ctctctgtat	ccatccatat	cgaaaaacca	gagatcggag	gaaggagaga	120
gagataccaa	ttctctgttc	tttggtttta	agggtttaga	ggagatgtca	aaccaccoga	180
agatcacatc	ggcgcatcag	aatgtggagg	agaagctaag	ggaacttcag	gagaggttct	240
gtcatcttca	agctgctagg	aaagaagggc	ggcatgggtga	ccttgcgctt	ttagaagccc	300
aaatctctca	gaattatcgg	gagtgcccaag	ctgaactcac	tgctctctct	cctgaatctt	360
ctctgttggg	tgaagggtatt	agccaattcc	ttgaggagtt	tgctctctct	ttgaattagg	420
acgaggagga	tgatgcaact	agtacgcata	aagaacatgc	tgaggcaaa	cctgatcctg	480
aggggttttc	tcaaagcttg	tgccctcctg	aatggacatc	tgagaatttt	agtcaaagtc	540
ctttcaacgg	aaatttctcc	tgccggctttg	aggatgctct	taatagcaca	gaacaacatg	600
gccagcaact	ccattatgga	tatgaagggt	ttgatccaag	cataaactcc	gtcctgatt	660
tccatgacca	aaaactcagc	agcaacttgg	atataacttc	tcagtatgat	tatatattct	720
ccgaagtgcg	tcagggaacta	gataaacagcc	cttccactaa	gcttgattct	tcggaagaga	780
ttgacaactt	tgctgaattt	tctactccat	caagtgtccg	tgtgctctca	ctcgcttttc	840
tggaacctaa	gtgtgcacta	tggaattgca	caaggcctgc	tcagggtctc	gagtggtacc	900
tggaattactg	cagtaactac	catgggactc	tagtctctga	tgaagattcg	ctcgccacag	960
caactgtatt	gagggcaggg	ggcatcagtt	tgaaagataa	tctattgatt	gatgctcttc	1020
atgcgaaagc	tcagggttaag	aattgtggga	tcccagtggt	tgaaggagct	gttaacacaa	1080
gaatgcccatg	gaacgcagca	gagctatttc	atcttgaact	ggttggaagg	gaacaactaa	1140
gagagtggct	ctcttttgac	aaacctagaa	gagcatatga	tacgggaaac	cgaaagcaaa	1200
gatcacttcc	agattacagt	ggaagaggtt	ggcatgaatc	aagaaaacaa	ctgatgaagg	1260
aaacaagaag	ccagaagaga	tcttactata	tggaaccaca	acctccaggt	ccctttgagt	1320
ggcatctctt	tgaattacaa	atcaatgaat	ctgacgcgatg	tgcggtatat	cgcttagaag	1380
ttaaagttagg	aaatggaaag	aagagtccta	agggaaag			

(2) INFORMATION FOR SEQ ID NO:600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..472
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498691

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:

Leu Ser Leu Val Leu Leu Leu His Arg Asp Ile Ser Gly Val Phe Phe
1 5 10 15
Val Ser Ile Arg Arg Ser Ser Leu Tyr Pro Ser Ile Ser Lys Asn
20 25 30
Gln Arg Ser Glu Glu Gly Glu Arg Asp Thr Asn Leu Cys Cys Phe Gly
35 40 45
Phe Lys Gly Leu Glu Glu Met Ser Asn His Pro Lys Ile Thr Ser Ala
50 55 60
His Gln Asn Val Glu Glu Lys Leu Arg Glu Leu Gln Glu Arg Phe Cys
65 70 75 80
His Leu Gln Ala Ala Arg Lys Glu Gly Arg His Gly Asp Leu Ala Leu
85 90 95
Leu Glu Ala Gln Ile Ser Gln Asn Ile Arg Glu Trp Gln Ala Glu Leu
100 105 110
Thr Ala Pro Ser Pro Glu Ser Ser Leu Leu Gly Glu Gly Ile Ser Gln
115 120 125
Phe Leu Glu Glu Phe Ala Pro Leu Leu Lys Leu Asp Glu Glu Asp Asp
130 135 140
Ala Thr Ser Thr Leu Lys Glu His Ala Gly Ala Lys Pro Asp Pro Glu
145 150 155 160
Gly Phe Ser Gln Ser Leu Cys Pro Pro Glu Trp Thr Ser Glu Asn Phe
165 170 175
Ser Gln Ser Pro Phe Asn Gly Asn Phe Ser Cys Gly Phe Glu Asp Ala
180 185 190
Leu Asn Ser Thr Glu Thr His Gly Gln Gln Leu His Tyr Gly Tyr Glu
195 200 205
Gly Phe Asp Pro Ser Ile Asn Ser Ala Pro Asp Phe His Asp Gln Lys
210 215 220
Leu Ser Ser Asn Leu Asp Ile Thr Ser Gln Tyr Asp Tyr Ile Phe Ser
225 230 235 240
Glu Val Arg Gln Glu Leu Asp Asn Ser Pro Ser Thr Lys Leu Asp Ser
245 250 255
Ser Glu Glu Ile Asp Asn Phe Ala Glu Phe Ser Thr Pro Ser Ser Val
260 265 270
Arg Val Pro Pro Ser Ala Phe Leu Gly Pro Lys Cys Ala Leu Trp Asp
275 280 285
Cys Thr Arg Pro Ala Gln Gly Ser Glu Trp Tyr Leu Asp Tyr Cys Ser
290 295 300
Asn Tyr His Gly Thr Leu Ala Leu Asn Glu Asp Ser Pro Gly Thr Ala
305 310 315 320
Pro Val Leu Arg Pro Gly Gly Ile Ser Leu Lys Asp Asn Leu Leu Ile
325 330 335
Asp Ala Leu Arg Ala Lys Thr Gln Gly Lys Asn Val Gly Ile Pro Val
340 345 350
Cys Glu Gly Ala Val Asn Thr Lys Cys Pro Trp Asn Ala Ala Glu Leu
355 360 365
Phe His Leu Glu Leu Val Glu Gly Glu Thr Ile Arg Glu Trp Leu Phe
370 375 380
Phe Asp Lys Pro Arg Arg Ala Tyr Asp Ser Gly Asn Arg Lys Gln Arg
385 390 395 400
Ser Leu Pro Asp Tyr Ser Gly Arg Gly Trp His Glu Ser Arg Lys Gln
405 410 415
Leu Met Lys Glu Gln Glu Gly Gln Lys Arg Ser Tyr Tyr Met Asp Pro
420 425 430
Gln Pro Pro Gly Pro Phe Glu Trp His Leu Phe Glu Tyr Gln Ile Asn
435 440 445
Glu Ser Asp Ala Cys Ala Leu Tyr Arg Leu Glu Leu Lys Val Gly Asn
450 455 460
Gly Lys Lys Ser Pro Lys Gly Lys
465 470

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 418 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..418
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498692
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

Met	Ser	Asn	His	Pro	Lys	Ile	Thr	Ser	Ala	His	Gln	Asn	Val	Glu	Glu
1				5				10						15	
Lys	Leu	Arg	Glu	Leu	Gln	Glu	Arg	Phe	Cys	His	Leu	Gln	Ala	Ala	Arg
			20				25						30		
Lys	Glu	Gly	Arg	His	Gly	Asp	Leu	Ala	Leu	Leu	Glu	Ala	Gln	Ile	Ser
		35				40					45				
Gln	Asn	Ile	Arg	Glu	Trp	Gln	Ala	Glu	Leu	Thr	Ala	Pro	Ser	Pro	Glu
	50				55					60					
Ser	Ser	Leu	Leu	Gly	Glu	Gly	Ile	Ser	Gln	Phe	Leu	Glu	Glu	Phe	Ala
65				70					75					80	
Pro	Leu	Leu	Lys	Leu	Asp	Glu	Glu	Asp	Asp	Ala	Thr	Ser	Thr	Leu	Lys
			85						90				95		
Glu	His	Ala	Gly	Ala	Lys	Pro	Asp	Pro	Glu	Gly	Phe	Ser	Gln	Ser	Leu
		100						105					110		
Cys	Pro	Pro	Glu	Trp	Thr	Ser	Glu	Asn	Phe	Ser	Gln	Ser	Pro	Phe	Asn
		115					120					125			
Gly	Asn	Phe	Ser	Cys	Gly	Phe	Glu	Asp	Ala	Leu	Asn	Ser	Thr	Glu	Thr
	130					135					140				
His	Gly	Gln	Gln	Leu	His	Tyr	Gly	Tyr	Glu	Gly	Phe	Asp	Pro	Ser	Ile
145				150					155					160	
Asn	Ser	Ala	Pro	Asp	Phe	His	Asp	Gln	Lys	Leu	Ser	Ser	Asn	Leu	Asp
		165						170					175		
Ile	Thr	Ser	Gln	Tyr	Asp	Tyr	Ile	Phe	Ser	Glu	Val	Arg	Gln	Glu	Leu
		180					185						190		
Asp	Asn	Ser	Pro	Ser	Thr	Lys	Leu	Asp	Ser	Ser	Glu	Glu	Ile	Asp	Asn
	195					200						205			
Phe	Ala	Glu	Phe	Ser	Thr	Pro	Ser	Ser	Val	Arg	Val	Pro	Pro	Ser	Ala
	210					215					220				
Phe	Leu	Gly	Pro	Lys	Cys	Ala	Leu	Trp	Asp	Cys	Thr	Arg	Pro	Ala	Gln
225				230					235					240	
Gly	Ser	Glu	Trp	Tyr	Leu	Asp	Tyr	Cys	Ser	Asn	Tyr	His	Gly	Thr	Leu
		245						250					255		
Ala	Leu	Asn	Glu	Asp	Ser	Pro	Gly	Thr	Ala	Pro	Val	Leu	Arg	Pro	Gly
		260						265					270		
Gly	Ile	Ser	Leu	Lys	Asp	Asn	Leu	Leu	Ile	Asp	Ala	Leu	Arg	Ala	Lys
	275					280					285				
Thr	Gln	Gly	Lys	Asn	Val	Gly	Ile	Pro	Val	Cys	Glu	Gly	Ala	Val	Asn
	290					295					300				
Thr	Lys	Cys	Pro	Trp	Asn	Ala	Ala	Glu	Leu	Phe	His	Leu	Glu	Leu	Val
305				310						315				320	
Glu	Gly	Glu	Thr	Ile	Arg	Glu	Trp	Leu	Phe	Phe	Asp	Lys	Pro	Arg	Arg
		325						330					335		
Ala	Tyr	Asp	Ser	Gly	Asn	Arg	Lys	Gln	Arg	Ser	Leu	Pro	Asp	Tyr	Ser
	340						345						350		
Gly	Arg	Gly	Trp	His	Glu	Ser	Arg	Lys	Gln	Leu	Met	Lys	Glu	Gln	Glu
	355					360						365			
Gly	Gln	Lys	Arg	Ser	Tyr	Tyr	Met	Asp	Pro	Gln	Pro	Pro	Gly	Pro	Phe
	370					375				380					
Glu	Trp	His	Leu	Phe	Glu	Tyr	Gln	Ile	Asn	Glu	Ser	Asp	Ala	Cys	Ala
385					390					395				400	

Leu Tyr Arg Leu Glu Leu Lys Val Gly Asn Gly Lys Lys Ser Pro Lys
405 410 415
Gly Lys

(2) INFORMATION FOR SEQ ID NO:602:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1896 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1896

(D) OTHER INFORMATION: / Ceres Seq. ID 1498703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

aaaaactcgc	cgccgtggag	agagaagaga	gaatggagga	tatcaggagat	ttgttgccgc	60
gaggagtcgg	tggtgcacca	ccgggattcc	gattaccctt	gaatgcagtc	gggattaatc	120
cgaagacgaa	taagagcaaa	cgtattagct	cgaaccgga	tcaaattact	gcttcgaatc	180
gtgactcgct	tgctccacca	tcgatgaaga	ttccaggaa	tcagacgata	tacatcaaga	240
cgtttggatg	tctcataat	cagagtata	gtgagtata	ggctggctcag	ctttctgcat	300
ttggctatgc	gttgacagaa	gtcccggagg	aagctgatt	atggctcatt	aacacctgta	360
ctgtgaagtc	ccttagccag	tctgcgatgt	ctactttgat	aacgaggggt	agaagtggga	420
aaaagcctct	tgtagtgca	ggatgtgttc	ctcagggcag	tcgtgatctt	aaagaactgg	480
aaggcgttag	tgtagttgga	gtcccaacaga	ttgatcgtgt	tggttgagatt	gttgaagaaa	540
ctcttaaggg	tcataagata	cggttgctga	ctcggaagac	tttgcctgcy	cttgatctcc	600
caaaagtgcy	gaggaacaat	tttatcgaaa	ttctcccat	taatgttgcy	tgtttgggtg	660
ccgtactcta	ctgcaagacc	aagcatgccc	gtggtcattt	aggaagtta	acagtgtata	720
ctcttttgga	gcgggtgaga	actgtaatct	ctgaaggagt	caaggagatt	tggttaagca	780
gcgagagac	tgagcatat	ggctgtgaca	taggagttaa	tcttccaata	ctgcttaattg	840
ctatcgttaa	ggaagttcct	tctgatcaaa	gcacaatgt	aaggattggg	atgactaatc	900
ctccctttat	tttagagcat	tgaaagaaa	tagcggcagt	gttacgtcac	ccatgtgtct	960
acacacctct	tcagtccct	gtgcaatctg	gtagcgatt	tggtgtgacg	gccatgaaca	1020
gggaatatat	agcaagttag	ttcaggactg	tggtagacac	cttaacagag	cttgtgccag	1080
gaatgcaaat	tgctactgat	ataaatatgc	gttttctcgg	tgaaaccgat	gaagattttt	1140
ctcagacagt	tgaactcatc	aaggattaca	agtttctcct	agttcatatt	tctcagtttt	1200
accccgagacc	agggacccca	gcagcaaaaga	tgaagaaggt	acaaagttaa	atagtgaagc	1260
aacgaagccg	tgaattgact	tctgtctttg	aggcttttgc	accttacacc	ggaatggagt	1320
gcagagaaga	gaggatatgg	ataactgaag	tagctactga	tggaaatcat	ttggtgggac	1380
atacgaaggg	atatgtacag	ctcttagtta	ctggaccaga	aagtatgctt	gggacttcag	1440
ctgtggcgag	gataacatct	gtggggagat	ggtcagtatt	tggggagagc	attgagacat	1500
ttagctctgc	aaatagagaa	acaaaatccc	gagaggaaac	aaagctgcct	tggtcgtcga	1560
atgttagcac	ttgttagact	gtcacttgct	ctgctgagag	ctgtggagaa	gagagatcag	1620
gagagcgctg	taacatttct	ggaatatctc	caggacaaga	tgataacaag	ggaaagtcaa	1680
agaaagaaga	gaaggaggtg	caagaggctg	tgtaaccggg	aagcagcgta	gcaaattggg	1740
gtttcattga	taaggcactt	gtctgtggag	tgttcgttaa	ctctgtcacc	attctgtgtt	1800
tggtgattag	cattgcatgt	agagttttgc	tgccgtaaat	aatcagtggt	tccgactaat	1860
gtagtcttct	gaataatttt	gcctctttac	ttgtct			

(2) INFORMATION FOR SEQ ID NO:603:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 611 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..611

(D) OTHER INFORMATION: / Ceres Seq. ID 1498704

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:

Lys Leu Ala Ala Val Glu Arg Glu Glu Arg Met Glu Asp Ile Glu Asp

1	5	10	15
Leu Leu Ala Gly Gly Val Gly Gly Ala Pro Pro Gly Phe Arg Leu Pro			
20	25	30	
Leu Asn Ala Val Gly Ile Asn Pro Lys Thr Asn Lys Ser Lys Arg Ile			
35	40	45	
Ser Ser Lys Pro Asp Gln Ile Thr Ala Ser Asn Arg Asp Ser Leu Ala			
50	55	60	
Pro Pro Ser Met Lys Ile Pro Gly Thr Gln Thr Ile Tyr Ile Lys Thr			
65	70	75	80
Phe Gly Cys Ser His Asn Gln Ser Asp Ser Glu Tyr Met Ala Gly Gln			
85	90	95	
Leu Ser Ala Phe Gly Tyr Ala Leu Thr Glu Val Pro Glu Glu Ala Asp			
100	105	110	
Leu Trp Leu Ile Asn Thr Cys Thr Val Lys Ser Pro Ser Gln Ser Ala			
115	120	125	
Met Ser Thr Leu Ile Thr Arg Gly Arg Ser Gly Lys Lys Pro Leu Val			
130	135	140	
Ile Ala Gly Cys Val Pro Gln Gly Ser Arg Asp Leu Lys Glu Leu Glu			
145	150	155	160
Gly Val Ser Val Val Gly Val Gln Gln Ile Asp Arg Val Val Glu Ile			
165	170	175	
val Glu Glu Thr Leu Lys Gly His Glu Val Arg Leu Leu Thr Arg Lys			
180	185	190	
Thr Leu Pro Ala Leu Asp Leu Pro Lys Val Arg Arg Asn Asn Phe Ile			
195	200	205	
Glu Ile Leu Pro Ile Asn Val Gly Cys Leu Gly Ala Cys Thr Tyr Cys			
210	215	220	
Lys Thr Lys His Ala Arg Gly His Leu Gly Ser Tyr Thr Val Asp Ser			
225	230	235	240
Leu Val Glu Arg Val Arg Thr Val Ile Ser Glu Gly Val Lys Glu Ile			
245	250	255	
Trp Leu Ser Ser Glu Asp Thr Gly Ala Thr Gly Arg Asp Ile Gly Val			
260	265	270	
Asn Leu Pro Ile Leu Leu Asn Ala Ile Val Lys Glu Leu Pro Ser Asp			
275	280	285	
Gln Ser Thr Met Leu Arg Ile Gly Met Thr Asn Pro Phe Ile Leu			
290	295	300	
Glu His Leu Lys Glu Ile Ala Ala Val Leu Arg His Pro Cys Val Tyr			
305	310	315	320
Thr Phe Leu His Val Pro Val Gln Ser Gly Ser Asp Ser Val Leu Thr			
325	330	335	
Ala Met Asn Arg Glu Tyr Thr Ala Ser Glu Phe Arg Thr Val Val Asp			
340	345	350	
Thr Leu Thr Glu Leu Val Pro Gly Met Gln Ile Ala Thr Asp Ile Ile			
355	360	365	
Cys Gly Phe Pro Gly Glu Thr Asp Glu Asp Phe Ser Gln Thr Val Glu			
370	375	380	
Leu Ile Lys Asp Tyr Lys Phe Pro Gln Val His Ile Ser Gln Phe Tyr			
385	390	395	400
Pro Arg Pro Gly Thr Pro Ala Ala Lys Met Lys Lys Val Gln Ser Lys			
405	410	415	
Ile Val Lys Gln Arg Ser Arg Glu Leu Thr Ser Val Phe Glu Ala Phe			
420	425	430	
Ala Pro Tyr Thr Gly Met Glu Cys Arg Glu Glu Arg Ile Trp Ile Thr			
435	440	445	
Glu Val Ala Thr Asp Gly Ile His Leu Val Gly His Thr Lys Gly Tyr			
450	455	460	
Val Gln Val Leu Val Thr Gly Pro Glu Ser Met Leu Gly Thr Ser Ala			
465	470	475	480
Met Ala Arg Ile Thr Ser Val Gly Arg Trp Ser Val Phe Gly Glu Val			
485	490	495	

Ile Glu Thr Phe Ser Ser Ala Asn Arg Glu Thr Lys Ser Arg Glu Glu
500 505 510
Thr Lys Leu Pro Cys Ser Ser Asn Val Ser Thr Cys Glu Thr Cys Thr
515 520 525
Cys Ser Ala Glu Ser Cys Gly Glu Glu Arg Ser Gly Glu Ala Cys Asn
530 535 540
Ile Ser Gly Asn Ile Ser Gly Gln Asp Asp Asn Lys Gly Lys Ser Lys
545 550 555 560
Lys Glu Glu Lys Glu Val Gln Glu Val Val Val Pro Gly Ser Ser Val
565 570 575
Ala Asn Trp Gly Phe Ile Asp Lys Ala Leu Val Cys Gly Val Phe Val
580 585 590
Ser Ser Val Thr Ile Leu Val Leu Leu Ile Ser Ile Ala Cys Arg Val
595 600 605
Leu Leu Arg
610

(2) INFORMATION FOR SEQ ID NO:604:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..601
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:

Met Glu Asp Ile Glu Asp Leu Leu Ala Gly Gly Val Gly Gly Ala Pro
1 5 10 15
Pro Gly Phe Arg Leu Pro Leu Asn Ala Val Gly Ile Asn Pro Lys Thr
20 25 30
Asn Lys Ser Lys Arg Ile Ser Ser Lys Pro Asp Gln Ile Thr Ala Ser
35 40 45
Asn Arg Asp Ser Leu Ala Pro Pro Ser Met Lys Ile Pro Gly Thr Gln
50 55 60
Thr Ile Tyr Ile Lys Thr Phe Gly Cys Ser His Asn Gln Ser Asp Ser
65 70 75 80
Glu Tyr Met Ala Gly Gln Leu Ser Ala Phe Gly Tyr Ala Leu Thr Glu
85 90 95
Val Pro Glu Glu Ala Asp Leu Trp Leu Ile Asn Thr Cys Thr Val Lys
100 105 110
Ser Pro Ser Gln Ser Ala Met Ser Thr Leu Ile Thr Arg Gly Arg Ser
115 120 125
Gly Lys Lys Pro Leu Val Ile Ala Gly Cys Val Pro Gln Gly Ser Arg
130 135 140
Asp Leu Lys Glu Leu Glu Gly Val Ser Val Val Gly Val Gln Gln Ile
145 150 155 160
Asp Arg Val Val Glu Ile Val Glu Glu Thr Leu Lys Gly His Glu Val
165 170 175
Arg Leu Leu Thr Arg Lys Thr Leu Pro Ala Leu Asp Leu Pro Lys Val
180 185 190
Arg Arg Asn Asn Phe Ile Glu Ile Leu Pro Ile Asn Val Gly Cys Leu
195 200 205
Gly Ala Cys Thr Tyr Cys Lys Thr Lys His Ala Arg Gly His Leu Gly
210 215 220
Ser Tyr Thr Val Asp Ser Leu Val Glu Arg Val Arg Thr Val Ile Ser
225 230 235 240
Glu Gly Val Lys Glu Ile Trp Leu Ser Ser Glu Asp Thr Gly Ala Tyr
245 250 255
Gly Arg Asp Ile Gly Val Asn Leu Pro Ile Leu Leu Asn Ala Ile Val

(a) Sequence alignment

Met	Lys	Ile	Pro	Gly	Thr	Gln	Thr	Ile	Tyr	Ile	Lys	Thr	Phe	Gly	Cys
1				5					10					15	
Ser	His	Asn	Gln	Ser	Asp	Ser	Glu	Tyr	Met	Ala	Gly	Gln	Leu	Ser	Ala
			20					25					30		
Phe	Gly	Tyr	Ala	Leu	Thr	Glu	Val	Pro	Glu	Glu	Ala	Asp	Leu	Trp	Leu
		35					40					45			

Ile Asn Thr Cys Thr Val Lys Ser Pro Ser Gln Ser Ala Met Ser Thr
50 55 60
Leu Ile Thr Arg Gly Arg Ser Gly Lys Lys Pro Leu Val Ile Ala Gly
65 70 75 80
Cys Val Pro Gln Gly Ser Arg Asp Leu Lys Glu Leu Glu Gly Val Ser
85 90 95
Val Val Gly Val Gln Gln Ile Asp Arg Val Val Glu Ile Val Glu Glu
100 105 110
Thr Leu Lys Gly His Glu Val Arg Leu Leu Thr Arg Lys Thr Leu Pro
115 120 125
Ala Leu Asp Leu Pro Lys Val Arg Arg Asn Asn Phe Ile Glu Ile Leu
130 135 140
Pro Ile Asn Val Gly Cys Leu Gly Ala Cys Thr Tyr Cys Lys Thr Lys
145 150 155 160
His Ala Arg Gly His Leu Gly Ser Tyr Thr Val Asp Ser Leu Val Glu
165 170 175
Arg Val Arg Thr Val Ile Ser Glu Gly Val Lys Glu Ile Trp Leu Ser
180 185 190
Ser Glu Asp Thr Gly Ala Tyr Gly Arg Asp Ile Gly Val Asn Leu Pro
195 200 205
Ile Leu Leu Asn Ala Ile Val Lys Glu Leu Pro Ser Asp Gln Ser Thr
210 215 220
Met Leu Arg Ile Gly Met Thr Asn Pro Pro Phe Ile Leu Glu His Leu
225 230 235 240
Lys Glu Ile Ala Ala Val Leu Arg His Pro Cys Val Tyr Thr Phe Leu
245 250 255
His Val Pro Val Gln Ser Gly Ser Asp Ser Val Leu Thr Ala Met Asn
260 265 270
Arg Glu Tyr Thr Ala Ser Glu Phe Arg Thr Val Val Asp Thr Leu Thr
275 280 285
Glu Leu Val Pro Gly Met Gln Ile Ala Thr Asp Ile Ile Cys Gly Phe
290 295 300
Pro Gly Glu Thr Asp Glu Asp Phe Ser Gln Thr Val Glu Leu Ile Lys
305 310 315 320
Asp Tyr Lys Phe Pro Gln Val His Ile Ser Gln Phe Tyr Pro Arg Pro
325 330 335
Gly Thr Pro Ala Ala Lys Met Lys Lys Val Gln Ser Lys Ile Val Lys
340 345 350
Gln Arg Ser Arg Glu Leu Thr Ser Val Phe Glu Ala Phe Ala Pro Tyr
355 360 365
Thr Gly Met Glu Cys Arg Glu Glu Arg Ile Trp Ile Thr Glu Val Ala
370 375 380
Thr Asp Gly Ile His Leu Val Gly His Thr Lys Gly Tyr Val Gln Val
385 390 395 400
Leu Val Thr Gly Pro Glu Ser Met Leu Gly Thr Ser Ala Met Ala Arg
405 410 415
Ile Thr Ser Val Gly Arg Trp Ser Val Phe Gly Glu Val Ile Glu Thr
420 425 430
Phe Ser Ser Ala Asn Arg Glu Thr Lys Ser Arg Glu Glu Thr Lys Leu
435 440 445
Pro Cys Ser Ser Asn Val Ser Thr Cys Glu Thr Cys Thr Cys Ser Ala
450 455 460
Glu Ser Cys Gly Glu Glu Arg Ser Gly Glu Ala Cys Asn Ile Ser Gly
465 470 475 480
Asn Ile Ser Gly Gln Asp Asp Asn Lys Gly Lys Ser Lys Lys Glu Glu
485 490 495
Lys Glu Val Gln Glu Val Val Val Pro Gly Ser Ser Val Ala Asn Trp
500 505 510
Gly Phe Ile Asp Lys Ala Leu Val Cys Gly Val Phe Val Ser Ser Val
515 520 525
Thr Ile Leu Val Leu Leu Ile Ser Ile Ala Cys Arg Val Leu Leu Arg

530

535

540

(2) INFORMATION FOR SEQ ID NO:606:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1444

(D) OTHER INFORMATION: / Ceres Seq. ID 1498718

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

```
ctctttctctt aagtgtcaaa ctcttgaaaa aactactttg aaggaaaaaa tgtctaagaa      60
gaagaagaagg agcaacaact ttaagcttct ctgttttttc ctgttttttg gtaggtttggt      120
tcagacagatg gcttcttttg gtagtaggagg cggcggttga gtaggaatcg gcggcgggcgg      180
cgggtggcggg ggcggtgggt ttggggttgg cgggtggata acaacgggtt gaaatcgtaa      240
tgctgttcca ggatcatcag ctccaaacag ggtagcttac aatgctcttc aagtttgaaa      300
atcagccatg agagaggatc catcaaatgt tctcaaaaca tgggttggat cagatgtttg      360
ttcttcaaaa ggtgtgttct gtcttggtca atctataacc tctatagatc ttaacctgc      420
aaatctcaaa ggcacattgt ccaagacctc agctttactc tcagacctca atattctcca      480
tctcaacagt aacagattct caggggcaat cccagattct tcaaatctct tagcttctct      540
tcaagaactt gatctaaagc acaataaact ctcaggctct tcccccttag tcacacteta      600
cataccaaat ctgggtttacc tggatctccg gtttaaatgt ttaacgggtt tcatccctga      660
agagcttttc aacaaacggg tagacgcgat tctctcaaat acaaatcaat tcgtcgagaa      720
aatcccaaga aacctcggaa attctccggc ttcgggtatt aatctcgaga ataacagatt      780
ttccggcgaa attccgacga gttttggtct gacgggatcg aggggttaag aagttttgct      840
tttgaataac cagtttaacc gttgtatacc ggaatctggt ggtatgttct ctgaaattga      900
agtctttgac gttagtctaa atgcaattgt gggctaatgt ccagatacga tctcttgctt      960
gtcggcgatt gaaattttga atcttgctca caataaatc tctggggagg tctctgattt      1020
ggttgttgct ttgaggaatc ttattaatct cactgttgct tcaatttct tctctgggtt      1080
tagctctgaa tgttcttcca ggggttagtt cgggttgat ttctgttgga attgtattcc      1140
cgggaggaat tgcagcggc cgcagccgga ttgttccggt tattccggcg gagctatgag      1200
ctgttttagg attccgacgc agcctttggc ttgtgtcgcg ataatgttg gattgagaga      1260
gagtaataat caatactaca ctctatctcc tccatgaaag ttctcaagt tagaagcttt      1320
tttttattaa tggttgatgc tgaatgatct atctttttt taacttatta attagttgat      1380
tagtgaccaa attaacggtt aattctctct ctgtgtaatc caatcgttgc taatgttggt      1440
ttgt
```

(2) INFORMATION FOR SEQ ID NO:607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..329

(D) OTHER INFORMATION: / Ceres Seq. ID 1498719

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

```
Met Arg Glu Asp Pro Ser Asn Val Leu Lys Thr Trp Val Gly Ser Asp
1      5      10      15
Val Cys Ser Tyr Lys Gly Val Phe Cys Ser Gly Gln Ser Ile Thr Ser
20      25      30
Ile Asp Leu Asn His Ala Asn Leu Lys Gly Thr Leu Val Lys Asp Leu
35      40      45
Ala Leu Leu Ser Asp Leu Asn Ile Leu His Leu Asn Ser Asn Arg Phe
50      55      60
Ser Gly Gln Ile Pro Asp Ser Phe Lys Ser Leu Ala Ser Leu Gln Glu
```

65	70	75	80
Leu Asp Leu Ser Asn Asn Lys Leu Ser Gly Pro Phe Pro Leu Val Thr			
	85	90	95
Leu Tyr Ile Pro Asn Leu Val Tyr Leu Asp Leu Arg Phe Asn Ser Leu			
	100	105	110
Thr Gly Phe Ile Pro Glu Glu Leu Phe Asn Lys Arg Leu Asp Ala Ile			
	115	120	125
Leu Leu Asn Asn Asn Gln Phe Val Gly Glu Ile Pro Arg Asn Leu Gly			
	130	135	140
Asn Ser Pro Ala Ser Val Ile Asn Leu Ala Asn Asn Arg Phe Ser Gly			
	145	150	155
Glu Ile Pro Thr Ser Phe Gly Leu Thr Gly Ser Arg Val Lys Glu Val			
	165	170	175
Leu Leu Leu Asn Asn Gln Leu Thr Gly Cys Ile Pro Glu Ser Val Gly			
	180	185	190
Met Phe Ser Glu Ile Glu Val Phe Asp Val Ser Tyr Asn Ala Leu Met			
	195	200	205
Gly His Val Pro Asp Thr Ile Ser Cys Leu Ser Ala Ile Glu Ile Leu			
	210	215	220
Asn Leu Ala His Asn Lys Phe Ser Gly Glu Val Pro Asp Leu Val Cys			
	225	230	235
Ser Leu Arg Asn Leu Ile Asn Leu Thr Val Ala Phe Asn Phe Phe Ser			
	245	250	255
Gly Phe Ser Ser Glu Cys Ser Ser Arg Val Ser Phe Gly Phe Asp Phe			
	260	265	270
Val Gly Asn Cys Ile Pro Gly Arg Asn Ser Gln Arg Pro Gln Pro Asp			
	275	280	285
Cys Ser Gly Tyr Ser Gly Gly Ala Met Ser Cys Phe Arg Ile Pro Thr			
	290	295	300
Gln Pro Leu Ala Cys Ala Ala Ile Ser Val Gly Leu Arg Glu Ser Asn			
	305	310	315
Asn Gln Tyr Tyr Thr Ser Ser Pro Pro			
	325		

(2) INFORMATION FOR SEQ ID NO:608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1981 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1981
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:

atcggttcacg	caaaacttca	cgattccagat	ctgtgtgtgg	cagaatttga	atcgaagcat	60
aggatacaatc	cggttaagcag	ccgttaacttg	caatcgatcg	ccgatctgga	tcoggttaaa	120
gacccctgcg	agtcccttgaa	gatatcgccg	tcctccgcga	ccgggaacag	gacccgttac	180
cggtcaacctt	ccgcttcttga	gcatttggag	cttggaactag	ccacccgagt	atccggttaac	240
cattctccta	cttccgactc	tcacacagga	cttggtgtcta	tcgacggagg	aaaaatgacg	300
gcgaagcgag	cgatcgagac	gcacgaatcc	cttgctgaca	aggtccatcg	acatcgttgt	360
cttctacttg	tgatttccat	ccccattgtg	ttgatagctc	ttgtgcttct	gttaatgccg	420
gggacgtcga	cgctccgtctc	tgatcatcag	tacacgatga	aaaaccacga	gggaggttcc	480
aattcgaggg	gtccgaagaa	ttaacgtctg	atttttgatg	ctggaagtgc	tggaagccgt	540
gtgcattgtt	actgtttcga	tcagaatttg	gatcttgttc	ctttggagaa	tgagctcgag	600
ctctctcttac	agctaaaaacc	gggttttaagt	gcatactcta	atgatccctg	gcaatcagca	660
aactctcttag	taactcttct	ggacaaagca	gaagcttccg	ttccccgtga	gttgctccca	720
aagactcctg	tcagagtttg	ggcaactgca	ggtttgagag	ctttgggtca	ccaagctctc	780
gaaaacattt	tgcaagcggg	agctctctca	aggtagaagt	aggtggaaga	ctgaggcaaa	840
tgcaagtact	gttctggatg	gtactcagga	aggatcttat	cagtggttga	caattaataa	900
cttgctaaag	actttgggaa	agccgtactc	ggacacagtt	ggagtgggtg	atctttggagg	960

ggggtcgggt	caaatggcat	atgctatacc	agaggaagat	gctgcaactg	cacaaaaacc	1020
agtagaaggc	gaggatttct	atgctcagaga	aatgtatttg	aagggacgaa	agtatttctc	1080
ctatgttcat	agctacctac	attacgggtt	actggctgct	cgggctgaga	ttttgaaagt	1140
ttctgaggac	tctaaacaac	cctgtatcgc	gactggatat	gctggtacct	acaaatatgg	1200
agggaaaagc	tttaaagctg	cagcttctcc	atccggtgca	agcttagatg	agtgcggcgc	1260
agtagctatt	aacgcactca	aagtcaataa	ttcattgtgc	acacacatga	aatgcacttt	1320
tggtggagta	tggaatgggt	gagggcggtg	tgggccagaag	aaaatgtttg	ttgcatcatt	1380
tttcttcgat	cgagccgcag	aggctgggtt	tggtgaccca	aaccaacctg	tggtgaggtg	1440
tcgaccactt	gacttttgaga	aagcggccaa	caaagcttgt	aacatgagaa	tggaagaagg	1500
gaaatcgaa	ttcccacgtg	tggaagaa	taacttctct	tacttgtgct	tggtatcttg	1560
ttaccaatat	actcttctgc	tcgatggatt	cggattgaag	ccatcacaga	caataacggt	1620
agtgaaagag	gtgaaatacg	gagattacgc	cgctggaagc	gcgtggccac	taggaagcgc	1680
catagaagca	gtatcctcac	catgaggaag	gcaattttgg	gtatttgac	taaacctctt	1740
attcttttag	tttctcccaa	aatcacocca	agcttttttt	gccttacctc	aaattttttt	1800
tatcgtaac	atcttctctta	catcaatttt	tgttacaata	atcatctaga	gaaaagagtt	1860
tcaattctta	atatacctat	aatttttttt	ttcttgtaat	ctaaactgct	taccgcatac	1920
gtaacctctg	tttctttctt	ataaaatatt	ttccttgctg	ttttttttct	tttgacgact	1980

(2) INFORMATION FOR SEQ ID NO:609:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 271 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..271

(D) OTHER INFORMATION: / Ceres Seq. ID 1498736

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:

Ile	Val	His	Ala	Lys	Leu	His	Asp	Ser	Asp	Leu	Cys	Val	Ala	Glu	Phe
1			5					10						15	
Glu	Ser	Lys	His	Arg	Ile	Asn	Pro	Val	Ser	Ser	Arg	Asn	Leu	Gln	Ser
		20						25				30			
Ile	Ala	Asp	Leu	Asp	Pro	Leu	Lys	Asp	Pro	Ser	Gln	Ser	Leu	Lys	Ile
		35					40					45			
Ser	Ala	Ser	Ser	Ala	Thr	Gly	Asn	Arg	Ile	Arg	Tyr	Arg	Ser	Pro	Ser
		50					55				60				
Ala	Ser	Glu	Leu	Leu	Glu	Ser	Gly	Leu	Ala	Thr	Gly	Leu	Ser	Gly	Asn
		65				70				75				80	
His	Ser	Pro	Thr	Ser	Asp	Ser	His	Gln	Gly	Leu	Val	Ser	Ile	Asp	Gly
			85					90					95		
Gly	Lys	Met	Thr	Ala	Lys	Arg	Ala	Ile	Gly	Arg	His	Glu	Ser	Leu	Ala
		100						105					110		
Asp	Lys	Val	His	Arg	His	Arg	Gly	Leu	Leu	Leu	Val	Ile	Ser	Ile	Pro
		115					120					125			
Ile	Val	Leu	Ile	Ala	Leu	Val	Leu	Leu	Leu	Met	Pro	Gly	Thr	Ser	Thr
		130				135					140				
Ser	Val	Ser	Val	Ile	Glu	Tyr	Thr	Met	Lys	Asn	His	Glu	Gly	Gly	Ser
		145				150				155				160	
Asn	Ser	Arg	Gly	Pro	Lys	Asn	Tyr	Ala	Val	Ile	Phe	Asp	Ala	Gly	Ser
			165					170					175		
Ser	Gly	Ser	Arg	Val	His	Val	Tyr	Cys	Phe	Asp	Gln	Asn	Leu	Asp	Leu
		180					185						190		
Val	Pro	Leu	Glu	Asn	Glu	Leu	Glu	Leu	Phe	Leu	Gln	Leu	Lys	Pro	Gly
		195					200					205			
Leu	Ser	Ala	Tyr	Pro	Asn	Asp	Pro	Arg	Gln	Ser	Ala	Asn	Ser	Leu	Val
		210				215					220				
Thr	Leu	Leu	Asp	Lys	Ala	Glu	Ala	Ser	Val	Pro	Arg	Glu	Leu	Arg	Pro
		225				230				235				240	
Lys	Thr	Pro	Val	Arg	Val	Gly	Ala	Thr	Ala	Gly	Leu	Arg	Ala	Leu	Gly

245 250 255
His Gln Ala Ser Glu Asn Ile Leu Gln Ala Gly Ala Pro Gln Arg
260 265 270

(2) INFORMATION FOR SEQ ID NO:610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..243

(D) OTHER INFORMATION: / Ceres Seq. ID 1498737

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

Met Ala Tyr Ala Ile Pro Glu Glu Asp Ala Ala Thr Ala Pro Lys Pro
1 5 10 15
Val Glu Gly Glu Asp Ser Tyr Val Arg Glu Met Tyr Leu Lys Gly Arg
20 25 30
Lys Tyr Phe Leu Tyr Val His Ser Tyr Leu His Tyr Gly Leu Leu Ala
35 40 45
Ala Arg Ala Glu Ile Leu Lys Val Ser Glu Asp Ser Asn Asn Pro Cys
50 55 60
Ile Ala Thr Gly Tyr Ala Gly Thr Tyr Lys Tyr Gly Gly Lys Ala Phe
65 70 75 80
Lys Ala Ala Ala Ser Pro Ser Gly Ala Ser Leu Asp Glu Cys Arg Arg
85 90 95
Val Ala Ile Asn Ala Leu Lys Val Asn Asn Ser Leu Cys Thr His Met
100 105 110
Lys Cys Thr Phe Gly Gly Val Trp Asn Gly Gly Gly Gly Gly Lys Gln
115 120 125
Lys Lys Met Phe Val Ala Ser Phe Phe Asp Arg Ala Ala Glu Ala
130 135 140
Gly Phe Val Asp Pro Asn Gln Pro Val Ala Glu Val Arg Pro Leu Asp
145 150 155 160
Phe Glu Lys Ala Ala Asn Lys Ala Cys Asn Met Arg Met Glu Glu Gly
165 170 175
Lys Ser Lys Phe Pro Arg Val Glu Glu Asp Asn Leu Pro Tyr Leu Cys
180 185 190
Leu Asp Leu Val Tyr Gln Tyr Thr Leu Leu Val Asp Gly Phe Gly Leu
195 200 205
Lys Pro Ser Gln Thr Ile Thr Leu Val Lys Lys Val Lys Tyr Gly Asp
210 215 220
Tyr Ala Val Glu Ala Ala Trp Pro Leu Gly Ser Ala Ile Glu Ala Val
225 230 235 240
Ser Ser Pro

(2) INFORMATION FOR SEQ ID NO:611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..217

(D) OTHER INFORMATION: / Ceres Seq. ID 1498738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:

Met Tyr Leu Lys Gly Arg Lys Tyr Phe Leu Tyr Val His Ser Tyr Leu
1 5 10 15

His Tyr Gly Leu Leu Ala Ala Arg Ala Glu Ile Leu Lys Val Ser Glu
20 25 30
Asp Ser Asn Asn Pro Cys Ile Ala Thr Gly Tyr Ala Gly Thr Tyr Lys
35 40 45
Tyr Gly Gly Lys Ala Phe Lys Ala Ala Ala Ser Pro Ser Gly Ala Ser
50 55 60
Leu Asp Glu Cys Arg Arg Val Ala Ile Asn Ala Leu Lys Val Asn Asn
65 70 75 80
Ser Leu Cys Thr His Met Lys Cys Thr Phe Gly Gly Val Trp Asn Gly
85 90 95
Gly Gly Gly Gly Gly Gln Lys Lys Met Phe Val Ala Ser Phe Phe
100 105 110
Asp Arg Ala Ala Glu Ala Gly Phe Val Asp Pro Asn Gln Pro Val Ala
115 120 125
Glu Val Arg Pro Leu Asp Phe Glu Lys Ala Ala Asn Lys Ala Cys Asn
130 135 140
Met Arg Met Glu Glu Gly Lys Ser Lys Phe Pro Arg Val Glu Glu Asp
145 150 155 160
Asn Leu Pro Tyr Leu Cys Leu Asp Leu Val Tyr Gln Tyr Thr Leu Leu
165 170 175
Val Asp Gly Phe Gly Leu Lys Pro Ser Gln Thr Ile Thr Leu Val Lys
180 185 190
Lys Val Lys Tyr Gly Asp Tyr Ala Val Glu Ala Ala Trp Pro Leu Gly
195 200 205
Ser Ala Ile Glu Ala Val Ser Ser Pro
210 215

(2) INFORMATION FOR SEQ ID NO:612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1418
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498739

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:

ttctctccgg	atatttctag	gttttcaatt	tttgttttac	cttcaaagg	tgttcctttg	60
tgatataaaa	atatagtttt	caccttcttt	caatctctgc	ggtttctaaa	tagaacattg	120
gagagatttg	tttctgcac	tgtaaatttt	gatttctttg	accatctctc	tgtttttgrt	180
ggcaacacac	gtattccaat	ccaaatcgac	aataacgcg	tctctgatgg	atatgttttg	240
gattcagtga	gaacaagaga	ttgatttttg	ttttctttaa	tcatggtgga	gccttatgag	300
acacgtaaca	acggtgaagc	atccagatgc	atcagatatt	agagttataa	ccatcacaat	360
tcacagactac	catcttcatt	atcatcgcca	ttgcttgatt	tgagagtgtt	ctatgttcaga	420
atcagtaatt	tcaagggtga	tcattcgaca	cctgaggttc	tcacattact	tcattttcct	480
ttgatctcag	attcattctt	ggagattaat	gggttagaaa	tgagcatgtg	ctctgaagga	540
gtttctcttc	agcttagcgc	tgatcgtggt	gataagaaat	ctgaagttyc	tacttttatc	600
agcaccggata	atatcaggtt	atctggtagt	gtgaagtttg	aggtttatga	taaaagtagg	660
ctgggttttg	ctggaaacgt	tgagatgtct	ggtagtaagt	gtttcaactg	tgaaactaa	720
catagcgtgta	agcgggtgaa	catgaattgt	gaagctgaga	tcactgcagg	gtctggtttc	780
ttgaagagga	aacatatgtg	tggttcggag	ttatctcttc	cattgcccaac	tattgaagtc	840
tatgtcactg	gctgtctttc	tggaactcct	atcatcttaa	cgaagactct	acagcttggt	900
ttcagaaga	agcaccggtg	agtgaactga	ttagattcga	ttcccagata	tgaaactgat	960
gagcctcata	aagggaactc	atctgagctt	gattatcagg	ttactgata	tggaagtatt	1020
aaacaagaat	atgaaggaga	acacagcgac	atgtactgga	atagagagta	cgcagatggt	1080
gaagatgggt	agatgctgtg	gttcaacgct	gggtgtgagg	ttggtgtggg	aattgttgtt	1140
gggtgctgtg	taggtcttgg	cattgggggt	ggcctctctg	tgcgtaacta	tcacatgacc	1200
accagaactc	tcagaaggag	gattatctag	tttcatctaa	atgtccctca	gcttcatcta	1260
ctctctccct	ctaaactcaa	tcctgtgcac	atcacttttg	actgcagaac	tttaagctat	1320
atagtctaag	ctaactatgc	tggttagtat	aatttttgtt	ttatgtactt	tttaactctt	1380

ttgtgccttc aaattttgaa agaaatcatt ttcccttg

(2) INFORMATION FOR SEQ ID NO:613:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..315

(D) OTHER INFORMATION: / Ceres Seq. ID 1498740

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:

Met	Val	Glu	Pro	Tyr	Glu	Thr	Arg	Asn	Asn	Gly	Glu	Ala	Ser	Gln	Met
1			5					10						15	
Ile	Arg	Tyr	Gln	Ser	Tyr	Asn	His	Asn	Ser	Arg	Leu	Pro	Ser	Ser	
			20			25					30				
Leu	Ser	Ser	Pro	Leu	Leu	Asp	Leu	Arg	Val	Phe	Tyr	Val	Arg	Ile	Ser
			35			40					45				
Asn	Phe	Lys	Val	Asp	His	Ser	Thr	Pro	Glu	Val	Leu	Thr	Ile	Thr	His
	50					55				60					
Ile	Pro	Leu	Asp	Pro	Asp	Ser	Leu	Leu	Glu	Ile	Asn	Gly	Val	Arg	Met
65					70					75				80	
Ser	Met	Tyr	Ser	Glu	Gly	Val	Ser	Ser	Gln	Leu	Arg	Arg	Asp	Arg	Val
				85						90				95	
Asp	Lys	Lys	Ser	Glu	Val	Ala	Thr	Phe	Ile	Ser	Thr	Asp	Asn	Ile	Arg
			100					105					110		
Leu	Ser	Gly	Ser	Val	Lys	Phe	Glu	Val	Tyr	Asp	Lys	Asp	Glu	Leu	Val
			115				120					125			
Leu	Ser	Gly	Thr	Leu	Glu	Met	Ser	Gly	Ser	Asn	Gly	Phe	Thr	Gly	Glu
			130			135				140					
Ser	Lys	His	Ser	Val	Lys	Arg	Trp	Asn	Met	Asn	Cys	Glu	Ala	Glu	Ile
145					150					155				160	
Thr	Ala	Gly	Ser	Gly	Phe	Leu	Lys	Glu	Lys	His	Ile	Gly	Gly	Ser	Glu
			165					170						175	
Leu	Ser	Ser	Pro	Leu	Pro	Thr	Ile	Glu	Val	Tyr	Val	Thr	Gly	Cys	Phe
			180					185					190		
Ser	Gly	Thr	Pro	Ile	Ile	Leu	Thr	Lys	Thr	Leu	Gln	Leu	Gly	Phe	Arg
			195			200						205			
Lys	Lys	His	Gly	Arg	Val	Thr	Ala	Leu	Asp	Ser	Ile	Pro	Glu	Tyr	Glu
			210			215					220				
Thr	Asp	Glu	Pro	His	Lys	Gly	Asn	Ser	Ser	Glu	Leu	Asp	Tyr	Gln	Val
225					230					235				240	
Thr	Glu	Tyr	Gly	Ser	Tyr	Lys	Gln	Glu	Tyr	Glu	Gly	Glu	His	Ser	Asp
			245					250					255		
Met	Tyr	Trp	Asn	Arg	Glu	Tyr	Ala	Asp	Gly	Glu	Asp	Gly	Glu	Met	Ser
			260					265					270		
Trp	Phe	Asn	Ala	Gly	Val	Arg	Val	Gly	Val	Gly	Ile	Gly	Leu	Gly	Val
			275			280						285			
Cys	Val	Gly	Leu	Gly	Ile	Gly	Val	Gly	Leu	Leu	Val	Arg	Thr	Tyr	Gln
			290			295					300				
Ser	Thr	Thr	Arg	Asn	Phe	Arg	Arg	Arg	Ile	Ile					
305				310					315						

(2) INFORMATION FOR SEQ ID NO:614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..300
(D) OTHER INFORMATION: / Ceres Seq. ID 1498741

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

Met Ile Arg Tyr Gln Ser Tyr Asn His His Asn Ser Arg Leu Pro Ser
1 5 10 15
Ser Leu Ser Ser Pro Leu Leu Asp Leu Arg Val Phe Tyr Val Arg Ile
20 25 30
Ser Asn Phe Phe Val Asp His Ser Thr Pro Glu Val Leu Thr Ile Thr
35 40 45
His Ile Pro Leu Asp Pro Asp Ser Leu Leu Glu Ile Asn Gly Val Arg
50 55 60
Met Ser Met Tyr Ser Glu Gly Val Ser Ser Gln Leu Arg Arg Asp Arg
65 70 75 80
Val Asp Lys Lys Ser Glu Val Ala Thr Phe Ile Ser Thr Asp Asn Ile
85 90 95
Arg Leu Ser Gly Ser Val Lys Phe Glu Val Tyr Asp Lys Asp Glu Leu
100 105 110
Val Leu Ser Gly Thr Leu Glu Met Ser Gly Ser Asn Gly Phe Thr Gly
115 120 125
Glu Ser Lys His Ser Val Lys Arg Trp Asn Met Asn Cys Glu Ala Glu
130 135 140
Ile Thr Ala Gly Ser Gly Phe Leu Lys Glu Lys His Ile Gly Gly Ser
145 150 155 160
Glu Leu Ser Ser Pro Leu Pro Thr Ile Glu Val Tyr Val Thr Gly Cys
165 170 175
Phe Ser Gly Thr Pro Ile Ile Leu Thr Lys Thr Leu Gln Leu Gly Phe
180 185 190
Arg Lys Lys His Gly Arg Val Thr Ala Leu Asp Ser Ile Pro Glu Tyr
195 200 205
Glu Thr Asp Glu Pro His Lys Gly Asn Ser Ser Glu Leu Asp Tyr Gln
210 215 220
Val Thr Glu Tyr Gly Ser Tyr Lys Gln Glu Tyr Glu Gly Glu His Ser
225 230 235 240
Asp Met Tyr Trp Asn Arg Glu Tyr Ala Asp Gly Glu Asp Gly Glu Met
245 250 255
Ser Trp Phe Asn Ala Gly Val Arg Val Gly Val Gly Ile Gly Leu Gly
260 265 270
Val Cys Val Gly Leu Gly Ile Gly Val Gly Leu Leu Val Arg Thr Tyr
275 280 285
Gln Ser Thr Thr Arg Asn Phe Arg Arg Ile Ile
290 295 300

(2) INFORMATION FOR SEQ ID NO:615:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..236
(D) OTHER INFORMATION: / Ceres Seq. ID 1498742

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

Met Ser Met Tyr Ser Glu Gly Val Ser Ser Gln Leu Arg Arg Asp Arg
1 5 10 15
Val Asp Lys Lys Ser Glu Val Ala Thr Phe Ile Ser Thr Asp Asn Ile
20 25 30
Arg Leu Ser Gly Ser Val Lys Phe Glu Val Tyr Asp Lys Asp Glu Leu
35 40 45
Val Leu Ser Gly Thr Leu Glu Met Ser Gly Ser Asn Gly Phe Thr Gly

50	55	60
Glu Ser Lys His Ser Val Lys Arg Trp Asn Met Asn Cys Glu Ala Glu		
65	70	75
Ile Thr Ala Gly Ser Gly Phe Leu Lys Glu Lys His Ile Gly Gly Ser		80
	85	90
Glu Leu Ser Ser Pro Leu Pro Thr Ile Glu Val Tyr Val Thr Gly Cys		95
	100	105
Phe Ser Gly Thr Pro Ile Ile Leu Thr Lys Thr Leu Gln Leu Gly Phe		110
	115	120
Arg Lys Lys His Gly Arg Val Thr Ala Leu Asp Ser Ile Pro Glu Tyr		125
	130	135
Glu Thr Asp Glu Pro His Lys Gly Asn Ser Ser Glu Leu Asp Tyr Gln		140
	145	150
Val Thr Glu Tyr Gly Ser Tyr Lys Gln Glu Tyr Glu Gly Glu His Ser		155
	165	170
Asp Met Tyr Trp Asn Arg Glu Tyr Ala Asp Gly Glu Asp Gly Glu Met		175
	180	185
Ser Trp Phe Asn Ala Gly Val Arg Val Gly Val Gly Ile Gly Leu Gly		190
	195	200
Val Cys Val Gly Leu Gly Ile Gly Val Gly Leu Leu Val Arg Thr Tyr		205
	210	215
Gln Ser Thr Thr Arg Asn Phe Arg Arg Arg Ile Ile		220
	225	230
		235

(2) INFORMATION FOR SEQ ID NO:616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1608 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1608

(D) OTHER INFORMATION: / Ceres Seq. ID 1498743

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

aatcgagagat	ttctctcct	tctcttttca	gcgcgcaatc	gccgcgcgcaa	tcttcttcac	60
cgccctccgt	tctacatcga	cgggtgtttgc	cgtaactctc	gtcaaaactct	cagaattttgc	120
ttaagtatac	cacctaaact	gagacgctat	gaacggtttc	tcagttcag	ccactatctt	180
cagtcgagcc	tcgctagctc	ttctctcgag	caatggcttc	aaacgatttt	cattcgtttc	240
ttcgtttttc	ttctccgcgc	cttactctcc	acctaaaaatg	aggaagcgctc	gctaccccaat	300
cgctctcgct	gttgatattg	gtggcgctgc	aatcgctaga	aatgatgtgg	tgagagagga	360
tgatccaaca	aataatgtac	cgatctcgat	tttctctaaa	ctaggaatac	agctacacag	420
aagagataag	atcccgattg	gtatcttaaa	aaacgctatc	tacgattact	ttgattccaa	480
ttactcaaac	aagtttgaga	agtttgaaga	cctttcccca	attgttacca	caaagcaaaa	540
ctttgatgat	gtgctagtc	ctgctgatca	tgtaagcaga	agtcttaagt	acacgtacta	600
tttagactga	caaaactgtt	tgagatgtca	tacgagtgtc	caccaagctg	agctgttgag	660
gaaaggtcat	agtcgtttcc	ttgtaacccg	ggatgtttac	cgaagagatt	ctattgaact	720
tactcaatt	cgggtttttc	atcagatgga	aggtttttgt	gttttctctc	ctgaggactg	780
gaacgggtct	ggcaaggatt	ccaactttgt	tgctgctgag	gatttgaaga	aatgtcttga	840
gggattggca	gcccaacttat	ttggttcggt	ggagatgaga	tggttgata	oatattcccc	900
atttaccatt	ccatcttttg	agcttgagat	atattttaag	gaagaactgtg	tggaagtttt	960
gggtctgtgg	gtgaccgagc	aagtaattct	gaacacaaat	ggataagaaa	ataatgtttg	1020
ttgggccttc	ggacttgagc	ttgagagact	tgctatgttt	ttgttgaca	tacctgatat	1080
acgatttttc	tggtcatccg	atgaacgatt	cacgtcccag	tttggaaaag	gagaacttgg	1140
agtgaatttc	aagccatatt	caaatgatcc	tcctttgtac	aaggacatca	gtttctggat	1200
aagtgtattg	ttcacagaga	ataatttttg	tgaagtgttt	agaggaattg	ctggggatct	1260
tgttgaagag	gtgaagttaa	ttgaccaatt	caccaataag	aagaaagggc	tgacgagtca	1320
ttgttacaga	atcgtgttcc	gttccatgga	gcggtctctt	accgagcagg	aggtcaatga	1380
ctctgcagagt	aaagtgcgtg	atgaggtgca	gaagaagcta	gtgttcgaat	taaggtgaga	1440
attttgaaaa	gagtagcgtt	gttcagacga	gtgatgaata	ttgaagtttt	ggcattgtta	1500
ttcctacata	aactttattt	acttctggca	gaattgcatt	accctcaaaa	aaatatatgt	1560

acattggttt cgttattcta aaggaatgaa aaataagggtg tccgtttt

(2) INFORMATION FOR SEQ ID NO:617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..285
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498744

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:

Met	Thr	Val	Phe	Ser	Val	Gln	Ser	Thr	Ile	Phe	Ser	Arg	Ala	Ser	Val
1			5					10						15	
Ala	Leu	Leu	Ser	Ser	Asn	Gly	Phe	Lys	Arg	Phe	Ser	Phe	Val	Ser	Ser
			20				25						30		
Phe	Ser	Ser	Ser	Ala	Ala	Tyr	Ser	Pro	Pro	Lys	Met	Arg	Lys	Arg	Arg
			35				40				45				
Tyr	Pro	Ile	Val	Ser	Ala	Val	Asp	Ile	Gly	Gly	Val	Ala	Ile	Ala	Arg
			50				55				60				
Asn	Asp	Val	Val	Arg	Glu	Asp	Asp	Pro	Thr	Asn	Asn	Val	Pro	Asp	Ser
65				70				75						80	
Ile	Phe	Ser	Lys	Leu	Gly	Xaa	Gln	Leu	His	Arg	Arg	Asp	Lys	His	Pro
				85				90					95		
Ile	Gly	Ile	Leu	Lys	Asn	Ala	Ile	Tyr	Asp	Tyr	Phe	Asp	Ser	Asn	Tyr
				100				105					110		
Ser	Asn	Lys	Phe	Glu	Lys	Phe	Glu	Asp	Leu	Ser	Pro	Ile	Val	Thr	Thr
				115				120				125			
Lys	Gln	Asn	Phe	Asp	Asp	Val	Leu	Val	Pro	Ala	Asp	His	Val	Ser	Arg
						135					140				
Ser	Leu	Asn	Asp	Thr	Tyr	Tyr	Val	Asp	Ser	Gln	Thr	Val	Leu	Arg	Cys
145					150				155					160	
His	Thr	Ser	Ala	His	Gln	Ala	Glu	Leu	Leu	Arg	Lys	Gly	His	Ser	Arg
				165				170					175		
Phe	Leu	Val	Thr	Gly	Asp	Val	Tyr	Arg	Arg	Asp	Ser	Ile	Asp	Ser	Thr
				180				185					190		
His	Tyr	Pro	Val	Phe	His	Gln	Met	Glu	Gly	Phe	Cys	Val	Phe	Ser	Pro
				195			200					205			
Glu	Asp	Trp	Asn	Gly	Ser	Gly	Lys	Asp	Ser	Thr	Leu	Tyr	Ala	Ala	Glu
						215					220				
Asp	Leu	Lys	Lys	Cys	Leu	Glu	Gly	Leu	Ala	Arg	His	Leu	Phe	Gly	Ser
225					230				235					240	
Val	Glu	Met	Arg	Trp	Val	Asp	Thr	Tyr	Phe	Pro	Phe	Thr	Asn	Pro	Ser
				245				250					255		
Phe	Glu	Leu	Glu	Ile	Tyr	Phe	Lys	Glu	Asp	Trp	Leu	Glu	Val	Leu	Gly
				260				265					270		
Cys	Gly	Val	Thr	Glu	Gln	Val	Ile	Leu	Lys	Gln	Ser	Gly			
				275			280					285			

(2) INFORMATION FOR SEQ ID NO:618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..242
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:618:

```

Met Arg Lys Arg Arg Tyr Pro Ile Val Ser Ala Val Asp Ile Gly Gly
1          5          10          15
Val Ala Ile Ala Arg Asn Asp Val Val Arg Glu Asp Asp Pro Thr Asn
          20          25          30
Asn Val Pro Asp Ser Ile Phe Ser Lys Leu Gly Xaa Gln Leu His Arg
          35          40          45
Arg Asp Lys His Pro Ile Gly Ile Leu Lys Asn Ala Ile Tyr Asp Tyr
          50          55          60
Phe Asp Ser Asn Tyr Ser Asn Lys Phe Glu Lys Phe Glu Asp Leu Ser
65          70          75          80
Pro Ile Val Thr Thr Lys Gln Asn Phe Asp Asp Val Leu Val Pro Ala
          85          90          95
Asp His Val Ser Arg Ser Leu Asn Asp Thr Tyr Tyr Val Asp Ser Gln
          100          105          110
Thr Val Leu Arg Cys His Thr Ser Ala His Gln Ala Glu Leu Leu Arg
          115          120          125
Lys Gly His Ser Arg Phe Leu Val Thr Gly Asp Val Tyr Arg Arg Asp
          130          135          140
Ser Ile Asp Ser Thr His Tyr Pro Val Phe His Gln Met Glu Gly Phe
145          150          155          160
Cys Val Phe Ser Pro Glu Asp Trp Asn Gly Ser Gly Lys Asp Ser Thr
          165          170          175
Leu Tyr Ala Ala Glu Asp Leu Lys Lys Cys Leu Glu Gly Leu Ala Arg
          180          185          190
His Leu Phe Gly Ser Val Glu Met Arg Trp Val Asp Thr Tyr Phe Pro
          195          200          205
Phe Thr Asn Pro Ser Phe Glu Leu Glu Ile Tyr Phe Lys Glu Asp Trp
          210          215          220
Leu Glu Val Leu Gly Cys Gly Val Thr Glu Gln Val Ile Leu Lys Gln
225          230          235          240
Ser Gly

```

(2) INFORMATION FOR SEQ ID NO:619:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1451

(D) OTHER INFORMATION: / Ceres Seq. ID 1498746

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:

```

accagaagaa gagccacaca ctcacaaatt aaaaagagag agagagagag agagacagag      60
agagagagag attctgcgga ggagctcttt cttcgtaggg tgttcatcgt tattaacggt      120
atcgccctca cgtcagctcc attctccagaa acatggggtc agtgcggttc atgcgggttc      180
ctactctctc caagaaatcg gaaaccgaca ccacaaagcg tgtgccgtgc gagaaccgac      240
ctttctcggt gggagatctg aagaagacaa tcccgccgca ttgtttcaaa cgctcaatcc      300
ctcgtctctt ctctacacct atcagtgaca tcattatagc ctcagtcttc coactctatt      360
ccaccaatta ctctctctct ctcctctcag ctctctctta cttggtgttg coactctatt      420
gggcctgtca agcgtgtgtc ctaactggta tctgggtcat agcccaagaa tgcggtcacc      480
acgcattcag cgcattacca tggctgggat acacagttgg tcttatcttc catctcttcc      540
tcctcgtccc ttactctctc ttgaagtata gtcctgcgcc tcaccattcc aacactggat      600
ccctcgaagg agatgaagta ttgttcccaa agcagaaatc agcaatcaag tggtagcgga      660
aataacctca caacctcttt ggaagcatca tgatgttaac cgtccagttt gtcctcgggt      720
ggcccttgta ctttagcctt aacgtctctg gcagaccgta tgacgggttc gcttgccatt      780
tcttccccaa cgctcccatc tacaatgacc gagaacgcct tgcgtgcaca gggatggcct      900
cggttatctc agcgcctctg ttgggtcttt acogttacgc tgcgttcttc gtcttgatca      960
cgatgatctg cctctacgga gtaccgcttc tgatagttaa ttcactcagag tgggactggc      1020
cttacttgca gcacactcat cctcgtttgc ctcaetacga

```

tcaggggagc ttgggtacc gtagacagag actacggaat ctgaacaag gtgttcacaa 1080
acattacaga cacacacgtg gctcatcacc tgttctcgac aatgcgcgat tataacgcaa 1140
tggaagctac aaaggcgata aagccaattc tgggagacta ttaccagttc gatggaacac 1200
cgtgttatgt ggcgatgtat agggaggcaa aggagtgtat ctatgtagaa ccggacaggg 1260
aaaggtgacaa gaaagggtgtg tactgtgtaca acaataagtt atgaggatga tggtagaaga 1320
attgtcgact ttctctctgt ctgtttgtct tttgttaaag aagctatgct tcgttttaat 1380
aatcttattg tccattttgt tgtgttatga cattttgget gctcattatg ttatgtggga 1440
agtttagtt c

(2) INFORMATION FOR SEQ ID NO:620:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..383
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498747

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620:

Met	Gly	Ala	Gly	Arg	Met	Pro	Val	Pro	Thr	Ser	Ser	Lys	Lys	Ser
1		5					10						15	
Glu	Thr	Asp	Thr	Lys	Arg	Val	Pro	Cys	Glu	Lys	Pro	Pro	Phe	Ser
		20					25					30		
Val	Gly	Asp	Leu	Lys	Lys	Ala	Ile	Pro	Pro	His	Cys	Phe	Lys	Arg
		35				40						45		
Ile	Pro	Arg	Ser	Phe	Ser	Tyr	Leu	Ile	Ser	Asp	Ile	Ile	Ala	Ser
		50				55					60			
Cys	Phe	Tyr	Tyr	Val	Ala	Thr	Asn	Tyr	Phe	Ser	Leu	Leu	Pro	Gln
65				70					75					80
Leu	Ser	Tyr	Leu	Ala	Trp	Pro	Leu	Tyr	Trp	Ala	Cys	Gln	Gly	Cys
				85					90				95	
Leu	Thr	Gly	Ile	Trp	Val	Ile	Ala	His	Glu	Cys	Gly	His	His	Ala
				100				105					110	
Ser	Asp	Tyr	Gln	Trp	Leu	Asp	Asp	Thr	Val	Gly	Leu	Ile	Phe	His
				115				120					125	
Phe	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Arg
				130				135				140		
His	Ser	Asn	Thr	Gly	Ser	Leu	Glu	Arg	Asp	Glu	Val	Phe	Val	Pro
145					150					155				160
Gln	Lys	Ser	Ala	Ile	Lys	Trp	Tyr	Gly	Lys	Tyr	Leu	Asn	Asn	Pro
				165					170					175
Gly	Arg	Ile	Met	Met	Leu	Thr	Val	Gln	Phe	Val	Leu	Gly	Trp	Pro
				180				185					190	
Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	Gly	Phe	Ala
				195				200				205		
His	Phe	Phe	Pro	Asn	Ala	Pro	Ile	Tyr	Asn	Asp	Arg	Glu	Arg	Leu
				210				215				220		
Ile	Tyr	Leu	Ser	Asp	Ala	Gly	Ile	Leu	Ala	Val	Cys	Phe	Gly	Leu
225					230					235				240
Arg	Tyr	Ala	Ala	Ala	Gln	Gly	Met	Ala	Ser	Met	Ile	Cys	Leu	Tyr
				245						250			255	
Val	Pro	Leu	Leu	Ile	Val	Asn	Ala	Phe	Leu	Val	Leu	Ile	Thr	Tyr
				260				265					270	
Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Ser	Glu	Trp
				275				280				285		
Trp	Leu	Arg	Gly	Ala	Leu	Ala	Thr	Val	Asp	Arg	Asp	Tyr	Gly	Ile
				290				295				300		
Asn	Lys	Val	Phe	His	Asn	Ile	Thr	Asp	Thr	His	Val	Ala	His	His
305					310					315				320
Phe	Ser	Thr	Met	Pro	His	Tyr	Asn	Ala	Met	Glu	Ala	Thr	Lys	Ala

			325						330						335
Lys	Pro	Ile	Leu	Gly	Asp	Tyr	Tyr	Gln	Phe	Asp	Gly	Thr	Pro	Trp	Tyr
			340						345					350	
Val	Ala	Met	Tyr	Arg	Glu	Ala	Lys	Glu	Cys	Ile	Tyr	Val	Glu	Pro	Asp
			355				360					365			
Arg	Glu	Gly	Asp	Lys	Lys	Gly	Val	Tyr	Trp	Tyr	Asn	Asn	Lys	Leu	
			370				375				380				

(2) INFORMATION FOR SEQ ID NO:621:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..377
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498748

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:621:

Met	Pro	Val	Pro	Thr	Ser	Ser	Lys	Lys	Ser	Glu	Thr	Asp	Thr	Thr	Lys
1			5					10						15	
Arg	Val	Pro	Cys	Glu	Lys	Pro	Pro	Phe	Ser	Val	Gly	Asp	Leu	Lys	Lys
			20				25						30		
Ala	Ile	Pro	Pro	His	Cys	Phe	Lys	Arg	Ser	Ile	Pro	Arg	Ser	Phe	Ser
			35				40					45			
Tyr	Leu	Ile	Ser	Asp	Ile	Ile	Ile	Ala	Ser	Cys	Phe	Tyr	Tyr	Val	Ala
			50				55					60			
Thr	Asn	Tyr	Phe	Ser	Leu	Leu	Pro	Gln	Pro	Leu	Ser	Tyr	Leu	Ala	Trp
			65				70				75			80	
Pro	Leu	Tyr	Trp	Ala	Cys	Gln	Gly	Cys	Val	Leu	Thr	Gly	Ile	Trp	Val
			85						90				95		
Ile	Ala	His	Glu	Cys	Gly	His	His	Ala	Phe	Ser	Asp	Tyr	Gln	Trp	Leu
			100					105					110		
Asp	Asp	Thr	Val	Gly	Leu	Ile	Phe	His	Ser	Phe	Leu	Leu	Val	Pro	Tyr
			115					120				125			
Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Arg	His	His	Ser	Asn	Thr	Gly	Ser
			130				135				140				
Leu	Glu	Arg	Asp	Glu	Val	Phe	Val	Pro	Lys	Gln	Lys	Ser	Ala	Ile	Lys
			145				150				155			160	
Trp	Tyr	Gly	Lys	Tyr	Leu	Asn	Asn	Pro	Leu	Gly	Arg	Ile	Met	Met	Leu
			165						170				175		
Thr	Val	Gln	Phe	Val	Leu	Gly	Trp	Pro	Leu	Tyr	Leu	Ala	Phe	Asn	Val
			180					185					190		
Ser	Gly	Arg	Pro	Tyr	Asp	Gly	Phe	Ala	Cys	His	Phe	Phe	Pro	Asn	Ala
			195				200					205			
Pro	Ile	Tyr	Asn	Asp	Arg	Glu	Arg	Leu	Gln	Ile	Tyr	Leu	Ser	Asp	Ala
			210				215					220			
Gly	Ile	Leu	Ala	Val	Cys	Phe	Gly	Leu	Tyr	Arg	Tyr	Ala	Ala	Ala	Gln
			225				230				235			240	
Gly	Met	Ala	Ser	Met	Ile	Cys	Leu	Tyr	Gly	Val	Pro	Leu	Leu	Ile	Val
			245						250				255		
Asn	Ala	Phe	Leu	Val	Leu	Ile	Thr	Tyr	Leu	Gln	His	Thr	His	Pro	Ser
			260					265					270		
Leu	Pro	His	Tyr	Asp	Ser	Ser	Glu	Trp	Asp	Trp	Leu	Arg	Gly	Ala	Leu
			275				280					285			
Ala	Thr	Val	Asp	Arg	Asp	Tyr	Gly	Ile	Leu	Asn	Lys	Val	Phe	His	Asn
			290				295				300				
Ile	Thr	Asp	Thr	His	Val	Ala	His	His	Leu	Phe	Ser	Thr	Met	Pro	His
			305				310				315			320	
Tyr	Asn	Ala	Met	Glu	Ala	Thr	Lys	Ala	Ile	Lys	Pro	Ile	Leu	Gly	Asp
			325					330					335		

Tyr Tyr Gln Phe Asp Gly Thr Pro Trp Tyr Val Ala Met Tyr Arg Glu
340 345 350
Ala Lys Glu Cys Ile Tyr Val Glu Pro Asp Arg Glu Gly Asp Lys Lys
355 360 365
Gly Val Tyr Trp Tyr Asn Asn Lys Leu
370 375

(2) INFORMATION FOR SEQ ID NO:622:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..204
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:622:

Met	Met	Leu	Thr	Val	Gln	Phe	Val	Leu	Gly	Trp	Pro	Leu	Tyr	Leu	Ala
1				5					10					15	
Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	Gly	Phe	Ala	Cys	His	Phe	Phe
				20				25					30		
Pro	Asn	Ala	Pro	Ile	Tyr	Asn	Asp	Arg	Glu	Arg	Leu	Gln	Ile	Tyr	Leu
				35				40				45			
Ser	Asp	Ala	Gly	Ile	Leu	Ala	Val	Cys	Phe	Gly	Leu	Tyr	Arg	Tyr	Ala
				50				55				60			
Ala	Ala	Gln	Gly	Met	Ala	Ser	Met	Ile	Cys	Leu	Tyr	Gly	Val	Pro	Leu
				65				70				75		80	
Leu	Ile	Val	Asn	Ala	Phe	Leu	Val	Leu	Ile	Thr	Tyr	Leu	Gln	His	Thr
				85				90					95		
His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Ser	Glu	Trp	Asp	Trp	Leu	Arg
				100				105					110		
Gly	Ala	Leu	Ala	Thr	Val	Asp	Arg	Asp	Tyr	Gly	Ile	Leu	Asn	Lys	Val
				115				120				125			
Phe	His	Asn	Ile	Thr	Asp	Thr	His	Val	Ala	His	His	Leu	Phe	Ser	Thr
				130				135				140			
Met	Pro	His	Tyr	Asn	Ala	Met	Glu	Ala	Thr	Lys	Ala	Ile	Lys	Pro	Ile
				145				150				155			160
Leu	Gly	Asp	Tyr	Tyr	Gln	Phe	Asp	Gly	Thr	Pro	Trp	Tyr	Val	Ala	Met
				165				170					175		
Tyr	Arg	Glu	Ala	Lys	Glu	Cys	Ile	Tyr	Val	Glu	Pro	Asp	Arg	Glu	Gly
				180				185					190		
Asp	Lys	Lys	Gly	Val	Tyr	Trp	Tyr	Asn	Asn	Lys	Leu				
				195				200							

(2) INFORMATION FOR SEQ ID NO:623:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1813 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1813
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:

ctcccttaga	gagagcgtgc	cattttttatt	tttctctttc	ttctctcatt	tttattttct	60
tttctttttt	ttcacccttt	tttttctctt	ttttttcttt	cttctctctt	ttacttgatt	120
ttgaaacctta	gcttaagggg	aattttctcg	ggaaacaaaa	gagatatttt	tatcgagtg	180
agaaagaaac	acaaaaaatg	cagaatcaaa	ggcttattaa	gcagcaacaa	caacaacac	240
aacagcaaca	tcaacaagct	atgattcaac	aagctatgat	gcaacaacat	ccttctcttt	300

atcatctcgtg	tggtatggct	cctcctcaga	tggagccttt	accaagtgga	aaccttcttc	360
ctggtttttg	tcacaactact	tgccgtagtg	tgtatgctgg	aaacattcat	acgcagggtca	420
cagagattct	tcttcaagag	atttttgcaa	gtactggtcc	tattgaaagc	tgtaaaactca	480
tcagaaaagg	taagtcatca	tatggatttg	ttcactactt	tgatcgaaag	tgtgctagta	540
tggtctataat	gactcttaac	ggaaggcata	tatttggaca	gcctatgaaa	gttaattggg	600
cgatgcaac	tggtcaaagg	gaagatcat	caagtcattt	caacattttt	gttgagagtc	660
ttagtcgca	ggttactagt	gcagcattgt	ttgatagctt	ttctgctttt	aacagctgct	720
cggaagcaag	agtaattgtg	gaccagaaaa	ctggacgctc	aagaggcttt	ggttttgttt	780
ccttccgtaa	tcagcaggat	gctcaaaactg	ccattaatga	gatgaatggg	aaatgggttaa	840
gtagcagaca	gatcagatgc	aactggggcga	caaaaagggtg	tacttttggc	gaggacaaaac	900
atagctctga	tgaaaaaagg	gtgttagaac	ttactaacgg	atcttcagag	gatgttagag	960
agctgtcaaa	tgaaagatgc	cctgaaaaaca	atctcaattt	tacaactgtc	tatgttagaaa	1020
atctctctcc	agaaaatact	cagcttgatc	tacaccgtct	attctatacc	cttggtgtctg	1080
gagtgatcga	agaggtccgt	gtccagcgag	acaaaagggtt	tggttttggg	agatataagaa	1140
ctcatgcaac	ggctgtctct	gctattcaga	tgggcaacgc	tcagcccttc	ctctttagca	1200
gacagcataag	gtgttctctg	ggaaaacaaac	caactccatc	aggcaacgac	tcaaaaccac	1260
ttccccacc	agccccggca	tcagtcctct	ctctgtctgc	aatggacctc	ttagcctaac	1320
agaggcaact	ggctctagcc	aagatgcac	ctcaggctca	acattctctg	aggcaagcag	1380
gtcttggagt	caatgttgct	ggaggaactg	cagctatgta	tgatgtgggc	tatcagaagt	1440
tagctgcccc	ccatcagcag	ctcatgtact	atcagtaata	aaacctcttc	actggtctctg	1500
agataacctt	tctgttttct	ttctttttct	tttataaact	tttataaact	tctgtgtttt	1560
tctagacctt	cctgtttcaa	gagtctttat	gtatgtgtct	ctttcattta	aagccgttgg	1620
ttttttttat	gtatgcagag	ctttatgctc	agtttggtaac	ctatagggtc	tacttggatt	1680
gtaagccaag	caataagaca	acatcaata	aaaggggatt	tggtttctg	gggttaagt	1740
ttgttgggt	tctgtaata	taggtttgaa	acaaagtaat	ttgtctttta	taaaagttt	1800
atagtttcat	ttc					

(2) INFORMATION FOR SEQ ID NO:624:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 426 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..426

(D) OTHER INFORMATION: / Ceres Seq. ID 1498751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:

Met	Gln	Asn	Gln	Arg	Leu	Ile	Lys	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln
1				5				10					15		
Gln	His	Gln	Gln	Ala	Met	Ile	Gln	Gln	Ala	Met	Met	Gln	Gln	His	Pro
				20				25				30			
Ser	Leu	Tyr	His	Pro	Gly	Val	Met	Ala	Pro	Pro	Gln	Met	Glu	Pro	Leu
		35				40					45				
Pro	Ser	Gly	Asn	Leu	Pro	Pro	Gly	Phe	Asp	Pro	Thr	Thr	Cys	Arg	Ser
		50				55				60					
Val	Tyr	Ala	Gly	Asn	Ile	His	Thr	Gln	Val	Thr	Glu	Ile	Leu	Leu	Gln
		65				70				75				80	
Glu	Ile	Phe	Ala	Ser	Thr	Gly	Pro	Ile	Glu	Ser	Cys	Lys	Leu	Ile	Arg
				85				90						95	
Lys	Asp	Lys	Ser	Ser	Tyr	Gly	Phe	Val	His	Tyr	Phe	Asp	Arg	Arg	Cys
				100				105					110		
Ala	Ser	Met	Ala	Ile	Met	Thr	Leu	Asn	Gly	Arg	His	Ile	Phe	Gly	Gln
		115				120						125			
Pro	Met	Lys	Val	Asn	Trp	Ala	Tyr	Ala	Thr	Gly	Gln	Arg	Glu	Asp	Thr
		130				135					140				
Ser	Ser	His	Phe	Asn	Ile	Phe	Val	Gly	Asp	Leu	Ser	Pro	Glu	Val	Thr
		145				150				155				160	
Asp	Ala	Ala	Leu	Phe	Asp	Ser	Phe	Ser	Ala	Phe	Asn	Ser	Cys	Ser	Asp
				165				170						175	
Ala	Arg	Val	Met	Trp	Asp	Gln	Lys	Thr	Gly	Arg	Ser	Arg	Gly	Phe	Gly

180										185										190									
Phe	Val	Ser	195	Phe	Arg	Asn	Gln	Gln	200	Asp	Ala	Gln	Thr	Ala	205	Ile	Asn	Glu											
Met	Asn	Gly	210	Lys	Trp	Val	Ser	Ser	215	Arg	Gln	Ile	Arg	220	Cys	Asn	Trp	Ala											
Thr	Lys	Gly	225	Ala	Thr	Phe	Gly	Glu	230	Asp	Lys	His	Ser	235	Ser	Asp	Glu	Lys	240										
Ser	Val	Val	250	Glu	Leu	Thr	Asn	Gly	260	Ser	Ser	Glu	Asp	265	Gly	Arg	Glu	Leu	270										
Ser	Asn	Glu	275	Asp	Ala	Pro	Glu	Asn	280	Asn	Pro	Gln	Phe	285	Thr	Thr	Val	Tyr	290										
Val	Gly	Asn	295	Leu	Ser	Pro	Glu	Ile	295	Thr	Gln	Leu	Asp	300	Leu	His	Arg	Leu											
Phe	Tyr	Thr	305	Leu	Gly	Ala	Gly	Val	310	Ile	Glu	Glu	Val	315	Arg	Val	Gln	Arg											
Asp	Lys	Gly	320	Phe	Gly	Phe	Val	Arg	325	Tyr	Asn	Thr	His	330	Asp	Glu	Ala	Ala	335										
Leu	Ala	Ile	340	Gln	Met	Gly	Asn	Ala	345	Gln	Pro	Phe	Leu	350	Phe	Ser	Arg	Gln											
Ile	Arg	Cys	355	Ser	Trp	Gly	Asn	Lys	360	Pro	Thr	Pro	Ser	365	Gly	Thr	Ala	Ser											
Asn	Pro	Leu	370	Pro	Pro	Pro	Ala	Pro	375	Ala	Ser	Val	Pro	380	Ser	Leu	Ser	Ala											
Met	Asp	Leu	385	Leu	Ala	Tyr	Glu	Arg	390	Gln	Leu	Ala	Leu	395	Ala	Lys	Met	His											
Pro	Gln	Ala	400	Gln	His	Ser	Leu	Arg	405	Ala	Gly	Gly	Val	410	Gly	Asn	Val	Ala											
Ala	Gly	Gly	415	Thr	Ala	Ala	Met	Tyr	420	Asp	Gly	Gly	Tyr	425	Gln	Asn	Val	Ala											
Ala	Ala	His	430	Gln	Gln	Leu	Met	Tyr	435	Tyr	Gln																		

(2) INFORMATION FOR SEQ ID NO:625:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 405 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..405
(D) OTHER INFORMATION

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:

(X1) SEQUENCE DESCRIPTION MET PRO GLN HIS PRO SER LEU TYR HIS PRO																	
Met	Val	Met	Gln	Ala	Met	Met	Gln	Gln	His	Pro	Ser	Leu	Tyr	His	Pro		
1				5					10					15			
Gly	Val	Met	Ala	Pro	Pro	Gln	Met	Glu	Pro	Leu	Pro	Ser	Gly	Asn	Leu		
			20					25					30				
Pro	Pro	Gly	Phe	Asp	Pro	Thr	Thr	Cys	Arg	Ser	Val	Tyr	Ala	Gly	Asn		
			35				40					45					
Ile	His	Thr	Gln	Val	Thr	Glu	Ile	Leu	Leu	Gln	Glu	Ile	Phe	Ala	Ser		
			50				55				60						
Thr	Gly	Pro	Ile	Glu	Ser	Cys	Lys	Leu	Ile	Arg	Lys	Asp	Lys	Ser	Ser		
65					70					75					80		
Tyr	Gly	Phe	Val	His	Tyr	Phe	Asp	Arg	Arg	Cys	Ala	Ser	Met	Ala	Ile		
				85					90					95			
Met	Thr	Leu	Asn	Gly	Arg	His	Ile	Phe	Gly	Gln	Pro	Met	Lys	Val	Asn		
			100					105					110				
Trp	Ala	Tyr	Ala	Thr	Gly	Gln	Arg	Glu	Asp	Thr	Ser	Ser	His	Phe	Asn		
			115					120				125					
Ile	Phe	Val	Gly	Asp	Leu	Ser	Pro	Glu	Val	Thr	Asp	Ala	Ala	His	Phe		
			130				135					140					

Asp Ser Phe Ser Ala Phe Asn Ser Cys Ser Asp Ala Arg Val Met Trp
145 150 155 160
Asp Gln Lys Thr Gly Arg Ser Arg Gly Phe Gly Phe Val Ser Phe Arg
165 170 175
Asn Gln Gln Asp Ala Gln Thr Ala Ile Asn Glu Met Asn Gly Lys Trp
180 185 190
Val Ser Ser Arg Gln Ile Arg Cys Asn Trp Ala Thr Lys Gly Ala Thr
195 200 205
Phe Gly Glu Asp Lys His Ser Ser Asp Glu Lys Ser Val Val Glu Leu
210 215 220
Thr Asn Gly Ser Ser Glu Asp Gly Arg Glu Leu Ser Asn Glu Asp Ala
225 230 235 240
Pro Glu Asn Asn Pro Gln Phe Thr Thr Val Tyr Val Gly Asn Leu Ser
245 250 255
Pro Glu Ile Thr Gln Leu Asp Leu His Arg Leu Phe Tyr Thr Leu Gly
260 265 270
Ala Gly Val Ile Glu Glu Val Arg Val Gln Arg Asp Lys Gly Phe Gly
275 280 285
Phe Val Arg Tyr Asn Thr His Asp Glu Ala Ala Leu Ala Ile Gln Met
290 295 300
Gly Asn Ala Gln Pro Phe Leu Phe Ser Arg Gln Ile Arg Cys Ser Trp
305 310 315 320
Gly Asn Lys Pro Thr Pro Ser Gly Thr Ala Ser Asn Pro Leu Pro Pro
325 330 335
Pro Ala Pro Ala Ser Val Pro Ser Leu Ser Ala Met Asp Leu Leu Ala
340 345 350
Tyr Glu Arg Gln Leu Ala Leu Ala Lys Met His Pro Gln Ala Gln His
355 360 365
Ser Leu Arg Gln Ala Gly Leu Gly Val Asn Val Ala Gly Gly Thr Ala
370 375 380
Ala Met Tyr Asp Gly Gly Tyr Gln Asn Val Ala Ala His Gln Gln
385 390 395 400
Leu Met Tyr Tyr Gln
405

(2) INFORMATION FOR SEQ ID NO:626:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..400

(D) OTHER INFORMATION: / Ceres Seq. ID 1498753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:

Met Met Gln Gln His Pro Ser Leu Tyr His Pro Gly Val Met Ala Pro
1 5 10 15
Pro Gln Met Glu Pro Leu Pro Ser Gly Asn Leu Pro Pro Gly Phe Asp
20 25 30
Pro Thr Thr Cys Arg Ser Val Tyr Ala Gly Asn Ile His Thr Gln Val
35 40 45
Thr Glu Ile Leu Leu Gln Glu Ile Phe Ala Ser Thr Gly Pro Ile Glu
50 55 60
Ser Cys Lys Leu Ile Arg Lys Asp Lys Ser Ser Tyr Gly Phe Val His
65 70 75 80
Tyr Phe Asp Arg Arg Cys Ala Ser Met Ala Ile Met Thr Leu Asn Gly
85 90 95
Arg His Ile Phe Gly Gln Pro Met Lys Val Asn Trp Ala Tyr Ala Thr
100 105 110
Gly Gln Arg Glu Asp Thr Ser Ser His Phe Asn Ile Phe Val Gly Asp

115	120	125
Leu Ser Pro Glu Val Thr Asp Ala Ala Leu Phe Asp Ser Phe Ser Ala		
130	135	140
Phe Asn Ser Cys Ser Asp Ala Arg Val Met Trp Asp Gln Lys Thr Gly		
145	150	155
Arg Ser Arg Gly Phe Gly Phe Val Ser Phe Arg Asn Gln Gln Asp Ala		
165	170	175
Gln Thr Ala Ile Asn Glu Met Asn Gly Lys Trp Val Ser Ser Arg Gln		
180	185	190
Ile Arg Cys Asn Trp Ala Thr Lys Gly Ala Thr Phe Gly Glu Asp Lys		
195	200	205
His Ser Ser Asp Glu Lys Ser Val Val Glu Leu Thr Asn Gly Ser Ser		
210	215	220
Glu Asp Gly Arg Glu Leu Ser Asn Glu Asp Ala Pro Glu Asn Asn Pro		
225	230	235
Gln Phe Thr Thr Val Tyr Val Gly Asn Leu Ser Pro Glu Ile Thr Gln		
245	250	255
Leu Asp Leu His Arg Leu Phe Tyr Thr Leu Gly Ala Gly Val Ile Glu		
260	265	270
Glu Val Arg Val Gln Arg Asp Lys Gly Phe Gly Phe Val Arg Tyr Asn		
275	280	285
Thr His Asp Glu Ala Ala Leu Ala Ile Gln Met Gly Asn Ala Gln Pro		
290	295	300
Phe Leu Phe Ser Arg Gln Ile Arg Cys Ser Trp Gly Asn Lys Pro Thr		
305	310	315
Pro Ser Gly Thr Ala Ser Asn Pro Leu Pro Pro Pro Ala Pro Ala Ser		
325	330	335
Val Pro Ser Leu Ser Ala Met Asp Leu Leu Ala Tyr Glu Arg Gln Leu		
340	345	350
Ala Leu Ala Lys Met His Pro Gln Ala Gln His Ser Leu Arg Gln Ala		
355	360	365
Gly Leu Gly Val Asn Val Ala Gly Thr Ala Ala Met Tyr Asp Gly		
370	375	380
Gly Tyr Gln Asn Val Ala Ala His Gln Gln Leu Met Tyr Tyr Gln		
385	390	395
		400

(2) INFORMATION FOR SEQ ID NO:627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1552
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:

gctgcttaga	ttttgttttc	tctattgtcg	tcgtcggagt	gaattaggga	ttcagaatat	60
acgatgaact	cgcttcgag	gagatttggg	aagaatcatg	gctatttggg	tcgagattat	120
cgaaacggaa	gacgatctgg	ttcagattcc	gatgaagaat	tgaagggtatt	gagtcacgaa	180
gagtatagga	ggcagaaacg	gcttaagatg	aggaatcag	ccaagtctcg	cttttgggag	240
aacacaccca	gtccacctag	agatcagaac	gaggattccg	atgagaaacg	cgacgagatt	300
caggacaaga	acggcgccga	aaagatgat	aattcgaag	ggaaagaag	gaaaggtaaa	360
tctgactcgg	aatctgaatc	tgatggtttg	agatctagga	agaggaagag	taagagctcg	420
aggtcaaaagc	gcaggagaaa	gagatcttat	gacagcgata	gtgaatccga	agggagtgaag	480
agtgtattcgg	aaagaggaaga	taggagacga	aggaggaaga	gttcttctaa	gaggaagaag	540
agtgaagaca	gccgtagtct	taggaaaaag	cgaagtcata	ggagaaaagac	gaaatacagt	600
gactctgatg	agagcagcga	tgaagatagt	aaagctgaga	ttagtgtctc	ttcgtctggg	660
gaggaagaag	ataccaagtc	aaagagcaag	agggcggaaga	aattcttcga	ttctagtcca	720

aaacgaagca	agggagagaa	gacgaagta	gggagtgaca	gcgatggtac	tgaggaagat	780
tcgaagatgc	aagtagacga	aacggtaaga	acactgagct	agaacttgat	gaagaagagt	840
tgaagaagtt	caaagagatg	attgaattaa	agaagaaatc	ttcagctggt	gatgaagagg	900
aagaagaagg	tgatgttgtt	ccaatgccat	tacataaagc	tgaaggtcac	atcagttatg	960
gtggtgtctt	aagaccgggt	gaaggagacg	ccrttgcvca	gtatgttcag	caaggtaaac	1020
gtatccccac	tagaggagaa	gtgggtctta	acgtgaaaga	gattcagaag	tttgaggatc	1080
ttggttatgt	gatgagtgga	agtaggcatc	aaaggatgaa	tgctattcgt	attagaaaag	1140
aaaaccaggt	ttacagtgtc	gaagacaaac	gggcattggc	catgtttaac	tacgaggaga	1200
aggcggaagc	cgaggctaag	gttatgtctg	atctgcagcg	gcttgtgcag	cgccatatgg	1260
gagaagaggt	ggggccaaat	catgaccctt	tcggtgctgg	aaagactgaa	gaagatgatg	1320
attgattttg	cttggcttcc	tgcttctgtt	atgtgggtac	tcattcttat	ctttatcttg	1380
ttgaatgttc	cttatttgca	tcatagatac	tgctgtttgc	tacttgcccg	taaatgagct	1440
tcgtagttaa	tgctttaatc	tactatgtat	ccgttaaatg	gcttcatagt	ttatgcgtta	1500
atctgctatg	tatcacatga	ttgtgtttgt	gtgtcaaaag	taatgatttc	tg	

(2) INFORMATION FOR SEQ ID NO:628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..254

(D) OTHER INFORMATION: / Ceres Seq. ID 1498755

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:

Met	Thr	Met	Asn	Ser	Leu	Pro	Arg	Arg	Phe	Gly	Lys	Asn	His	Gly	Tyr
1			5					10					15		
Leu	Asp	Arg	Asp	Tyr	Arg	Asn	Gly	Arg	Ser	Gly	Ser	Asp	Ser	Asp	
			20					25				30			
Glu	Glu	Leu	Lys	Gly	Leu	Ser	His	Glu	Glu	Tyr	Arg	Arg	Gln	Lys	Arg
			35				40					45			
Leu	Lys	Met	Arg	Lys	Ser	Ala	Lys	Phe	Cys	Phe	Trp	Glu	Asn	Thr	Pro
			50				55				60				
Ser	Pro	Pro	Arg	Asp	Gln	Asn	Glu	Asp	Ser	Asp	Glu	Asn	Ala	Asp	Glu
			65				70			75				80	
Ile	Gln	Asp	Lys	Asn	Gly	Gly	Glu	Arg	Asp	Asp	Asn	Ser	Lys	Gly	Lys
			85					90				95			
Glu	Arg	Lys	Gly	Lys	Ser	Asp	Ser	Glu	Ser	Glu	Ser	Asp	Gly	Leu	Arg
			100					105				110			
Ser	Arg	Lys	Arg	Lys	Ser	Lys	Ser	Ser	Arg	Ser	Lys	Arg	Arg	Arg	Lys
			115					120				125			
Arg	Ser	Tyr	Asp	Ser	Asp	Ser	Glu	Ser	Glu	Gly	Ser	Glu	Ser	Asp	Ser
			130				135				140				
Glu	Glu	Glu	Asp	Arg	Arg	Arg	Arg	Lys	Ser	Ser	Ser	Lys	Arg	Lys	
			145				150			155				160	
Lys	Ser	Arg	Ser	Ser	Arg	Ser	Phe	Arg	Lys	Lys	Arg	Ser	His	Arg	Arg
			165					170					175		
Lys	Thr	Lys	Tyr	Ser	Asp	Ser	Asp	Glu	Ser	Ser	Asp	Glu	Asp	Ser	Lys
			180					185				190			
Ala	Glu	Ile	Ser	Ala	Ser	Ser	Ser	Gly	Glu	Glu	Glu	Asp	Thr	Lys	Ser
			195					200				205			
Lys	Ser	Lys	Arg	Arg	Lys	Lys	Ser	Ser	Asp	Ser	Ser	Ser	Lys	Arg	Ser
			210				215					220			
Lys	Gly	Glu	Lys	Thr	Lys	Ser	Gly	Ser	Asp	Ser	Asp	Gly	Thr	Glu	Glu
			225				230			235				240	
Asp	Ser	Lys	Met	Gln	Val	Asp	Glu	Thr	Val	Arg	Thr	Leu	Ser		
			245					250							

(2) INFORMATION FOR SEQ ID NO:629:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..252
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498756
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:
Met Asn Ser Leu Pro Arg Arg Phe Gly Lys Asn His Gly Tyr Leu Asp
1 5 10 15
Arg Asp Tyr Arg Asn Gly Arg Arg Ser Gly Ser Asp Ser Asp Glu Glu
 20 25 30
Leu Lys Gly Leu Ser His Glu Glu Tyr Arg Arg Gln Lys Arg Leu Lys
 35 40 45
Met Arg Lys Ser Ala Lys Phe Cys Phe Trp Glu Asn Thr Pro Ser Pro
 50 55 60
Pro Arg Asp Gln Asn Glu Asp Ser Asp Glu Asn Ala Asp Glu Ile Gln
65 70 75 80
Asp Lys Asn Gly Gly Glu Arg Asp Asp Asn Ser Lys Gly Lys Glu Arg
 85 90 95
Lys Gly Lys Ser Asp Ser Glu Ser Glu Ser Asp Gly Leu Arg Ser Arg
 100 105 110
Lys Arg Lys Ser Lys Ser Ser Arg Ser Lys Arg Arg Arg Lys Arg Ser
 115 120 125
Tyr Asp Ser Asp Ser Glu Ser Glu Gly Ser Glu Ser Asp Ser Glu Glu
 130 135 140
Glu Asp Arg Arg Arg Arg Arg Lys Ser Ser Ser Lys Arg Lys Lys Ser
145 150 155 160
Arg Ser Ser Arg Ser Phe Arg Lys Lys Arg Ser His Arg Arg Lys Thr
 165 170 175
Lys Tyr Ser Asp Ser Asp Glu Ser Ser Asp Glu Asp Ser Lys Ala Glu
 180 185 190
Ile Ser Ala Ser Ser Ser Gly Glu Glu Asp Thr Lys Ser Lys Ser
 195 200 205
Lys Arg Arg Lys Lys Ser Ser Asp Ser Ser Ser Lys Arg Ser Lys Gly
 210 215 220
Glu Lys Thr Lys Ser Gly Ser Asp Ser Asp Gly Thr Glu Glu Asp Ser
225 230 235 240
Lys Met Gln Val Asp Glu Thr Val Arg Thr Leu Ser
 245 250
(2) INFORMATION FOR SEQ ID NO:630:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 204 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..204
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498757
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:
Met Arg Lys Ser Ala Lys Phe Cys Phe Trp Glu Asn Thr Pro Ser Pro
1 5 10 15
Pro Arg Asp Gln Asn Glu Asp Ser Asp Glu Asn Ala Asp Glu Ile Gln
 20 25 30
Asp Lys Asn Gly Gly Glu Arg Asp Asp Asn Ser Lys Gly Lys Glu Arg
 35 40 45
Lys Gly Lys Ser Asp Ser Glu Ser Glu Ser Asp Gly Leu Arg Ser Arg
 50 55 60

Lys Arg Lys Ser Lys Ser Ser Arg Ser Lys Arg Arg Arg Lys Arg Ser
65 70 75 80
Tyr Asp Ser Asp Ser Glu Ser Glu Gly Ser Glu Ser Asp Ser Glu Glu
85 90 95
Glu Asp Arg Arg Arg Arg Lys Ser Ser Lys Arg Lys Lys Ser
100 105 110
Arg Ser Ser Arg Ser Phe Arg Lys Lys Arg Ser His Arg Arg Lys Thr
115 120 125
Lys Tyr Ser Asp Ser Asp Glu Ser Ser Asp Glu Asp Ser Lys Ala Glu
130 135 140
Ile Ser Ala Ser Ser Ser Gly Glu Glu Glu Asp Thr Lys Ser Lys Ser
145 150 155 160
Lys Arg Arg Lys Lys Ser Ser Asp Ser Ser Lys Arg Ser Lys Gly
165 170 175
Glu Lys Thr Lys Ser Gly Ser Asp Ser Asp Gly Thr Glu Glu Asp Ser
180 185 190
Lys Met Gln Val Asp Glu Thr Val Arg Thr Leu Ser
195 200

(2) INFORMATION FOR SEQ ID NO:631:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1275 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1275

(D) OTHER INFORMATION: / Ceres Seq. ID 1498758

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:

aatctttttt	tttttgcctta	ttattttttt	gaactttgato	tcccatcagtt	tcactttctt	60
cttcttcttc	tgatcaacca	tggctgctgc	tataaagtgt	gcagtctctt	taacctcttc	120
caagtcatacc	tctctcctca	ccaaatcttc	ctctgtatcc	ccctcaaggga	ttttcctcaa	180
gaagagcaca	gtgtgtttca	gaagagttgt	gtcagtgaa	gctcaggtga	caacagatac	240
taccgaggca	ccaccagtta	aagtagtcaa	ggagtctaa	aaacaggaa	aagggattgt	300
tgtcaacaaa	ttcaaaccta	agaaccctta	cactggtcgc	tgccctttga	acaccaagat	360
caccggtgat	gagcgtcccg	gtgagacttg	gcacattgtc	ttcaccacgc	aaggtgaggt	420
tccgtataga	gaaggacaat	cgataggagt	gattccagag	ggaatagaca	agaacggaaa	480
gcgcacaaag	ctcaggcttt	actctatcgc	gagtagtgcc	attggtgact	ttggagactc	540
caagaccgtt	tctctctgtg	tcaagagact	agtttacaca	aatgatggcg	gagagattgt	600
taagggggctc	tgctccaact	ctttgtgtga	cttgaagccg	ggtgatgaag	ctaatgatac	660
tggaacctgtt	ggcaaggaaa	tgcttatgcc	aaaagacccc	aatgccacca	tcatacatgt	720
tggaacaggga	actggaatag	ctccattcag	atcatttttg	tggaataatg	tttttgaggga	780
gcacgaggac	tacaagtcca	atggtttggc	gtggcttttc	ttgggtgtac	ccagaaggac	840
ctcactgcta	tacaaggagg	agtttgagaa	gatgaaggag	aagaaccocag	acaacttcag	900
gctggacttt	gcggtgagca	gagagcagag	gaacgagaag	ggagagaaaa	tgtaacattca	960
gacaagaatg	gcagagtatg	cagaagaagc	tgtgggagtt	gctgaagaaa	gacaaacact	1020
ttgtttacat	gtgtggtctt	aagggtatgg	agaagggatg	cgatgacatt	attggtctcgc	1080
ttgctgctaa	agatgggagc	gattggttgg	agtacaagaa	gcaattgaag	aggagtgaa	1140
agtggaatgt	tgaagtctac	taaggaaagt	tctgaggagg	taattatata	atttagataaa	1200
aaagcttcag	atgcattgtg	aaatcttcat	atctgcttct	ttttcttttc	tcaaggatttt	1260
tcaatcaaaa	catcc					

(2) INFORMATION FOR SEQ ID NO:632:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 320 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..320

(D) OTHER INFORMATION: / Ceres Seq. ID 1498759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:

Met Ala Ala Ala Ile Ser Ala Ala Val Ser Leu Pro Ser Ser Lys Ser
1 5 10 15
Ser Ser Leu Leu Thr Lys Ile Ser Ser Val Ser Pro Gln Arg Ile Phe
20 25 30
Leu Lys Lys Ser Thr Val Cys Tyr Arg Arg Val Val Ser Val Lys Ala
35 40 45
Gln Val Thr Thr Asp Thr Thr Glu Ala Pro Pro Val Lys Val Val Lys
50 55 60
Glu Ser Lys Lys Gln Glu Gly Ile Val Val Asn Lys Phe Lys Pro
65 70 75 80
Lys Asn Pro Tyr Thr Gly Arg Cys Leu Leu Asn Thr Lys Ile Thr Gly
85 90 95
Asp Asp Ala Pro Gly Glu Thr Trp His Ile Val Phe Thr Thr Glu Gly
100 105 110
Glu Val Pro Tyr Arg Glu Gly Gln Ser Ile Gly Val Ile Pro Glu Gly
115 120 125
Ile Asp Lys Asn Gly Lys Pro His Lys Leu Arg Leu Tyr Ser Ile Ala
130 135 140
Ser Ser Ala Ile Gly Asp Phe Gly Asp Ser Lys Thr Val Ser Leu Cys
145 150 155 160
Val Lys Arg Leu Val Tyr Thr Asn Asp Gly Gly Glu Ile Val Lys Gly
165 170 175
Val Cys Ser Asn Phe Leu Cys Asp Leu Lys Pro Gly Asp Glu Ala Lys
180 185 190
Ile Thr Gly Pro Val Gly Lys Glu Met Leu Met Pro Lys Asp Pro Asn
195 200 205
Ala Thr Ile Ile Met Leu Gly Thr Gly Thr Gly Ile Ala Pro Phe Arg
210 215 220
Ser Phe Leu Trp Lys Met Phe Phe Glu Glu His Glu Asp Tyr Lys Phe
225 230 235 240
Asn Gly Leu Ala Trp Leu Phe Leu Gly Val Pro Arg Ser Ser Ser Leu
245 250 255
Leu Tyr Lys Glu Glu Phe Glu Lys Met Lys Glu Lys Asn Pro Asp Asn
260 265 270
Phe Arg Leu Asp Phe Ala Val Ser Arg Glu Gln Thr Asn Glu Lys Gly
275 280 285
Glu Lys Met Tyr Ile Gln Thr Arg Met Ala Glu Tyr Ala Glu Arg Ala
290 295 300
Val Gly Val Ala Glu Glu Arg Gln His Leu Cys Leu His Val Trp Ser
305 310 315 320

(2) INFORMATION FOR SEQ ID NO:633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1854 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1854

(D) OTHER INFORMATION: / Ceres Seq. ID 1498760

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:

ataatacttc tctgtttaca tctctgttc cgaggagaaa agtctcgatc tcttgatct 60
ggggttttgt ttgggtttggg ttgactcgg ttttgactcg ggacaagtc tctcgtgaga 120
tggatgtctc tctgtttatta gtatctcttt gagagtctgt cttctcgggt tcaatagatt 180
cttatagttt cgcttagaaa cagcacaaaa aagatgtcgt tgaagcatca tcacagagga 240

ttagagctct	ctgcttcgaa	gagttttgtc	tcaaagaat	ggactttatt	tctctgtatc	300
ggtttttttc	gcgcaggaat	tctcttctcc	gacagaatgt	ggccagagcc	tgaatccaat	360
gttgatataa	gggacacagt	agcatcagat	gaacggctgc	ggttagagtc	tgaggactgt	420
gattcatcaa	aaaaggggtt	taaaagcgtga	atcgaaagac	atccttgagg	atgtttacaa	480
gagtcacagt	gcaattcaaa	cgcttgataa	aacgatttca	aagctggaaa	cagaactggc	540
cgatgcaaga	gtgcgcgaag	aattctatcat	gaatgggttca	ccagtttctg	atgactttaa	600
gctccctgaa	actgtcacta	aaagaaagta	tctgatgggt	gttggtgtta	atactgcgtt	660
tagcagcaga	aagcgcaggg	attcagtcog	tgctacttgg	atgctctccg	gtgaggagag	720
aaagaagctc	gagggaagaga	aagggatcgt	gatgcgggtt	gtgataggcc	atagttctac	780
tcccgttgga	attcttgata	gagcgattca	ggctgaagaa	agtaaacatg	gagacttctt	840
gaggctggat	catgttgaa	gttatctcga	gctgtcagca	aagactaaaa	cttaactttc	900
cacggttttt	gcaatgtggg	atgcagactt	ctactgtcaa	tgcgatgatg	atgtgcattg	960
aaatatagcc	acgcttgagg	cagaatttagc	aagataccgg	atgaagcccc	gagtgatcat	1020
tggttgcatg	aaatctggac	ctgttcttgc	tcagaaagga	gtgagatata	atgaacccca	1080
atactggaaa	tttggaaga	agggtaacaa	atacttccgc	catgccacag	gtcagctcta	1140
tgcaataatc	agggagtggg	cgtcttcat	atcgataaac	caaaacgtac	ttcaacaaata	1200
tgtgaatgaa	gatgtctctt	taggatacat	gtttcttggg	ttagatgtgg	agcatgtaga	1260
tgaccgtagg	ctatgtttgt	gtacaacaga	ttgtgagttg	aaggcgcagg	cgggcaacat	1320
ctgtgtgtcc	tcgttcgatt	ggagctgcag	tggtatttgg	agatcagcgg	ataggatgaa	1380
ggatgttcat	cgtagtggtg	gagaaggtga	aaagcccttt	ctggctgcgt	ctttctgaaa	1440
cacaataact	aaagaaacac	attgaggaag	aagagtacag	agacaaatcc	gctcgcagat	1500
ctacactgtg	tagtataagc	acacagtcac	actctctcta	tatatgtatt	tatgtatgta	1560
tgtatgtatc	tttgaaactg	agatgagaag	gggtgctttt	gcctctcttt	cttgtttctt	1620
tatgcttttc	tcaattctct	gaaggtctgg	agttcttttc	acacagaaaa	tgacagatttt	1680
agctgcaaaa	gcggactcca	tgagtgcaac	ttcagagtc	tttcattgag	gcggtttctc	1740
tgccctttga	gctttttctc	ttcatttctt	tttggaattt	gcctattttg	ttcatttttt	1800
cccttgccat	gattgtggtg	aaacatgggt	tgtttatgtg	tgtaacttgaa	acgc	

(2) INFORMATION FOR SEQ ID NO:634:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 289 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..289

(D) OTHER INFORMATION: / Ceres Seq. ID 1498761

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:

Met	Asn	Gly	Ser	Pro	Val	Ser	Asp	Asp	Phe	Lys	Leu	Pro	Glu	Thr	Val
1			5					10					15		
Thr	Lys	Arg	Lys	Tyr	Leu	Met	Val	Val	Gly	Val	Asn	Thr	Ala	Phe	Ser
			20				25					30			
Ser	Arg	Lys	Arg	Arg	Asp	Ser	Val	Arg	Ala	Thr	Trp	Met	Pro	Pro	Gly
		35					40				45				
Glu	Glu	Arg	Lys	Lys	Leu	Glu	Glu	Glu	Lys	Gly	Ile	Val	Met	Arg	Phe
		50				55					60				
Val	Ile	Gly	His	Ser	Ser	Thr	Pro	Gly	Gly	Ile	Leu	Asp	Arg	Ala	Ile
		65				70				75				80	
Gln	Ala	Glu	Glu	Ser	Lys	His	Gly	Asp	Phe	Leu	Arg	Leu	Asp	His	Val
			85					90					95		
Glu	Gly	Tyr	Leu	Glu	Leu	Ser	Ala	Lys	Thr	Lys	Thr	Tyr	Phe	Thr	Thr
			100					105					110		
Ala	Phe	Ala	Met	Trp	Asp	Ala	Asp	Phe	Tyr	Val	Lys	Val	Asp	Asp	Asp
			115				120				125				
Val	His	Val	Asn	Ile	Ala	Thr	Leu	Gly	Ala	Glu	Leu	Ala	Arg	Tyr	Arg
		130				135					140				
Met	Lys	Pro	Arg	Val	Tyr	Ile	Gly	Cys	Met	Lys	Ser	Gly	Pro	Val	Leu
		145				150				155				160	
Ala	Gln	Lys	Gly	Val	Arg	Tyr	His	Glu	Pro	Glu	Tyr	Trp	Lys	Phe	Gly
			165					170						175	

Glu Glu Gly Asn Lys Tyr Phe Arg His Ala Thr Gly Gln Leu Tyr Ala
180 185 190
Ile Ser Arg Glu Leu Ala Ser Tyr Ile Ser Ile Asn Gln Asn Val Leu
195 200 205
His Lys Tyr Val Asn Glu Asp Val Ser Leu Gly Ser Trp Phe Leu Gly
210 215 220
Leu Asp Val Glu His Val Asp Asp Arg Arg Leu Cys Cys Gly Thr Thr
225 230 235 240
Asp Cys Glu Trp Lys Ala Gln Ala Gly Asn Ile Cys Val Ala Ser Phe
245 250 255
Asp Trp Ser Cys Ser Gly Ile Cys Arg Ser Ala Asp Arg Met Lys Asp
260 265 270
Val His Arg Arg Cys Gly Glu Gly Glu Lys Ala Leu Leu Ala Ala Ser
275 280 285
Phe

(2) INFORMATION FOR SEQ ID NO:635:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..267
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498762

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:635:

Met Val Val Gly Val Asn Thr Ala Phe Ser Ser Arg Lys Arg Arg Asp
1 5 10 15
Ser Val Arg Ala Thr Trp Met Pro Pro Gly Glu Glu Arg Lys Lys Leu
20 25 30
Glu Glu Glu Lys Gly Ile Val Met Arg Phe Val Ile Gly His Ser Ser
35 40 45
Thr Pro Gly Gly Ile Leu Asp Arg Ala Ile Gln Ala Glu Glu Ser Lys
50 55 60
His Gly Asp Phe Leu Arg Leu Asp His Val Glu Gly Tyr Leu Glu Leu
65 70 75 80
Ser Ala Lys Thr Lys Thr Tyr Phe Thr Thr Ala Phe Ala Met Trp Asp
85 90 95
Ala Asp Phe Tyr Val Lys Val Asp Asp Asp Val His Val Asn Ile Ala
100 105 110
Thr Leu Gly Ala Glu Leu Ala Arg Tyr Arg Met Lys Pro Arg Val Tyr
115 120 125
Ile Gly Cys Met Lys Ser Gly Pro Val Leu Ala Gln Lys Gly Val Arg
130 135 140
Tyr His Glu Pro Glu Tyr Trp Lys Phe Gly Glu Glu Gly Asn Lys Tyr
145 150 155 160
Phe Arg His Ala Thr Gly Gln Leu Tyr Ala Ile Ser Arg Glu Leu Ala
165 170 175
Ser Tyr Ile Ser Ile Asn Gln Asn Val Leu His Lys Tyr Val Asn Glu
180 185 190
Asp Val Ser Leu Gly Ser Trp Phe Leu Gly Leu Asp Val Glu His Val
195 200 205
Asp Asp Arg Arg Leu Cys Cys Gly Thr Thr Asp Cys Glu Trp Lys Ala
210 215 220
Gln Ala Gly Asn Ile Cys Val Ala Ser Phe Asp Trp Ser Cys Ser Gly
225 230 235 240
Ile Cys Arg Ser Ala Asp Arg Met Lys Asp Val His Arg Arg Cys Gly
245 250 255
Glu Gly Glu Lys Ala Leu Leu Ala Ala Ser Phe

260 265
(2) INFORMATION FOR SEQ ID NO:636:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 245 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..245
(D) OTHER INFORMATION: / Ceres Seq. ID 1498763
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:636:
Met Pro Pro Gly Glu Glu Arg Lys Lys Leu Glu Glu Glu Lys Gly Ile
1 5 10 15
Val Met Arg Phe Val Ile Gly His Ser Ser Thr Pro Gly Gly Ile Leu
20 25 30
Asp Arg Ala Ile Gln Ala Glu Glu Ser Lys His Gly Asp Phe Leu Arg
35 40 45
Leu Asp His Val Glu Gly Tyr Leu Glu Leu Ser Ala Lys Thr Lys Thr
50 55 60
Tyr Phe Thr Thr Ala Phe Ala Met Trp Asp Ala Asp Phe Tyr Val Lys
65 70 75 80
Val Asp Asp Asp Val His Val Asn Ile Ala Thr Leu Gly Ala Glu Leu
85 90 95
Ala Arg Tyr Arg Met Lys Pro Arg Val Tyr Ile Gly Cys Met Lys Ser
100 105 110
Gly Pro Val Leu Ala Gln Lys Gly Val Arg Tyr His Glu Pro Glu Tyr
115 120 125
Trp Lys Phe Gly Glu Glu Gly Asn Lys Tyr Phe Arg His Ala Thr Gly
130 135 140
Gln Leu Tyr Ala Ile Ser Arg Glu Leu Ala Ser Tyr Ile Ser Ile Asn
145 150 155 160
Gln Asn Val Leu His Lys Tyr Val Asn Glu Asp Val Ser Leu Gly Ser
165 170 175
Trp Phe Leu Gly Leu Asp Val Glu His Val Asp Asp Arg Arg Leu Cys
180 185 190
Cys Gly Thr Thr Asp Cys Glu Trp Lys Ala Gln Ala Gly Asn Ile Cys
195 200 205
Val Ala Ser Phe Asp Trp Ser Cys Ser Gly Ile Cys Arg Ser Ala Asp
210 215 220
Arg Met Lys Asp Val His Arg Arg Cys Gly Glu Gly Glu Lys Ala Leu
225 230 235 240
Leu Ala Ala Ser Phe
245

(2) INFORMATION FOR SEQ ID NO:637:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 865 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..865
(D) OTHER INFORMATION: / Ceres Seq. ID 1498764
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637:
acacacacacac aaactcaaga gagactttgt ggccatggca gacctctctc aatccaccgc 60
tacattctctc cagtcggcgga agatcgccac cgctccttct cgcggaagtgt ctcaactctc 120
atcgactcaa gccctcgcca aatcttttgg gctcgaaact tctcggctc gctctacgtt 180
ctccttccag tctgacttta aggactttcac cggtaaatgc tccgacgctg tcaaaatcgc 240

cggattcgcgt	cttgccacct	ctgctctcgt	cgtctcggga	gcaagtgcgg	agggagctcc	300
aaagagattg	acctatgacg	agatcgaag	acccttcgag	gttgcttcag	acggaagcgt	360
caatttcaag	gaagaagatg	gaatcgacta	tgctgcagtc	acagtccaac	ttccaggagg	420
tgaacgtgtg	ccattctctt	tcacagtcac	acagcttgac	tcctcaggca	aaccagacag	480
cttcaccgga	aaattctctg	ttccatcgta	ccgtggctct	tccttcttgg	acccaaaggg	540
ccgtgggtga	tcacacagga	atgacaacgc	cgtggcattg	ccagctggag	gcagaggaga	600
cgaggaggag	cttgtaaaag	agaacgtgaa	gaacactgcc	gcttcagtg	gagagatcac	660
tctgaagtg	acaaagagca	agccggagac	aggagaggtg	atcggagtgt	tccgagagct	720
tcagccgtcg	gatactgact	tggtgtctaa	ggtaccaaa	gatgtgaaga	tccaaggggt	780
gtggtatggt	caacttgagt	gatcatgtta	ttatatcttc	cgttgattgt	gtttgatgat	840
aatgataaca	tcttttgatg	ctttc				

(2) INFORMATION FOR SEQ ID NO:638:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..266
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:

Pro	Lys	Lys	Lys	Leu	Lys	Arg	Asp	Phe	Val	Ala	Met	Ala	Ala	Ser	Leu	
1				5					10					15		
Gln	Ser	Thr	Ala	Thr	Phe	Leu	Gln	Ser	Ala	Lys	Ile	Ala	Thr	Ala	Pro	
			20					25					30			
Ser	Arg	Gly	Ser	Ser	His	Leu	Arg	Ser	Thr	Gln	Ala	Val	Gly	Lys	Ser	
		35				40				45						
Phe	Gly	Leu	Glu	Thr	Ser	Ser	Ala	Arg	Leu	Thr	Cys	Ser	Phe	Gln	Ser	
	50				55				60							
Asp	Phe	Lys	Asp	Phe	Thr	Gly	Lys	Cys	Ser	Asp	Ala	Val	Lys	Ile	Ala	
	65				70				75					80		
Gly	Phe	Ala	Leu	Ala	Thr	Ser	Ala	Leu	Val	Ser	Gly	Ala	Ser	Ala		
			85					90					95			
Glu	Gly	Ala	Pro	Lys	Arg	Leu	Thr	Tyr	Asp	Glu	Ile	Glu	Gly	Pro	Phe	
	100					105							110			
Glu	Val	Ala	Ser	Asp	Gly	Ser	Val	Asn	Phe	Lys	Glu	Glu	Asp	Gly	Ile	
	115					120						125				
Asp	Tyr	Ala	Ala	Val	Thr	Val	Gln	Leu	Pro	Gly	Gly	Glu	Arg	Val	Pro	
	130				135					140						
Phe	Leu	Phe	Thr	Val	Lys	Gln	Leu	Asp	Ser	Ser	Gly	Lys	Pro	Asp	Ser	
	145				150					155				160		
Phe	Thr	Gly	Lys	Phe	Leu	Val	Pro	Ser	Tyr	Arg	Gly	Ser	Ser	Phe	Leu	
		165							170					175		
Asp	Pro	Lys	Gly	Arg	Gly	Gly	Ser	Thr	Gly	Tyr	Asp	Asn	Ala	Val	Ala	
		180					185						190			
Leu	Pro	Ala	Gly	Gly	Arg	Gly	Asp	Glu	Glu	Leu	Val	Lys	Glu	Asn		
	195					200						205				
Val	Lys	Asn	Thr	Ala	Ala	Ser	Val	Gly	Glu	Ile	Thr	Leu	Lys	Val	Thr	
	210				215					220						
Lys	Ser	Lys	Pro	Glu	Thr	Gly	Glu	Val	Ile	Gly	Val	Phe	Glu	Ser	Leu	
	225				230					235				240		
Gln	Pro	Ser	Asp	Thr	Asp	Leu	Gly	Ala	Lys	Val	Pro	Lys	Asp	Val	Lys	
		245						250					255			
Ile	Gln	Gly	Val	Trp	Tyr	Gly	Gln	Leu	Glu							
	260					265										

(2) INFORMATION FOR SEQ ID NO:639:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..255
(D) OTHER INFORMATION: / Ceres Seq. ID 1498766
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:639:
Met Ala Ala Ser Leu Gln Ser Thr Ala Thr Phe Leu Gln Ser Ala Lys
1 5 10 15
Ile Ala Thr Ala Pro Ser Arg Gly Ser Ser His Leu Arg Ser Thr Gln
20 25 30
Ala Val Gly Lys Ser Phe Gly Leu Glu Thr Ser Ser Ala Arg Leu Thr
35 40 45
Cys Ser Phe Gln Ser Asp Phe Lys Asp Phe Thr Gly Lys Cys Ser Asp
50 55 60
Ala Val Lys Ile Ala Gly Phe Ala Leu Ala Thr Ser Ala Leu Val Val
65 70 75 80
Ser Gly Ala Ser Ala Glu Gly Ala Pro Lys Arg Leu Thr Tyr Asp Glu
85 90 95
Ile Glu Gly Pro Phe Glu Val Ala Ser Asp Gly Ser Val Asn Phe Lys
100 105 110
Glu Glu Asp Gly Ile Asp Tyr Ala Ala Val Thr Val Gln Leu Pro Gly
115 120 125
Gly Glu Arg Val Pro Phe Leu Phe Thr Val Lys Gln Leu Asp Ser Ser
130 135 140
Gly Lys Pro Asp Ser Phe Thr Gly Lys Phe Leu Val Pro Ser Tyr Arg
145 150 155 160
Gly Ser Ser Phe Leu Asp Pro Lys Gly Arg Gly Gly Ser Thr Gly Tyr
165 170 175
Asp Asn Ala Val Ala Leu Pro Ala Gly Gly Arg Gly Asp Glu Glu Glu
180 185 190
Leu Val Lys Glu Asn Val Lys Asn Thr Ala Ala Ser Val Gly Glu Ile
195 200 205
Thr Leu Lys Val Thr Lys Ser Lys Pro Glu Thr Gly Glu Val Ile Gly
210 215 220
Val Phe Glu Ser Leu Gln Pro Ser Asp Thr Asp Leu Gly Ala Lys Val
225 230 235 240
Pro Lys Asp Val Lys Ile Gln Gly Val Trp Gly Gln Leu Glu
245 250 255

(2) INFORMATION FOR SEQ ID NO:640:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..2144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498771

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:640:

aaggaatcga	aaacccagaa	gaggactcag	tgaacaaatt	tcttoaggtt	aaatttcctc	60
actattctac	tgtgtttttg	ttctcagaat	cctcgaaaat	cgtaaatgtg	tttttcgtat	120
gctccctaaaa	tcctgggcaat	tcattagatt	tcgttcgcta	gataaaccta	agcttgatgt	180
attcttttggt	acaatgtaa	tctgttttagt	tcctataactt	ggaatcactc	taagtgtaat	240
gtatattgat	gcgaagtcaa	atgttgctga	atttttgctc	tcttgcaatt	ttccccaatt	300
ttttctgagc	cagtatttgt	aaaaattgga	gtctgagaaa	actgaaaaag	ttaatgtatt	360
ctcatttaac	cagtggttcat	agattcacta	gttggtttgac	cagggcctag	ctctaatcat	420
tcttgtgaca	cttggttttc	ttttaaatct	gttttgatgt	tcaggtttct	ttggaagcta	480
tatacccata	aacttaaaat	gaataaagat	ggaagcttta	gctgatataa	tttgggtggt	540

tctttctttc	ttccttggtg	tgaagctggt	tcaaaatgct	tcggaggtat	gatagtcgca	600
ccacgatctt	ctcaccggaa	ggctgctctt	accagggtga	atatgctatg	gaagctattg	660
gcaatgctgt	ttctgccatt	ggatctttgg	caaaagacgg	agtgggtttg	gttgggtaga	720
agaaagtcac	ttctaaactt	cttcaaacct	cttcatccat	ggagaaaatg	tacaagatcg	780
atgaccatgt	ggcttgtgca	gttgctggta	taatgtctga	tgccaaacatt	ctgatttaaca	840
ctgctctgagt	tcaagctcag	egttacacct	ttatgtacca	agagccaatg	cccgttttagc	900
agctgggttca	gtctctttgt	gacaccaagc	aaggatacac	ccagtttggt	ggctctccgcc	960
cgtttggagt	ttcctttctt	tttgcaggct	gggacaggaa	ccacgggttt	cgactgtata	1020
tgagtgcacc	aagtggaaac	tatgggtgat	ggcaagctgc	agctgtttgga	gcaaaataatc	1080
aagcggttca	gtctattctt	aagcaagact	ataaggatga	tgcaacgagg	gaagaagtgg	1140
ttcagctcgc	tatcaagttg	ttgagcaaga	cgatggacag	cacgagcttt	acagctgaaa	1200
aactcgagct	tgctgagttg	tatctgactc	cttcaaaaatg	tgtaagtac	catgttcaact	1260
cgctcgactc	gctcactaag	ctcttgggtt	agcatgggtg	gactcaacca	gcgcagaaaa	1320
cttcctaagc	tagaaaactg	tgacagtttt	acctgaccgc	cctggttact	gtagatgtcc	1380
atttgccttc	tttccctttt	gagatatcgt	atcagaatca	atttaccact	ctgattatgt	1440
catgtgatcc	atttgggttg	actattcttt	atcttgagat	tgactcttct	ctagtctaaa	1500
gtaaagttag	acttttagag	ttttattcaa	taaatgaatg	agcaatcacc	aacggggccca	1560
ttagaagacc	cataacattc	attgatttag	gtaacggggt	ttaatggctc	aaatttaacga	1620
agaatcagaa	tctcttttaag	tttcaccacg	tcgattttaac	ggtaacagagt	gtctgttttat	1680
taacagaaaa	gtaaaaatgt	taccgcctca	agcgatatct	ttgagcgcca	aatggaattt	1740
catgtgtaca	atgccacaga	gttctggggc	agaaactggcc	tcattgtaag	agattttttta	1800
ggagatttat	cgagatgtgc	aaaaacaagt	ttttctctct	tggtattatct	acaaaaatatt	1860
atttacttta	gtagtgttca	gttagacaat	gccctgaatc	caaggaattg	tatcgaccgg	1920
gattgaagag	accattcttg	catcgtctct	tctttttgca	gcacgcgat	tgatgaaac	1980
attgatggcc	agatctttct	tctataagtc	aatcaaccgg	ccaccggaa	taccctaaaa	2040
acatagaaaa	tatgttgaaa	tatatggaga	tatttagcat	cgactatgac	taagtgtcac	2100
aaacttttgt	gtgataggat	tcaatcaatc	caatggatct	tagt		

(2) INFORMATION FOR SEQ ID NO:641:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641:

Met	Ser	Arg	Arg	Tyr	Asp	Ser	Arg	Thr	Thr	Ile	Phe	Ser	Pro	Glu	Gly
1			5					10						15	
Arg	Leu	Tyr	Gln	Val	Glu	Tyr	Ala	Met	Glu	Ala	Ile	Gly	Asn	Ala	Gly
			20					25					30		
Ser	Ala	Ile	Gly	Ile	Leu	Ala	Lys	Asp	Gly	Val	Val	Leu	Val	Gly	Glu
			35					40				45			
Lys	Lys	Val	Thr	Ser	Lys	Leu	Leu	Gln	Thr	Ser	Ser	Ser	Met	Glu	Lys
			50				55				60				
Met	Tyr	Lys	Ile	Asp	Asp	His	Val	Ala	Cys	Ala	Val	Ala	Gly	Ile	Met
			70					75						80	
Ser	Asp	Ala	Asn	Ile	Leu	Ile	Asn	Thr	Ala	Arg	Val	Gln	Ala	Gln	Arg
			85					90					95		
Tyr	Thr	Phe	Met	Tyr	Gln	Glu	Pro	Met	Pro	Val					
			100					105							

(2) INFORMATION FOR SEQ ID NO:642:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..83
(D) OTHER INFORMATION: / Ceres Seq. ID 1498773
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:642:
Met Glu Ala Ile Gly Asn Ala Gly Ser Ala Ile Gly Ile Leu Ala Lys
1 5 10 15
Asp Gly Val Val Leu Val Gly Glu Lys Lys Val Thr Ser Lys Leu Leu
20 25 30
Gln Thr Ser Ser Ser Met Glu Lys Met Tyr Lys Ile Asp Asp His Val
35 40 45
Ala Cys Ala Val Ala Gly Ile Met Ser Asp Ala Asn Ile Leu Ile Asn
50 55 60
Thr Ala Arg Val Gln Ala Gln Arg Tyr Thr Phe Met Tyr Gln Glu Pro
65 70 75 80
Met Pro Val

(2) INFORMATION FOR SEQ ID NO:643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..102
(D) OTHER INFORMATION: / Ceres Seq. ID 1498774

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:643:

Met Ser Asp Pro Ser Gly Asn Tyr Gly Gly Trp Gln Ala Ala Val
1 5 10 15
Gly Ala Asn Asn Gln Ala Ala Gln Ser Ile Leu Lys Gln Asp Tyr Lys
20 25 30
Asp Asp Ala Thr Arg Glu Glu Val Val Gln Leu Ala Ile Lys Val Leu
35 40 45
Ser Lys Thr Met Asp Ser Thr Ser Phe Thr Ala Glu Lys Leu Glu Leu
50 55 60
Ala Glu Leu Tyr Leu Thr Pro Ser Lys Cys Val Lys Tyr His Val His
65 70 75 80
Ser Pro Asp Ser Leu Thr Lys Leu Leu Val Lys His Gly Val Thr Gln
85 90 95
Pro Ala Ala Glu Thr Ser
100

(2) INFORMATION FOR SEQ ID NO:644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1245 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1245
(D) OTHER INFORMATION: / Ceres Seq. ID 1498775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:644:

attgcttttg ctctgtatag tcaactgattt agggtttttc gaactctgaac ttcttctttt 60
ttgagtttcc aaagcaatgg cggcgctcgca agataagttg gataagatga aacttaggca 120
agattaccgg aatttatggc actccgatct catgggcacc gtcaccgccg acactcccta 180
ttgctgcatt tcgtgtctgt gtggaccttg tgtgtcattc atgcttcgga gaagagcaact 240
ttacaatgac atgtcaagggt ataacttgcgt tgcgtggatat atgacctgta gtggaaggtg 300
tgagagaagc aaatgtcttc aactttgcct tgccactgag gtcttctctt gcttcggaaa 360
ctctgtggcc tctaccgcgt ttcttctgca ggatgaattc aacatccaga caacacaatg 420

cgacaattgc	ataattggat	ttaatgtctg	cctcagccaa	gttgcttgca	tattctctat	480
agttgcttgc	attgttggtg	gtgatgaact	ttccgaggct	tctcagatag	tctcttctgt	540
tgctgatatg	gtctacttgc	cggtctgccc	atgtatgcag	acacaacaca	aacttgagat	600
ggacaaaaag	gatggagtgt	ttggatgcga	gccaatgggt	gtgccaccag	ctcagcagat	660
gtctcgtttt	gatcaacctg	tcctctctcc	agtcggatag	cctcagtcgt	atccaccgcc	720
tgctcaaggc	taccctctct	catcttaacc	gcctcccggt	tatctctcag	attaagaaat	780
ttaaccagta	tcttctattt	atgtgtcaga	ataggggacac	cgcgaatgac	aaccggagge	840
tgatatagtg	ctgatttcga	gacaatggcg	gattttctga	taaaagccgc	tcagataaaca	900
agtgcgttgc	agagagagca	tggaaagtca	cacaaggagt	ttgtgaaaag	tttatgcacc	960
aacaaagaca	tagctgagct	tagaaaaccga	gtcgaagcat	ttgcttttgc	gtatgagatg	1020
cctgcttctc	tatttcgaat	tgaatgaaag	aaaactccac	acaacagcgt	tatttcagat	1080
tgaattttat	attatctctg	gttcaatttt	tttttttttt	tttgaggttc	tatcttgtaa	1140
attagagtaa	atatataatt	atattgggat	tgatttgcac	tatttttttc	cattgttaatt	1200
ctgtaaaacat	tttgataaat	gggaatgatt	actacaaatt	tacttt		

(2) INFORMATION FOR SEQ ID NO:645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..232
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498776

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:645:

Met	Ala	Ala	Ser	Gln	Asp	Lys	Leu	Asp	Lys	Met	Lys	Leu	Arg	Gln	Asp
1			5				10					15			
Tyr	Arg	Asn	Leu	Trp	His	Ser	Asp	Leu	Met	Gly	Thr	Val	Thr	Ala	Asp
			20				25					30			
Thr	Pro	Tyr	Cys	Cys	Ile	Ser	Cys	Leu	Cys	Gly	Pro	Cys	Val	Ser	Tyr
			35				40					45			
Met	Leu	Arg	Arg	Arg	Ala	Leu	Tyr	Asn	Asp	Met	Ser	Arg	Tyr	Thr	Cys
			50				55					60			
Cys	Ala	Gly	Tyr	Met	Pro	Cys	Ser	Gly	Arg	Cys	Gly	Glu	Ser	Lys	Cys
			65				70					75			
Pro	Gln	Leu	Cys	Leu	Ala	Thr	Glu	Val	Phe	Leu	Cys	Phe	Gly	Asn	Ser
			85				90					95			
Val	Ala	Ser	Thr	Arg	Phe	Leu	Leu	Gln	Asp	Glu	Phe	Asn	Ile	Gln	Thr
			100				105					110			
Thr	Gln	Cys	Asp	Asn	Cys	Ile	Ile	Gly	Phe	Met	Phe	Cys	Leu	Ser	Gln
			115				120					125			
Val	Ala	Cys	Ile	Phe	Ser	Ile	Val	Ala	Cys	Ile	Val	Gly	Ser	Asp	Glu
			130				135					140			
Leu	Ser	Glu	Ala	Ser	Gln	Ile	Leu	Ser	Cys	Cys	Ala	Asp	Met	Val	Tyr
			145				150					155			
Cys	Thr	Val	Cys	Ala	Cys	Met	Gln	Thr	Gln	His	Lys	Leu	Glu	Met	Asp
			165				170					175			
Lys	Arg	Asp	Gly	Val	Phe	Gly	Ser	Gln	Pro	Met	Gly	Val	Pro	Pro	Ala
			180				185					190			
Gln	Gln	Met	Ser	Arg	Phe	Asp	Gln	Pro	Val	Pro	Pro	Pro	Val	Gly	Tyr
			195				200					205			
Pro	Gln	Ser	Tyr	Pro	Pro	Pro	Ala	Gln	Gly	Tyr	Pro	Pro	Ala	Ser	Tyr
			210				215					220			
Pro	Pro	Pro	Gly	Tyr	Pro	Gln	His								
			225				230								

(2) INFORMATION FOR SEQ ID NO:646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..222
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498777
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:646:
Met Lys Leu Arg Gln Asp Tyr Arg Asn Leu Trp His Ser Asp Leu Met
1 5 10 15
Gly Thr Val Thr Ala Asp Thr Pro Tyr Cys Cys Ile Ser Cys Leu Cys
 20 25 30
Gly Pro Cys Val Ser Tyr Met Leu Arg Arg Ala Leu Tyr Asn Asp
 35 40 45
Met Ser Arg Tyr Thr Cys Cys Ala Gly Tyr Met Pro Cys Ser Gly Arg
 50 55 60
Cys Gly Glu Ser Lys Cys Pro Gln Leu Cys Leu Ala Thr Glu Val Phe
65 70 75 80
Leu Cys Phe Gly Asn Ser Val Ala Ser Thr Arg Phe Leu Leu Gln Asp
 85 90 95
Glu Phe Asn Ile Gln Thr Thr Gln Cys Asp Asn Cys Ile Ile Gly Phe
 100 105 110
Met Phe Cys Leu Ser Gln Val Ala Cys Ile Phe Ser Ile Val Ala Cys
 115 120 125
Ile Val Gly Ser Asp Glu Leu Ser Glu Ala Ser Gln Ile Leu Ser Cys
 130 135 140
Cys Ala Asp Met Val Tyr Cys Thr Val Cys Ala Cys Met Gln Thr Gln
145 150 155 160
His Lys Leu Glu Met Asp Lys Arg Asp Gly Val Phe Gly Ser Gln Pro
 165 170 175
Met Gly Val Pro Pro Ala Gln Gln Met Ser Arg Phe Asp Gln Pro Val
 180 185 190
Pro Pro Pro Val Gly Tyr Pro Gln Ser Tyr Pro Pro Pro Ala Gln Gly
 195 200 205
Tyr Pro Pro Ala Ser Tyr Pro Pro Pro Gly Tyr Pro Gln His
 210 215 220
(2) INFORMATION FOR SEQ ID NO:647:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 207 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..207
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498778
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:647:
Met Gly Thr Val Thr Ala Asp Thr Pro Tyr Cys Cys Ile Ser Cys Leu
1 5 10 15
Cys Gly Pro Cys Val Ser Tyr Met Leu Arg Arg Ala Leu Tyr Asn
 20 25 30
Asp Met Ser Arg Tyr Thr Cys Cys Ala Gly Tyr Met Pro Cys Ser Gly
 35 40 45
Arg Cys Gly Glu Ser Lys Cys Pro Gln Leu Cys Leu Ala Thr Glu Val
 50 55 60
Phe Leu Cys Phe Gly Asn Ser Val Ala Ser Thr Arg Phe Leu Leu Gln
65 70 75 80
Asp Glu Phe Asn Ile Gln Thr Thr Gln Cys Asp Asn Cys Ile Ile Gly
 85 90 95
Phe Met Phe Cys Leu Ser Gln Val Ala Cys Ile Phe Ser Ile Val Ala
 100 105 110

Cys Ile Val Gly Ser Asp Glu Leu Ser Glu Ala Ser Gln Ile Leu Ser
115 120 125
Cys Cys Ala Asp Met Val Tyr Cys Thr Val Cys Ala Cys Met Gln Thr
130 135 140
Gln His Lys Leu Glu Met Asp Lys Arg Asp Gly Val Phe Gly Ser Gln
145 150 155 160
Pro Met Gly Val Pro Pro Ala Gln Gln Met Ser Arg Phe Asp Gln Pro
165 170 175
Val Pro Pro Pro Val Gly Tyr Pro Gln Ser Tyr Pro Pro Ala Gln
180 185 190
Gly Tyr Pro Pro Ala Ser Tyr Pro Pro Gly Tyr Pro Gln His
195 200 205

(2) INFORMATION FOR SEQ ID NO:648:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1182

(D) OTHER INFORMATION: / Ceres Seq. ID 1498779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:648:

aataggtcag	agagaaacatt	tcttattggt	ttagtttgac	gtctggtctc	tgttttgcwt	60
ctttctaatac	aacccatagc	tttcattctt	ttctctctt	cagcagtggt	ttcaagaaaa	120
tgctagtaaat	actttttgtg	tctgtcaatt	tcaggagaaa	aggcattttc	ttgttcgcga	180
tcgatttgaa	ccggccocta	tctgaacaa	ggccatttga	tgttgttttg	cataaagttgt	240
tgggaaaaga	gtgggaagag	gttattgagg	attaccaaca	aaaacaccca	gaagtgaactg	300
tgcttgatcc	tccaggatca	atacagcgta	tataataatc	acaatcgatg	cttcagggta	360
tggcagattt	gaaactgtca	gattgcagtg	gcagcctttt	tgttccaaga	caaattggttg	420
tcttgaaaga	tccagcagct	agtgtgatg	cagttgtgga	agctggtctc	aaatttccac	480
tagttgcaag	ccgctctgga	tcgattggac	tgcaaaagtc	catcaattgt	acttggtcta	540
tgacaggcgc	tcgcttgccg	agcttgatcc	gccttttagt	cttcaagagt	ttgtaataca	600
tggtggagtt	atgttcaagg	tatttgtggt	gggtgatggt	ataaaagtc	tgagacggtt	660
ttctctacca	aatgtgaag	attgtgaaaa	agccaaagtt	gatggcggtc	tccaattccc	720
aagggtttca	tcagctgctg	cttcagctga	taacgcagac	ttggaccctc	gtgttgctga	780
gtcactccca	aagcctttcc	tcgaggcgct	tgtgaaagag	ctaagaagct	tattgggact	840
tcggcttttc	aacatagaca	tgatcaggga	acatggggagc	aaaaacgtgt	tttatgttat	900
tgacatcaac	tattttcctg	gttacggaaa	actgccagac	tacgagcaag	cttttgtaga	960
ttcttcccaa	aatctggcgc	aggtcaataa	taagaagaga	caacatttga	aatgaaagaa	1020
aatggcgcca	gttttttagat	ggtctactaa	gaagcgacaa	ataataaaat	gtctaatat	1080
ggattgtgat	agaatttagc	tctcccttat	ggaagcagta	tcagataaac	aagttttgat	1140
tactgatttt	gaattttcag	tgaaataaac	gtctcttcat	cc		

(2) INFORMATION FOR SEQ ID NO:649:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..152

(D) OTHER INFORMATION: / Ceres Seq. ID 1498780

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:649:

Met	Leu	Val	Ile	Leu	Phe	Val	Ser	Val	Asn	Phe	Arg	Arg	Lys	Gly	Ile
1		5						10						15	
Phe	Phe	Val	Ala	Ile	Asp	Leu	Asn	Arg	Pro	Leu	Ser	Glu	Gln	Gly	Pro
		20					25					30			
Phe	Asp	Val	Val	Leu	His	Lys	Leu	Gly	Lys	Glu	Trp	Glu	Glu	Val	

35 40 45
Ile Glu Asp Tyr Gln Gln Lys His Pro Glu Val Thr Val Leu Asp Pro
50 55 60
Pro Gly Ser Ile Gln Arg Ile Tyr Asn Arg Gln Ser Met Leu Gln Gly
65 70 75 80
Met Ala Asp Leu Lys Leu Ser Asp Cys Ser Gly Ser Leu Phe Val Pro
85 90 95
Lys Gln Met Val Val Leu Lys Asp Ser Ala Ala Ser Ala Asp Ala Val
100 105 110
Val Glu Ala Gly Leu Lys Phe Pro Leu Val Ala Ser Arg Ser Gly Ser
115 120 125
Met Gly Leu Gln Ser His Ile Asn Cys Thr Trp Leu Met Thr Gly Ala
130 135 140
Arg Leu Gln Ser Leu Ile Arg Leu
145 150

(2) INFORMATION FOR SEQ ID NO:650:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498781

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:650:

Met Phe Lys Val Phe Val Val Gly Asp Val Ile Lys Val Met Arg Arg
1 5 10 15
Phe Ser Leu Pro Asn Val Ser Asn Cys Glu Lys Ala Lys Val Asp Gly
20 25 30
Val Phe Gln Phe Pro Arg Val Ser Ser Ala Ala Ala Ser Ala Asp Asn
35 40 45
Ala Asp Leu Asp Pro Arg Val Ala Glu Leu Pro Pro Lys Pro Phe Leu
50 55 60
Glu Ala Leu Val Lys Glu Leu Arg Ser Leu Leu Gly Leu Arg Leu Phe
65 70 75 80
Asn Ile Asp Met Ile Arg Glu His Gly Ser Lys Asn Val Phe Tyr Val
85 90 95
Ile Asp Ile Asn Tyr Phe Pro Gly Tyr Gly Lys Leu Pro Asp Tyr Glu
100 105 110
Gln Val Phe Val Asp Phe Phe Gln Asn Leu Ala Gln Val Lys Tyr Lys
115 120 125
Lys Arg Gln His Cys Lys
130

(2) INFORMATION FOR SEQ ID NO:651:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..121
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498782

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:651:

Met Arg Arg Phe Ser Leu Pro Asn Val Ser Asn Cys Glu Lys Ala Lys
1 5 10 15
Val Asp Gly Val Phe Gln Phe Pro Arg Val Ser Ser Ala Ala Ala Ser
20 25 30

(A1) SEQUENCE BLOCK															
Xaa	Ser	Phe	Lys	Glu	Ile	Val	Ser	Lys	Tyr	Ser	Arg	Glu	Val	Arg	Glu
1				5					10					15	
Val	Gly	Phe	Lys	Ile	Glu	Glu	Leu	Ile	Ser	Glu	Ser	Leu	Gly	Leu	Glu
			20					25					30		
Lys	Asp	Tyr	Met	Lys	Lys	Val	Leu	Gly	Gln	Gly	Gln	His	Met	Ala	
		35					40					45			
Val	Asn	Tyr	Tyr	Pro	Pro	Cys	Pro	Glu	Pro	Glu	Leu	Thr	Tyr	Gly	Leu
	50					55					60				
Pro	Ala	His	Thr	Asp	Pro	Asn	Ala	Leu	Thr	Ile	Leu	Leu	Gln	Asp	Thr
65					70				75					80	
Thr	Val	Cys	Gly	Leu	Gln	Ile	Leu	Ile	Asp	Gly	Gln	Trp	Phe	Ala	Val
			85						90					95	

Asn Pro His Pro Asp Ala Phe Val Ile Asn Ile Gly Asp Gln Leu Gln
100 105 110
Ala Leu Ser Asn Gly Val Tyr Lys Ser Val Trp Arg Arg Ala Val Thr
115 120 125
Asn Thr Glu Asn Pro Arg Leu Ser Val Ala Ser Phe Leu Cys Pro Ala
130 135 140
Asp Cys Ala Val Met Ser Pro Ala Lys Pro Leu Trp Glu Ala Glu Asp
145 150 155 160
Asp Glu Thr Lys Pro Val Tyr Lys Asp Phe Thr Tyr Ala Glu Tyr Tyr
165 170 175
Lys Lys Phe Trp Ser Arg Asn Leu Asp Gln Glu His Phe Leu Glu Asn
180 185 190
Phe Leu Asn Asn
195

(2) INFORMATION FOR SEQ ID NO:654:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..161

(D) OTHER INFORMATION: / Ceres Seq. ID 1498785

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:654:

Met Lys Lys Val Leu Gly Glu Gln Gly Gln His Met Ala Val Asn Tyr
1 5 10 15
Tyr Pro Pro Cys Pro Glu Pro Glu Leu Thr Tyr Gly Leu Pro Ala His
20 25 30
Thr Asp Pro Asn Ala Leu Thr Ile Leu Leu Gln Asp Thr Thr Val Cys
35 40 45
Gly Leu Gln Ile Leu Ile Asp Gly Gln Trp Phe Ala Val Asn Pro His
50 55 60
Pro Asp Ala Phe Val Ile Asn Ile Gly Asp Gln Leu Gln Ala Leu Ser
65 70 75 80
Asn Gly Val Tyr Lys Ser Val Trp Arg Arg Ala Val Thr Asn Thr Glu
85 90 95
Asn Pro Arg Leu Ser Val Ala Ser Phe Leu Cys Pro Ala Asp Cys Ala
100 105 110
Val Met Ser Pro Ala Lys Pro Leu Trp Glu Ala Glu Asp Asp Glu Thr
115 120 125
Lys Pro Val Tyr Lys Asp Phe Thr Tyr Ala Glu Tyr Tyr Lys Lys Phe
130 135 140
Trp Ser Arg Asn Leu Asp Gln Glu His Phe Leu Glu Asn Phe Leu Asn
145 150 155 160
Asn

(2) INFORMATION FOR SEQ ID NO:655:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1498786

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:655:

Met Ala Val Asn Tyr Tyr Pro Pro Cys Pro Glu Pro Glu Leu Thr Tyr

1	5	10	15
Gly Leu Pro Ala His Thr Asp Pro Asn Ala Leu Thr Ile Leu Leu Gln			
20	25	30	
Asp Thr Thr Val Cys Gly Leu Gln Ile Leu Ile Asp Gly Gln Trp Phe			
35	40	45	
Ala Val Asn Pro His Pro Asp Ala Phe Val Ile Asn Ile Gly Asp Gln			
50	55	60	
Leu Gln Ala Leu Ser Asn Gly Val Tyr Lys Ser Val Trp Arg Arg Ala			
65	70	75	80
Val Thr Asn Thr Glu Asn Pro Arg Leu Ser Val Ala Ser Phe Leu Cys			
85	90	95	
Pro Ala Asp Cys Ala Val Met Ser Pro Ala Lys Pro Leu Trp Glu Ala			
100	105	110	
Glu Asp Asp Glu Thr Lys Pro Val Tyr Lys Asp Phe Thr Tyr Ala Glu			
115	120	125	
Tyr Tyr Lys Lys Phe Trp Ser Arg Asn Leu Asp Gln Glu His Phe Leu			
130	135	140	
Glu Asn Phe Leu Asn Asn			
145	150		

(2) INFORMATION FOR SEQ ID NO:656:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1676 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1676
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:656:

attaagacgg gatgttgtaa ttaaacacct accaacagac aaaaacaaaa gataggaagc	60
cacgtatgca tatatttagg tgaagctttt gataaaacaa agcgttgggc tcttccaaat	120
atcaaaacaa gttttttttt ttgtttggct tataattcac ctgagaaaaa caatatcaat	180
cggtctggtt tctctctcca gtgtttcttc agtagtcctg cgagatcgta taagagattc	240
gaaaccctaa tctatcaatt tgatcctgtc cattctctgt tattgtttga gaattgtgca	300
atccgatggg gacgatgcac cggagtggtg ctcccagaag gacaaatgaa aatgcgaagc	360
ttatcataac gacaatcgtg ggagtggtgt ttgtttttt tggttggtatc acattaccat	420
taggttctct tagaagatt agcttacct caggccttat gtcattctct gatgtagcca	480
tgtcagatgg gaaattgttt tctggtggca gatcacctga agatattggt tcaagaagaat	540
ctcctaagat atattgtcca accaatccgc atggtgcaga actactctct ctctgggatta	600
tagtggcaga aacagatttc tacttgcgcc gattatgggg tgaacctagt gaagatttga	660
agaagaagcc aaagtatctc gtaactttta cagttggatt tgagcagaga aacaacaaa	720
atgcagctgt taagaagttt tctgaagatt tccaaatatt gttattccat tatgtgggcc	780
gaacaactga gtgggaccag tttagtggtt ctaaaaatgc aatacatatc atgcaaaaaa	840
agcaaacaaa atggttggtat gcaaaagagt ttgtgcatcc tgatgtgtgc tcatgcttag	900
agtatatatt tatatgggat gaagatcttg gagtcgagca cttcaatgca gatagtgaa	960
ttactgtctt gaaattgtag ttgcagatca gtgacaatct ttacaattt tattttaaat	1020
tttcaggtac gttgagttag ttaagaagca tgggtttggag atttctcaac caggcttaga	1080
gccaaacaa cgaactacat gggaaaatgc aaagaggaga ggtgaccgag atgtccacaa	1140
agaaactaag gaaaaaccag gatggtgcag tgatccacat ttacctccat gtgctcgctt	1200
tggtgatgat atggcacctg tattttctag agaagcatgg cgatgtatgt ggcattgat	1260
tcagaaatgat ctgtttcatg gatgggtctc cgattttgct ctacagacat gcgttgagcc	1320
gctctgatgc aagattgggtg tggtagattc acagttgatt atccatcaag tgattccctc	1380
ttcttgaagt cagggtgagt cggaggaggg gaaatctcca tggcgaaggg tgaggagagat	1440
atgcagaaac gaatggacga tgttccagaa tcgcgtggca gaagctacat aagcatcat	1500
ggacaacaac aaggtaaaag aataatttgg gccctctctt actctgtctc tgttaaatga	1560
gcttacgttt cccgatgcaa gtgagtgtag ggagagagat ctatgtagtc ccctatttag	1620
tttaaaacat ctacagatata tctacattat tagcttttta cctaataatat ttcttc	

(2) INFORMATION FOR SEQ ID NO:657:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..217
(D) OTHER INFORMATION: / Ceres Seq. ID 1498790
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657:
Met Gly Thr Met His Arg Ser Gly Ala Pro Arg Arg Thr Asn Glu Asn
1 5 10 15
Ala Lys Leu Ile Ile Thr Thr Ile Val Gly Val Val Phe Gly Phe Phe
20 25 30
Val Gly Ile Thr Leu Pro Leu Gly Ser Phe Arg Lys Ile Ser Leu Pro
35 40 45
Ser Gly Leu Met Ser Ser Leu Asp Val Ala Met Ser Asp Gly Lys Leu
50 55 60
Phe Ser Gly Gly Arg Ser Pro Glu Asp Ile Gly Ser Arg Lys Ser Pro
65 70 75 80
Lys Ile Tyr Val Pro Thr Asn Pro His Gly Ala Glu Leu Leu Pro Pro
85 90 95
Gly Ile Ile Val Ala Glu Thr Asp Phe Tyr Leu Arg Arg Leu Trp Gly
100 105 110
Glu Pro Ser Glu Asp Leu Lys Lys Lys Pro Lys Tyr Leu Val Thr Phe
115 120 125
Thr Val Gly Phe Glu Gln Arg Asn Asn Ile Asn Ala Ala Val Lys Lys
130 135 140
Phe Ser Glu Asp Phe Gln Ile Leu Leu Phe His Tyr Asp Gly Arg Thr
145 150 155 160
Thr Glu Trp Asp Gln Phe Glu Trp Ser Lys Asn Ala Ile His Ile Ser
165 170 175
Ala Lys Lys Gln Thr Lys Trp Trp Tyr Ala Lys Arg Phe Leu His Pro
180 185 190
Asp Val Val Ser Ala Tyr Glu Tyr Ile Phe Ile Trp Asp Glu Asp Leu
195 200 205
Gly Val Glu His Phe Asn Ala Asp Arg
210 215
(2) INFORMATION FOR SEQ ID NO:658:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 214 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..214
(D) OTHER INFORMATION: / Ceres Seq. ID 1498791
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:658:
Met His Arg Ser Gly Ala Pro Arg Arg Thr Asn Glu Asn Ala Lys Leu
1 5 10 15
Ile Ile Thr Thr Ile Val Gly Val Val Phe Gly Phe Phe Val Gly Ile
20 25 30
Thr Leu Pro Leu Gly Ser Phe Arg Lys Ile Ser Leu Pro Ser Gly Leu
35 40 45
Met Ser Ser Leu Asp Val Ala Met Ser Asp Gly Lys Leu Phe Ser Gly
50 55 60
Gly Arg Ser Pro Glu Asp Ile Gly Ser Arg Lys Ser Pro Lys Ile Tyr
65 70 75 80
Val Pro Thr Asn Pro His Gly Ala Glu Leu Leu Pro Pro Gly Ile Ile

85 90 95
Val Ala Glu Thr Asp Phe Tyr Leu Arg Leu Trp Gly Glu Pro Ser
100 105 110
Glu Asp Leu Lys Lys Lys Pro Lys Tyr Leu Val Thr Phe Thr Val Gly
115 120 125
Phe Glu Gln Arg Asn Asn Ile Asn Ala Ala Val Lys Lys Phe Ser Glu
130 135 140
Asp Phe Gln Ile Leu Leu Phe His Tyr Asp Gly Arg Thr Thr Glu Trp
145 150 155 160
Asp Gln Phe Glu Trp Ser Lys Asn Ala Ile His Ile Ser Ala Lys Lys
165 170 175
Gln Thr Lys Trp Trp Tyr Ala Lys Arg Phe Leu His Pro Asp Val Val
180 185 190
Ser Ala Tyr Glu Tyr Ile Phe Ile Trp Asp Glu Asp Leu Gly Val Glu
195 200 205
His Phe Asn Ala Asp Arg
210

(2) INFORMATION FOR SEQ ID NO:659:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..166
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498792

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:659:

Met Ser Ser Leu Asp Val Ala Met Ser Asp Gly Lys Leu Phe Ser Gly
1 5 10 15
Gly Arg Ser Pro Glu Asp Ile Gly Ser Arg Lys Ser Pro Lys Ile Tyr
20 25 30
Val Pro Thr Asn Pro His Gly Ala Glu Leu Leu Pro Pro Gly Ile Ile
35 40 45
Val Ala Glu Thr Asp Phe Tyr Leu Arg Arg Leu Trp Gly Glu Pro Ser
50 55 60
Glu Asp Leu Lys Lys Lys Pro Lys Tyr Leu Val Thr Phe Thr Val Gly
65 70 75 80
Phe Glu Gln Arg Asn Asn Ile Asn Ala Ala Val Lys Lys Phe Ser Glu
85 90 95
Asp Phe Gln Ile Leu Leu Phe His Tyr Asp Gly Arg Thr Thr Glu Trp
100 105 110
Asp Gln Phe Glu Trp Ser Lys Asn Ala Ile His Ile Ser Ala Lys Lys
115 120 125
Gln Thr Lys Trp Trp Tyr Ala Lys Arg Phe Leu His Pro Asp Val Val
130 135 140
Ser Ala Tyr Glu Tyr Ile Phe Ile Trp Asp Glu Asp Leu Gly Val Glu
145 150 155 160
His Phe Asn Ala Asp Arg
165

(2) INFORMATION FOR SEQ ID NO:660:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1373

(D) OTHER INFORMATION: / Ceres Seq. ID 1498801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:660:

(X1) SEQUENCE DESCRIPTION: SLP 2						
atgtcttggtc	tttatgtttaa	cgcgcgcgac	ctctctctct	ggtcggagaa	atctccagat	60
ttgtgtcattt	ctccaattctt	ctcgggaacc	taattttaac	aaacctctcc	tccttcagat	120
ttcaatctct	ctcaatctcc	ctaaaaagct	aaacctttct	ctactcaaat	ctataaacat	180
ggcaattcaga	gcacaacaaca	aatctccaga	atcgcgattc	cgctccaatt	cacacaaccac	240
ggaatttcgat	ccagcaataca	tggttcctga	tcacaaacac	actcttaaat	ttctgccaat	300
aatggtgcgc	ggttcaabgc	ctggctcagt	cgaaacaatg	gctatgttct	catgtatgac	360
agctaaaaac	catatgcag	ctctctgttc	atgtccgatt	aaaccaatct	gacatcgcta	420
atgcttcogt	tcfaatatca	aaaccgatgg	accttctgt	ttatatagag	gtatttggcg	480
ttgtggcaat	ggtgtgcgac	cacctcacgc	tggtttattc	tcattctatg	aagtccttaa	540
gaagtttttta	tcoggtggaa	acgctaataa	ctctctgcga	cacgctattt	ccggtgtttt	600
cgtcactata	ctatagtatg	ctgtgtttac	tcocattggat	atggttaaga	aaaggtgtga	660
atggttgaat	ggaacttata	aaggaattac	ggatgtgtat	aagagagtaa	ccgctgagga	720
agggtttggg	gcttttttaac	ctctgtatat	aactactgtg	ttgatgaatg	ctccgtttac	780
cgctgtcgat	ttcactaact	atgagcggct	taagagaggt	tttagggaga	tgtttctcga	840
gcactgtctt	ggagttagag	atgaggaaag	ttggttgatt	ttatgctaact	ctggagctgc	900
ggctgtgtgg	ttgtcggctg	ctgaataact	tcctgctgat	gtttgttaaga	cgcagattga	960
atgtcagggt	gtgtgttggt	gtgaccgttt	caagagcagt	tcataaatgc	atgtgttcgc	1020
tacaaatagt	aagaaagacg	gttatagagc	acttgctaga	ggatggctga	caagaatgct	1080
ctctccagct	ccagcagctg	cgattttgct	gtccacttat	gaacacgtca	aatctttctt	1140
ctcaagatct	atggtgtga	caaacgcgac	ttgaaaagac	acaaacatca	atcgcttgtt	1200
cataatttca	ttgtcgtgat	caggtcttat	attcttcata	gacagactga	ctggtgtggt	1260
agattaaaca	ctgtcctatta	gagaagatct	ctggtttgat	aattttttct	ttttcttcac	1320
cgaaataatc	tatcacttta	gaggtataac	accccacgag	ctctttttct	ggt	

(2) INFORMATION FOR SEQ ID NO:661:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 331 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

```
(ix) FEATURE:
```

(A) NAME/KEY: peptide

(B) LOCATION: 1..331

(D) OTHER INFORMATION: / Ceres Seq. ID 1498802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:661:

Met	Ala	Thr	Thr	Glu	Ala	Thr	Thr	Lys	Phe	Pro	Glu	Ser	Asp	Leu	Arg	Pro
1				5						10					15	
Ile	Pro	Gln	Pro	Pro	Asp	Phe	His	Pro	Ala	Ile	Ile	Val	Pro	Ala	Gln	
			20					25						30		
Asn	Thr	Thr	Leu	Lys	Phe	Trp	Gln	Leu	Met	Val	Ala	Gly	Ser	Ile	Ala	
			35				40					45				
Gly	Ser	Val	Glu	His	Met	Ala	Met	Phe	Pro	Val	Asp	Thr	Val	Lys	Thr	
			50				55				60					
His	Met	Gln	Ala	Leu	Arg	Ser	Cys	Pro	Ile	Lys	Pro	Ile	Gly	Ile	Arg	
65					70					75					80	
Gln	Ala	Phe	Arg	Ser	Ile	Ile	Lys	Thr	Asp	Gly	Pro	Ser	Ala	Leu	Tyr	
				85					90					95		
Arg	Gly	Ile	Trp	Ala	Met	Gly	Leu	Gly	Ala	Gly	Pro	Ala	His	Ala	Val	
			100					105					110			
Tyr	Phe	Ser	Phe	Tyr	Glu	Val	Ser	Lys	Lys	Phe	Leu	Ser	Gly	Gly	Asn	
			115					120				125				
Pro	Asn	Asn	Ser	Ala	Ala	His	Ala	Ile	Ser	Gly	Val	Phe	Ala	Thr	Ile	
			130				135					140				
Ser	Ser	Asp	Ala	Val	Phe	Thr	Pro	Met	Asp	Met	Val	Lys	Gln	Arg	Leu	
145					150					155					160	
Gln	Ile	Gly	Asn	Gly	Thr	Tyr	Lys	Gly	Val	Trp	Asp	Cys	Ile	Lys	Arg	
				165					170					175		
Val	Thr	Arg	Glu	Glu	Gly	Phe	Gly	Ala	Phe	Tyr	Ala	Ser	Tyr	Arg	Thr	
			180					185						190		

Thr	Val	Leu	Met	Asn	Ala	Pro	Phe	Thr	Ala	Val	His	Phe	Thr	Thr	Tyr
	195						200					205			
Glu	Ala	Val	Lys	Arg	Gly	Leu	Arg	Glu	Met	Phe	Pro	Glu	His	Ala	Val
	210					215					220				
Gly	Val	Glu	Asp	Glu	Glu	Gly	Trp	Leu	Ile	Tyr	Ala	Thr	Ala	Gly	Ala
	225				230					235				240	
Ala	Ala	Gly	Gly	Leu	Ala	Ala	Ala	Val	Thr	Thr	Pro	Leu	Asp	Val	Val
				245					250					255	
Lys	Thr	Gln	Leu	Gln	Cys	Gln	Gly	Val	Cys	Gly	Cys	Asp	Arg	Phe	Lys
			260					265						270	
Ser	Ser	Ser	Ile	Ser	Asp	Val	Phe	Arg	Thr	Ile	Val	Lys	Lys	Asp	Gly
			275					280						285	
Tyr	Arg	Gly	Leu	Ala	Arg	Gly	Trp	Leu	Pro	Arg	Met	Leu	Phe	His	Ala
			290				295				300				
Pro	Ala	Ala	Ala	Ile	Cys	Trp	Ser	Thr	Tyr	Glu	Thr	Val	Lys	Ser	Phe
					310						315				320
Phe	Gln	Asp	Leu	Asn	Gly	Glu	Ala	Asn	Ala	Ala					
					325					330					

(2) INFORMATION FOR SEQ ID NO:662:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 290 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..290

(D) OTHER INFORMATION: / Ceres Seq. ID 1498803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:662:

Met	Val	Ala	Gly	Ser	Ile	Ala	Gly	Ser	Val	Glu	His	Met	Ala	Met	Phe
1			5					10					15		
Pro	Val	Asp	Thr	Val	Lys	Thr	His	Met	Gln	Ala	Leu	Arg	Ser	Cys	Pro
			20				25						30		
Ile	Lys	Pro	Ile	Gly	Ile	Arg	Gln	Ala	Phe	Arg	Ser	Ile	Ile	Lys	Thr
			35				40					45			
Asp	Gly	Pro	Ser	Ala	Leu	Tyr	Arg	Gly	Ile	Trp	Ala	Met	Gly	Leu	Gly
			50				55				60				
Ala	Gly	Pro	Ala	His	Ala	Val	Tyr	Phe	Ser	Phe	Tyr	Glu	Val	Ser	Lys
				70						75				80	
Lys	Phe	Leu	Ser	Gly	Gly	Asn	Pro	Asn	Asn	Ser	Ala	Ala	His	Ala	Ile
				85					90				95		
Ser	Gly	Val	Phe	Ala	Thr	Ile	Ser	Ser	Asp	Ala	Val	Phe	Thr	Pro	Met
			100					105					110		
Asp	Met	Val	Lys	Gln	Arg	Leu	Gln	Ile	Gly	Asn	Gly	Thr	Tyr	Lys	Gly
			115				120					125			
Val	Trp	Asp	Cys	Ile	Lys	Arg	Val	Thr	Arg	Glu	Glu	Gly	Phe	Gly	Ala
			130				135				140				
Phe	Tyr	Ala	Ser	Tyr	Arg	Thr	Thr	Val	Leu	Met	Asn	Ala	Pro	Phe	Thr
			145			150				155				160	
Ala	Val	His	Phe	Thr	Thr	Tyr	Glu	Ala	Val	Lys	Arg	Gly	Leu	Arg	Glu
			165						170					175	
Met	Phe	Pro	Glu	His	Ala	Val	Gly	Val	Glu	Asp	Glu	Glu	Gly	Trp	Leu
			180					185					190		
Ile	Tyr	Ala	Thr	Ala	Gly	Ala	Ala	Ala	Gly	Gly	Leu	Ala	Ala	Ala	Val
			195					200				205			
Thr	Thr	Pro	Leu	Asp	Val	Val	Lys	Thr	Gln	Leu	Gln	Cys	Gln	Gly	Val
			210				215					220			
Cys	Gly	Cys	Asp	Arg	Phe	Lys	Ser	Ser	Ser	Ile	Ser	Asp	Val	Phe	Arg
			225			230				235				240	
Thr	Ile	Val	Lys	Lys	Asp	Gly	Tyr	Arg	Gly	Leu	Ala	Arg	Gly	Trp	Leu

(2) INFORMATION FOR SEQ ID NO:663:

(i) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:

(2) INFORMATION FOR SEQ ID NO:664:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1186 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1186

(D) OTHER INFORMATION: / Ceres Seq. ID 1498808

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:664:

accatccact	ctactcaaca	tggaactctc	caaactctca	tctctctctc	tttgccctctt	60
cctcatttgc	attatctatc	tcccaccaaca	ttctctcgca	tgcggctctt	gcaaccaca	120
gaagggcgga	aagcactccc	ctaagctacc	agttccctcg	gtgaccgtcc	ctaagctacc	180
agttctctcg	gtgaccgtcc	ctaagctacc	agttccctcg	gtgaccgtcc	ctaagctacc	240
cggttctctc	gtgaccatcc	ctaagctacc	cggttccacca	gtgactgtac	ctaagctacc	300
cggttctctc	gtgaccgtcc	ctaagctacc	cggttctctca	gtgaccgtcc	ctaagctacc	360
cggttctctca	gtgaccgtcc	ctaagctacc	cggttccctcg	gtgactgtac	ctaagctacc	420
cggttctctca	gtgaccgtcc	ctaagctacc	ccttccctcg	atttcagggc	taccataacc	480
tccagtggtg	ggtcccaatc	tgccattgcc	acctttgcc	attgtaggtc	ctattctctc	540
acgggggaaca	accccaccag	ccacaggagg	gaaggactgt	cctccaccgc	caggggagcgt	600
aaagccacca	tcagggggcg	ggaaggcgac	atgtccaata	gacacgctga	agttagggtgc	660
ttgctgtcag	ttgttgggag	gtttagtaaa	gatagggctt	ggggatccag	cagttaaaca	720
atgtgtgtcg	ttacttaaac	gcctcgttga	aatcgaagcc	gcggcttgtc	tctgcactac	780
ccctcaagctc	aaagctcttg	acctcaaatc	ttatgtccct	gatgtctctc	agctctctct	840
tacctgtggc	aaaaaatccc	ctccgggcta	cacttgttcc	atatgataaa	ctcactccac	900
ttataaaagg	tgctttggag	aaaaaagtga	gaagagaatg	gcagagctcc	aatctttctc	960
gtcttggttt	accaaaatac	tcataatcaa	tcctatccct	ttgattcttt	ctctatcgct	1020
tccttatatg	ttgtatcatt	aattaatgtg	tgctttttag	attaatgatt	cttctcttgt	1080
attaaagtat	gatttgaat	cccttttttt	tctctatctc	tttttttga	attgattgaa	1140
ctgcgttcat	gatactgtca	aaaagagaga	aaaagagtac	aatttt		

(2) INFORMATION FOR SEQ ID NO:665:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 294 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..294

(D) OTHER INFORMATION: / Ceres Seq. ID 1498809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:665:

Pro	Ser	Thr	Leu	Leu	Asn	Met	Asp	Ser	Ser	Ser	Lys	Leu	Ser	
1				5					10			15		
Leu	Cys	Leu	Phe	Leu	Ile	Cys	Ile	Ile	Tyr	Leu	Pro	Gln	His	Ser
				20				25				30		
Ala	Cys	Gly	Ser	Cys	Asn	Pro	Arg	Lys	Gly	Gly	Lys	His	Ser	Pro
				35			40					45		
Leu	Pro	Val	Pro	Pro	Val	Thr	Val	Pro	Lys	Leu	Pro	Val	Pro	Val
				50			55			60				
Thr	Val	Pro	Lys	Leu	Pro	Val	Pro	Pro	Val	Thr	Val	Pro	Lys	Leu
				65			70			75				80
Val	Pro	Pro	Val	Thr	Ile	Pro	Lys	Leu	Pro	Val	Pro	Pro	Val	Thr
				85				90						95
Pro	Lys	Leu	Pro	Val	Pro	Pro	Val	Thr	Val	Pro	Lys	Leu	Pro	Val
				100			105					110		
Pro	Val	Thr	Val	Pro	Lys	Leu	Pro	Val	Pro	Pro	Val	Thr	Val	Pro
				115			120					125		
Leu	Pro	Val	Pro	Pro	Val	Thr	Val	Pro	Lys	Leu	Pro	Val	Pro	Val
				130			135			140				
Thr	Val	Pro	Lys	Leu	Pro	Leu	Pro	Pro	Ile	Ser	Gly	Leu	Pro	Ile
				145			150			155				160
Pro	Val	Val	Gly	Pro	Asn	Leu	Pro	Leu	Pro	Pro	Leu	Pro	Ile	Val
				165				170						175
Pro	Ile	Leu	Pro	Pro	Gly	Thr	Thr	Pro	Pro	Ala	Thr	Gly	Gly	Lys

1	Net	Asp	Ser	Ser	5	Leu	Ser	Ser	10	Leu	Ser	Cys	Leu	Pro	15	Pro
Cys	Ile	Ile	Tyr	20	Leu	Pro	Gln	His	25	Ser	Leu	Ala	Cys	Gly	30	Cys
Pro	Arg	Lys	Gly	35	Gly	Lys	His	Ser	40	Ser	Pro	Lys	Leu	Pro	Val	Pro
Thr	Val	Pro	Lys	50	Leu	Pro	Val	Pro	55	Pro	Val	Thr	Val	Pro	Lys	Leu
Val	Pro	Pro	Val	65	Thr	Val	Pro	Lys	70	Leu	Pro	Val	Pro	Pro	Val	Ile
Pro	Lys	Leu	Pro	85	Val	Pro	Pro	Val	90	Thr	Val	Pro	Lys	Leu	Pro	Val
Pro	Val	Thr	Val	100	Pro	Lys	Leu	Pro	105	Val	Pro	Pro	Val	Thr	Val	Lys
Leu	Pro	Val	Pro	115	Pro	Val	Thr	Val	120	Pro	Lys	Leu	Pro	Val	Pro	Val
Thr	Val	Pro	Lys	130	Leu	Pro	Val	Pro	135	Pro	Val	Thr	Val	Pro	Lys	Leu
Leu	Pro	Pro	Ile	145	Ser	Gly	Leu	Pro	150	Pro	Pro	Val	Val	Gly	Pro	Asn
Leu	Pro	Leu	Pro	165	Pro	Leu	Pro	Ile	170	Val	Gly	Pro	Ile	Leu	Pro	Pro
Thr	Thr	Pro	Pro	180	Ala	Thr	Gly	Gly	185	Lys	Asp	Cys	Pro	Pro	Pro	Gly
Ser	Val	Lys	Pro	195	Pro	Ser	Gly	Gly	200	Lys	Ala	Thr	Cys	Pro	Ile	Asp
Thr	Leu	Lys	Leu	210	Gly	Ala	Cys	Val	215	Asp	Leu	Leu	Gly	Gly	Leu	Val
Ile	Gly	Leu	Gly	225	Asp	Pro	Ala	Val	230	Asn	Lys	Cys	Cys	Pro	Leu	Leu
Gly	Leu	Val	Glu	245	Ile	Glu	Ala	Ala	250	Ala	Cys	Leu	Cys	Thr	Leu	Lys
Leu	Lys	Ala	Leu	260	Asp	Leu	Asn	Leu	265	Tyr	Val	Pro	Asp	Ala	Leu	Gln

Leu Leu Thr Cys Gly Lys Asn Pro Pro Pro Gly Tyr Thr Cys Ser Ile
275 280 285

(2) INFORMATION FOR SEQ ID NO:667:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1777
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498811

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:667:

gaagacgaag	aagaagaaga	agaagaagaa	agcttgagac	ttctctctg	tgtgcaattt	60
cgaaatcgat	aaagacttca	actttcgggt	ctaacaatga	caatttccgt	atagtttgat	120
tttgtccacc	ttttccaccg	attacctgat	ttcatcgctg	gcgttagtca	tcaaatggga	180
gctcgttgct	caaaagtctc	attctgcttg	ttcccttctc	acttcaaatc	cgcttcagtt	240
ctcgagtctc	ctgatatcga	gaatggagga	aaagtgtggc	cgacttttaa	ggaattcaaa	300
ttggagcagc	tgaaatctgc	gaccggaggt	ttctcttcag	acaacattgt	atcagaacac	360
ggcgcagaaa	ctccaaacgt	tgctcacaga	ggaaggcttg	atgatggctg	tttgattgct	420
gtcaaacgat	tcaatcgctc	tgcttgggct	gatcatcgac	agttccttga	tgaagctaaa	480
gctgttggga	gcttgaggag	tgatagatta	gcaaactctga	ttggatgttg	ctttgaagga	540
gaagagagat	tactagttgc	tgagtttatg	cctcatgaaa	cgcttgcaaa	gcattctttc	600
cactgggaga	ataatccgat	gaaatggggc	atgagattaa	agttgtcatt	tggttttagca	660
caagcattgg	aataattgtag	taataaaggg	gagagctttg	tatcatgac	tcaatgotta	720
cagggttttg	tttgacaagg	atgggaatcc	caggttgtct	tggtttggac	tcatgaaaaa	780
tagcagagat	gggaagagtt	atagcacaaa	cttggcattt	actcctccag	agtattttgc	840
aacgggttga	gttacaccag	agagtgttgt	attcagtttt	ggaaccggtt	tgctcgatct	900
catgacttga	aaacatatcc	caccgagtca	tcgcgttgac	ctaactcagag	gtaacgaactg	960
tgcaatgtta	atggattctg	ctctcgaggg	tcattttcca	aacgaagacg	gaactgagctg	1020
agtaactgtta	gccacacgtt	gtctgcagta	tgaagctcga	gaaagaccac	atgtgaaatc	1080
tctcgtgact	tcacttgtca	cactccagaa	ggaactctga	gtagcttctc	acgttcttat	1140
gggtataccc	catgaaaccg	aggctgaaga	agagctctcg	ctttcttttg	cacccttttg	1200
tgatgcacgc	ttaagagtgg	atcttacagc	catacaggaa	atactcagta	agattgggata	1260
caaggatgat	gaagggaattg	ccaatgagct	ctcgtttcaa	atgtgggaca	atcagatgca	1320
ggaatctctc	aattcgaaga	agcaaggcga	cttagctttc	cgttccaaag	attttacaac	1380
cgcggtcgat	tgctacacac	agttcataga	tggggggaaca	atggtgtcac	caacagcata	1440
cgacgcgcgg	tgctgttcat	attctgatga	cgacaacgca	caagaggctc	tgacagatgc	1500
attgcagaca	caggttgtgt	ctccggattg	gccaaacggc	ttgtatctcg	aagcggcttg	1560
ctgtgttcaa	ctgggtatgg	aagccgatgc	tcagcaagct	cttaaggatg	ggactacatt	1620
ggaagctaa	aaagagtaaca	agcgtcgata	aaatagcggt	ttcaaaagct	ttgtatatg	1680
ctttattttg	tttctcttct	ctctatttcc	atctatatgc	gcatacatac	acatatgcgg	1740
gtgtatttat	tatatatgtg	catatacttt	tgatggcc			

(2) INFORMATION FOR SEQ ID NO:668:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..291
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:668:

Met	Lys	Asn	Ser	Arg	Asp	Gly	Lys	Ser	Tyr	Ser	Thr	Asn	Leu	Ala	Phe
1			5					10					15		
Thr	Pro	Pro	Glu	Tyr	Leu	Arg	Thr	Gly	Arg	Val	Thr	Pro	Glu	Ser	Val

20	25	30
Val Phe Ser Phe Gly Thr Val Leu Leu Asp Leu Met Ser Gly Lys His		
35	40	45
Ile Pro Pro Ser His Ala Leu Asp Leu Ile Arg Gly Lys Asn Cys Ala		
50	55	60
Met Leu Met Asp Ser Ala Leu Glu Gly His Phe Ser Asn Glu Asp Gly		
65	70	75
Thr Glu Leu Val Arg Leu Ala Thr Arg Cys Leu Gln Tyr Glu Ala Arg		
85	90	95
Glu Arg Pro Asn Val Lys Ser Leu Val Thr Ser Leu Val Thr Leu Gln		
100	105	110
Lys Glu Ser Asp Val Ala Ser Tyr Val Leu Met Gly Ile Pro His Glu		
115	120	125
Thr Glu Ala Glu Glu Glu Ser Pro Leu Ser Leu Thr Pro Phe Gly Asp		
130	135	140
Ala Cys Leu Arg Val Asp Leu Thr Ala Ile Gln Glu Ile Leu Ser Lys		
145	150	155
Ile Gly Tyr Lys Asp Asp Glu Gly Ile Ala Asn Glu Leu Ser Phe Gln		
165	170	175
Met Trp Thr Asn Gln Met Gln Glu Ser Leu Asn Ser Lys Lys Gln Gly		
180	185	190
Asp Leu Ala Phe Arg Ser Lys Asp Phe Thr Thr Ala Val Asp Cys Tyr		
195	200	205
Thr Gln Phe Ile Asp Gly Gly Thr Met Val Ser Pro Thr Val His Ala		
210	215	220
Arg Arg Cys Leu Ser Tyr Leu Met Asn Asp Asn Ala Gln Glu Ala Leu		
225	230	235
Thr Asp Ala Leu Gln Thr Gln Val Val Ser Pro Asp Trp Pro Thr Ala		
245	250	255
Leu Tyr Leu Gln Ala Ala Cys Leu Phe Lys Leu Gly Met Glu Ala Asp		
260	265	270
Ala Gln Gln Ala Leu Lys Asp Gly Thr Thr Leu Glu Ala Lys Lys Ser		
275	280	285
Asn Lys Arg		
290		

(2) INFORMATION FOR SEQ ID NO:669:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..248
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:669:

Met Ser Gly Lys His Ile Pro Pro Ser His Ala Leu Asp Leu Ile Arg	
1	5
Gly Lys Asn Cys Ala Met Leu Met Asp Ser Ala Leu Glu Gly His Phe	
20	25
Ser Asn Glu Asp Gly Thr Glu Leu Val Arg Leu Ala Thr Arg Cys Leu	
35	40
Gln Tyr Glu Ala Arg Glu Arg Pro Asn Val Lys Ser Leu Val Thr Ser	
50	55
Leu Val Thr Leu Gln Lys Glu Ser Asp Val Ala Ser Tyr Val Leu Met	
65	70
Gly Ile Pro His Glu Thr Glu Ala Glu Glu Ser Pro Leu Ser Leu	
85	90
Thr Pro Phe Gly Asp Ala Cys Leu Arg Val Asp Leu Thr Ala Ile Gln	
100	105
	110

Glu Ile Leu Ser Lys Ile Gly Tyr Lys Asp Asp Glu Gly Ile Ala Asn
115 120 125
Glu Leu Ser Phe Gln Met Trp Thr Asn Gln Met Gln Glu Ser Leu Asn
130 135 140
Ser Lys Lys Gln Gly Asp Leu Ala Phe Arg Ser Lys Asp Phe Thr Thr
145 150 155 160
Ala Val Asp Cys Tyr Thr Gln Phe Ile Asp Gly Gly Thr Met Val Ser
165 170 175
Pro Thr Val His Ala Arg Arg Cys Leu Ser Tyr Leu Met Asn Asp Asn
180 185 190
Ala Gln Glu Ala Leu Thr Asp Ala Leu Gln Thr Gln Val Val Ser Pro
195 200 205
Asp Trp Pro Thr Ala Leu Tyr Leu Gln Ala Ala Cys Leu Phe Lys Leu
210 215 220
Gly Met Glu Ala Asp Ala Gln Gln Ala Leu Lys Asp Gly Thr Thr Leu
225 230 235 240
Glu Ala Lys Lys Ser Asn Lys Arg
245

(2) INFORMATION FOR SEQ ID NO:670:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 227 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..227

(D) OTHER INFORMATION: / Ceres Seq. ID 1498814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:670:

Met Leu Met Asp Ser Ala Leu Glu Gly His Phe Ser Asn Glu Asp Gly
1 5 10 15
Thr Glu Leu Val Arg Leu Ala Thr Arg Cys Leu Gln Tyr Glu Ala Arg
20 25 30
Glu Arg Pro Asn Val Lys Ser Leu Val Thr Ser Leu Val Thr Leu Gln
35 40 45
Lys Glu Ser Asp Val Ala Ser Tyr Val Leu Met Gly Ile Pro His Glu
50 55 60
Thr Glu Ala Glu Glu Glu Ser Pro Leu Ser Leu Thr Pro Phe Gly Asp
65 70 75 80
Ala Cys Leu Arg Val Asp Leu Thr Ala Ile Gln Glu Ile Leu Ser Lys
85 90 95
Ile Gly Tyr Lys Asp Asp Glu Gly Ile Ala Asn Glu Leu Ser Phe Gln
100 105 110
Met Trp Thr Asn Gln Met Gln Glu Ser Leu Asn Ser Lys Lys Gln Gly
115 120 125
Asp Leu Ala Phe Arg Ser Lys Asp Phe Thr Thr Ala Val Asp Cys Tyr
130 135 140
Thr Gln Phe Ile Asp Gly Gly Thr Met Val Ser Pro Thr Val His Ala
145 150 155 160
Arg Arg Cys Leu Ser Tyr Leu Met Asn Asp Asn Ala Gln Glu Ala Leu
165 170 175
Thr Asp Ala Leu Gln Thr Gln Val Val Ser Pro Asp Trp Pro Thr Ala
180 185 190
Leu Tyr Leu Gln Ala Ala Cys Leu Phe Lys Leu Gly Met Glu Ala Asp
195 200 205
Ala Gln Gln Ala Leu Lys Asp Gly Thr Thr Leu Glu Ala Lys Lys Ser
210 215 220
Asn Lys Arg
225

(2) INFORMATION FOR SEQ ID NO:671:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1368 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1368

(D) OTHER INFORMATION: / Ceres Seq. ID 1498815

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:671:

```
aaaataagct tatcattctt acaaaaatat ttctgggttt ctgatattgt tcttgttctc      60
ttgaatctttt attacttgaa aaacataataa agtgatggcg gttgtggttg aagaagggtg      120
gggtgttgaat catggagggtg aagagctttgt ggatttgcca cctggtttca ggtttcattc      180
aacagacgaa gagatcataa catgtttacct taaggagaag gttttaaaca gccgattcac      240
ggctgtggcc atggggagaag ctgatctcaa caagtgtgag ccttgggatt tgccaattgg      300
gcaaaagatgg gggagaaga gttctacttc ttctgtcaaa gggacaggaa gtatccgact      360
gggatgagga cgaaccgtgc gacggagtca ggatactgga aagccaccgg gaaggataag      420
gagatcttca aaggcaaaag ttgtctcggt gggatgaaga aaacacttgt gttttataga      480
ggaagagctc caaaagggtg aaagactaat tgggtcatgc atgaatatcg tcttgaaggc      540
aaatattcgt attacaatct cccaaaatct gcaaggggacg aatgggtcgt gtgtagggtt      600
tttcacaaga caaatccttc taccacaacc caaccaatga cgagaatacc cgttgaagat      660
ttcacaagga tggattctct agagaacatt gatcatctcc tagacttctc atctcttctc      720
cctctcatag acccgagttt catgagtcac accgaacaac caaacttcaa acccatcaac      780
cctccaactt acgatattct atcaccaatc caaccccattc atttcaactt ttaccaatca      840
atctttaacc accagggtttt tggttctgct tgctgtcctc cgtacaacaa caacaacgag      900
atgatcaaga tggagcaatc acttggttagt gtatctcagg aaacatgcct aagctcagat      960
gtgaacgcga acatgactac aaccacggag gtatcttcgg gtctctgtaat gaacaacgaa      1020
atggggatga tgggaatggt gaatggtagc aagtcgtatg aagatcatag tgacttgagg      1080
ggggactctg gggacttcta attaatcatt tgactgttgt gaagagtagt atttgttggg      1140
atttaaatca tgttagttaa tacatataca tataggattt actagaggct taatcctagt      1200
taaatatttt cacttcattg attattatta attagttgat tgtttaatta gtttaactgt      1260
tatagtgtgg ttaaaaaaga aaagaaggga ttgtgataat ttgggatttt agtgcataag      1320
ttatatctca atgtaaactg tattgtata catataatta gtcttctc
```

(2) INFORMATION FOR SEQ ID NO:672:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 264 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..264

(D) OTHER INFORMATION: / Ceres Seq. ID 1498816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:672:

```
Met Gly Glu Lys Glu Phe Tyr Phe Phe Cys Gln Arg Asp Arg Lys Tyr
1      5      10      15
Pro Thr Gly Met Arg Thr Asn Arg Ala Thr Glu Ser Gly Tyr Trp Lys
20     25     30
Ala Thr Gly Lys Asp Lys Glu Ile Phe Lys Gly Lys Gly Cys Leu Val
35     40     45
Gly Met Lys Lys Thr Leu Val Phe Tyr Arg Gly Arg Ala Pro Lys Gly
50     55     60
Glu Lys Thr Asn Trp Val Met His Glu Tyr Arg Leu Glu Gly Lys Tyr
65     70     75     80
Ser Tyr Tyr Asn Leu Pro Lys Ser Ala Arg Asp Glu Trp Val Val Cys
85     90     95
Arg Val Phe His Lys Asn Asn Pro Ser Thr Thr Thr Gln Pro Met Thr
100    105    110
Arg Ile Pro Val Glu Asp Phe Thr Arg Met Asp Ser Leu Glu Asn Ile
```

115	120	125
Asp His Leu Leu Asp Phe Ser Ser Leu Pro Pro Leu Ile Asp Pro Ser		
130	135	140
Phe Met Ser Gln Thr Glu Gln Pro Asn Phe Lys Pro Ile Asn Pro Pro		
145	150	155
Thr Tyr Asp Ile Ser Ser Pro Ile Gln Pro His His Phe Asn Ser Tyr		
165	170	175
Gln Ser Ile Phe Asn His Gln Val Phe Gly Ser Ala Ser Gly Ser Thr		
180	185	190
Tyr Asn Asn Asn Asn Glu Met Ile Lys Met Glu Gln Ser Leu Val Ser		
195	200	205
Val Ser Gln Glu Thr Cys Leu Ser Ser Asp Val Asn Ala Asn Met Thr		
210	215	220
Thr Thr Thr Glu Val Ser Ser Gly Pro Val Met Lys Gln Glu Met Gly		
225	230	235
Met Met Gly Met Val Asn Gly Ser Lys Ser Tyr Glu Asp Leu Cys Asp		
245	250	255
Leu Arg Gly Asp Leu Trp Asp Phe		
260		

(2) INFORMATION FOR SEQ ID NO:673:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..245
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:673:

Met Arg Thr Asn Arg Ala Thr Glu Ser Gly Tyr Trp Lys Ala Thr Gly	
1	5
Lys Asp Lys Glu Ile Phe Lys Gly Lys Gly Cys Leu Val Gly Met Lys	10
20	25
Lys Thr Leu Val Phe Tyr Arg Gly Arg Ala Pro Lys Gly Glu Lys Thr	30
35	40
Asn Trp Val Met His Glu Tyr Arg Leu Glu Gly Lys Tyr Ser Tyr Tyr	45
50	55
Asn Leu Pro Lys Ser Ala Arg Asp Glu Trp Val Val Cys Arg Val Phe	60
65	70
His Lys Asn Asn Pro Ser Thr Thr Thr Gln Pro Met Thr Arg Ile Pro	75
85	90
Val Glu Asp Phe Thr Arg Met Asp Ser Leu Glu Asn Ile Asp His Leu	95
100	105
Leu Asp Phe Ser Ser Leu Pro Pro Leu Ile Asp Pro Ser Phe Met Ser	110
115	120
Gln Thr Glu Gln Pro Asn Phe Lys Pro Ile Asn Pro Pro Thr Tyr Asp	125
130	135
Ile Ser Ser Pro Ile Gln Pro His His Phe Asn Ser Tyr Gln Ser Ile	140
145	150
Phe Asn His Gln Val Phe Gly Ser Ala Ser Gly Ser Thr Tyr Asn Asn	155
165	170
Asn Asn Glu Met Ile Lys Met Glu Gln Ser Leu Val Ser Val Ser Gln	175
180	185
Glu Thr Cys Leu Ser Ser Asp Val Asn Ala Asn Met Thr Thr Thr Thr	190
195	200
Glu Val Ser Ser Gly Pro Val Met Lys Gln Glu Met Gly Met Met Gly	205
210	215
Met Val Asn Gly Ser Lys Ser Tyr Glu Asp Leu Cys Asp Leu Arg Gly	220
225	230
	235
	240

Asp Leu Trp Asp Phe
245

(2) INFORMATION FOR SEQ ID NO:674:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..215
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:674:

```
Met Lys Lys Thr Leu Val Phe Tyr Arg Gly Arg Ala Pro Lys Gly Glu
1      5      10      15
Lys Thr Asn Trp Val Met His Glu Tyr Arg Leu Glu Gly Lys Tyr Ser
20      25      30
Tyr Tyr Asn Leu Pro Lys Ser Ala Arg Asp Glu Trp Val Val Cys Arg
35      40      45
Val Phe His Lys Asn Asn Pro Ser Thr Thr Thr Gln Pro Met Thr Arg
50      55      60
Ile Pro Val Glu Asp Phe Thr Arg Met Asp Ser Leu Glu Asn Ile Asp
65      70      75      80
His Leu Leu Asp Phe Ser Ser Leu Pro Pro Leu Ile Asp Pro Ser Phe
85      90      95
Met Ser Gln Thr Glu Gln Pro Asn Phe Lys Pro Ile Asn Pro Pro Thr
100     105     110
Tyr Asp Ile Ser Ser Pro Ile Gln Pro His His Phe Asn Ser Tyr Gln
115     120     125
Ser Ile Phe Asn His Gln Val Phe Gly Ser Ala Ser Gly Ser Thr Tyr
130     135     140
Asn Asn Asn Asn Glu Met Ile Lys Met Glu Gln Ser Leu Val Ser Val
145     150     155     160
Ser Gln Glu Thr Cys Leu Ser Ser Asp Val Asn Ala Asn Met Thr Thr
165     170     175
Thr Thr Glu Val Ser Ser Gly Pro Val Met Lys Gln Glu Met Gly Met
180     185     190
Met Gly Met Val Asn Gly Ser Lys Ser Tyr Glu Asp Leu Cys Asp Leu
195     200     205
Arg Gly Asp Leu Trp Asp Phe
210     215
```

(2) INFORMATION FOR SEQ ID NO:675:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1898 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1898
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498823

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:675:

```
aaaaaattaa gtgatcatca ctctctctcc ttatcgaga gcttcagttt tagagcaaca      60
atgtctctat ttctgaagcc ctctctcttc ctatacgaca ccactcttag tcttctctta      120
ctctctgttca atggatggag tcttgaggat acagcagcag cccaaaagag gcgtgaagca      180
gacaaaaaatg ctgcagaaac tgaatggatc caactccaat acttgtagag caaacaagg      240
agtgttgtac tactctccgt ttccaagggt ttggtgggta tgtgtttggt tctatccatt      300
atagtggtct tcgagagttt ttacatgaac ttgtgtgata tcttcgtcaa gttatttaa      360
cgtaaacccc ataaagtgtg caaatgggag gccatgcaag aagatgttga ggttgagacc      420
```

gataactacc	caatggttct	tatccaaata	ccaatgtaca	atgaaaaaga	ggtctttcaa	480
ttatctatag	cagcaaatag	tagtttggtc	tggccatcga	gcgcgtctagt	agttcaaagtt	540
gtagatgatt	ctacggtagc	ggccgtaagg	gaaggtgtgg	acgtagagat	tgcaaaatgg	600
caaaagccaag	gcataaacat	aaggtgtgaa	aggagagata	acaggaaacgg	ctacaaagacc	660
ggagctatga	aagaagctct	tacgcagagc	tacgtcaagc	aatgcgactt	cgttagcagtc	720
ttcgatgtga	atttccaacc	cgagcccgat	tatctcatcc	gcgcgtgtccc	tttctctgtc	780
cacaaccctg	acgtttgctc	agtttcaagcc	cgatggatatt	ttgttaacgc	gaacaaatgc	840
ttgatgacga	ggatgcgaaga	gatgtctctc	aactatcatt	tcaaagtggga	acaagaatca	900
gggtcgacta	gacatgcttt	cttcgggttt	aatggaaacgg	cgggtgtatg	gagaatatcg	960
gcaatggagg	cagcaggagg	atggaaatca	aggaccacag	tagaggacat	ggacttggct	1020
gttcgtgttg	gtcttcatgg	ctggaaattt	gtctacttta	acgacctcac	ggtagaatac	1080
gagcttccaa	gcacaaattaa	ggcctacaga	tccagcaaac	ataggttgctc	ctgtggaccg	1140
gcgaatctat	ttagaaaaat	gacgatggag	atcattttca	ataagagagt	atcaatttgg	1200
aagaagtttt	atgtgatcta	cagctttttc	ttcgttaagg	aagtggcggt	acacttcttg	1260
acattctttc	tctactgtat	aattgtgccca	acaagtgtct	tcttccctga	aatccacatc	1320
ctactcttgg	ctacactttta	cgttccctct	ttgatcagta	tcttcccaac	cctggcaact	1380
ccaagatcct	tctacctcgt	gatattttgg	gtcttgttcg	agaagtgaat	ggctatgcgt	1440
cgaaaccaaag	gtacgtgcat	tggcctactt	gaaggaggaa	gagtaaacga	atgggttgtg	1500
accgaaaaaac	taggagatgc	tttgaagagt	aagctactct	ctcgggtagt	ccaaaagaaa	1560
tcttggttac	aaagagttaa	ttccaaaggaa	gtgatgggtg	gggtatacat	attaggtatg	1620
gcactctatg	gcctgatctta	tgggcacaca	tggttacatt	tctatctttt	tcttcaggcc	1680
acagcctttt	tgcctctcgg	ttttggtttt	gtcggaaacgg	cctaagaacc	ttccctgccc	1740
attatttttta	gtcaccaaat	aaattctcca	tgttttagtt	cttattttaca	ctttattatta	1800
ttttgacacc	attgtacggt	ttggacccca	tatcatcatg	ttgtataagt	ataacgaata	1860
atgatttttt	gtttgtttga	atgtatgcgt	cactcggt			

(2) INFORMATION FOR SEQ ID NO:676:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 574 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) SEQUENCE FEATURE:

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..574

(D) OTHER INFORMATION: / Ceres Seq. ID 1498824

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:676:

Lys	Lys	Leu	Ser	Asp	His	His	Phe	Ser	Ser	Phe	Ile	Glu	Ser	Phe	Ser
1			5					10					15		
Phe	Arg	Ala	Thr	Met	Ser	Leu	Phe	Leu	Lys	Pro	Phe	Leu	Phe	Leu	Tyr
		20						25				30			
Asp	Thr	Thr	Leu	Ser	Leu	Leu	Leu	Leu	Phe	Asn	Gly	Trp	Ser	Leu	
		35					40			45					
Glu	Asp	Thr	Ala	Ala	Ala	Gln	Lys	Arg	Arg	Glu	Ala	Asp	Lys	Asn	Ala
		50					55			60					
Ala	Glu	Thr	Glu	Trp	Ile	Gln	Leu	Gln	Tyr	Leu	Trp	Thr	Lys	Thr	Arg
		65				70				75					
Ser	Val	Val	Leu	Leu	Pro	Val	Phe	Lys	Gly	Leu	Val	Val	Met	Cys	Leu
			85						90					95	
Val	Leu	Ser	Ile	Ile	Val	Phe	Phe	Glu	Ser	Phe	Tyr	Met	Asn	Phe	Val
			100					105					110		
Ile	Leu	Phe	Val	Lys	Leu	Phe	Lys	Arg	Lys	Pro	His	Lys	Val	Tyr	Lys
			115				120					125			
Trp	Glu	Ala	Met	Gln	Glu	Asp	Val	Glu	Val	Gly	Pro	Asp	Asn	Tyr	Pro
			130				135				140				
Met	Val	Leu	Ile	Gln	Ile	Pro	Met	Tyr	Asn	Glu	Lys	Glu	Val	Phe	Gln
			145				150			155					160
Leu	Ser	Ile	Ala	Ala	Ile	Cys	Ser	Leu	Val	Trp	Pro	Ser	Ser	Arg	Leu
			165					170						175	
Val	Val	Gln	Val	Val	Asp	Asp	Ser	Thr	Asp	Pro	Ala	Val	Arg	Glu	Gly
			180					185						190	

Val Asp Val Glu Ile Ala Lys Trp Gln Ser Gln Gly Ile Asn Ile Arg
195 200 205
Cys Glu Arg Arg Asp Asn Arg Asn Gly Tyr Lys Ala Gly Ala Met Lys
210 215 220
Glu Ala Leu Thr Gln Ser Tyr Val Lys Gln Cys Asp Phe Val Ala Val
225 230 235 240
Phe Asp Ala Asp Phe Gln Pro Glu Pro Asp Tyr Leu Ile Arg Ala Val
245 250 255
Pro Phe Leu Val His Asn Pro Asp Val Ala Leu Val Gln Ala Arg Trp
260 265 270
Ile Phe Val Asn Ala Asn Lys Cys Leu Met Thr Arg Met Gln Glu Met
275 280 285
Ser Leu Asn Tyr His Phe Lys Val Glu Gln Glu Ser Gly Ser Thr Arg
290 295 300
His Ala Phe Phe Gly Phe Asn Gly Thr Ala Gly Val Trp Arg Ile Ser
305 310 315 320
Ala Met Glu Ala Ala Gly Gly Trp Lys Ser Arg Thr Thr Val Glu Asp
325 330 335
Met Asp Leu Ala Val Arg Val Gly Leu His Gly Trp Lys Phe Val Tyr
340 345 350
Leu Asn Asp Leu Thr Val Arg Asn Glu Leu Pro Ser Lys Phe Lys Ala
355 360 365
Tyr Arg Phe Gln Gln His Arg Trp Ser Cys Gly Pro Ala Asn Leu Phe
370 375 380
Arg Lys Met Thr Met Glu Ile Ile Phe Asn Lys Arg Val Ser Ile Trp
385 390 395 400
Lys Lys Phe Tyr Val Ile Tyr Ser Phe Phe Val Arg Lys Val Ala
405 410 415
Val His Phe Leu Thr Phe Phe Phe Tyr Cys Ile Ile Val Pro Thr Ser
420 425 430
Val Phe Phe Pro Glu Ile His Ile Pro Ser Trp Ser Thr Ile Tyr Val
435 440 445
Pro Ser Leu Ile Ser Ile Phe His Thr Leu Ala Thr Pro Arg Ser Phe
450 455 460
Tyr Leu Val Ile Phe Trp Val Leu Phe Glu Asn Val Met Ala Met His
465 470 475 480
Arg Thr Lys Gly Thr Cys Ile Gly Leu Leu Glu Gly Gly Arg Val Asn
485 490 495
Glu Trp Val Val Thr Glu Lys Leu Gly Asp Ala Leu Lys Ser Lys Leu
500 505 510
Leu Ser Arg Val Val Gln Arg Lys Ser Cys Tyr Gln Arg Val Asn Ser
515 520 525
Lys Glu Val Met Val Gly Val Tyr Ile Leu Gly Cys Ala Leu Tyr Gly
530 535 540
Leu Ile Tyr Gly His Thr Trp Leu His Phe Tyr Leu Phe Leu Gln Ala
545 550 555 560
Thr Ala Phe Phe Val Ser Gly Phe Gly Phe Val Gly Thr Ala
565 570

(2) INFORMATION FOR SEQ ID NO:677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 554 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..554

(D) OTHER INFORMATION: / Ceres Seq. ID 1498825

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:677:

Met Ser Leu Phe Leu Lys Pro Phe Leu Phe Leu Tyr Asp Thr Thr Leu

1	5	10	15
Ser Leu Leu Leu Leu Leu Phe Asn Gly Trp Ser Leu Glu Asp Thr Ala			
20		25	30
Ala Ala Gln Lys Arg Arg Glu Ala Asp Lys Asn Ala Ala Glu Thr Glu			
35		40	45
Trp Ile Gln Leu Gln Tyr Leu Trp Thr Lys Thr Arg Ser Val Val Leu			
50	55	60	
Leu Pro Val Phe Lys Gly Leu Val Val Met Cys Leu Val Leu Ser Ile			
65	70	75	80
Ile Val Phe Phe Glu Ser Phe Tyr Met Asn Phe Val Ile Leu Phe Val			
85	90		95
Lys Leu Phe Lys Arg Lys Pro His Lys Val Tyr Lys Trp Glu Ala Met			
100	105		110
Gln Glu Asp Val Glu Val Gly Pro Asp Asn Tyr Pro Met Val Leu Ile			
115	120		125
Gln Ile Pro Met Tyr Asn Glu Lys Glu Val Phe Gln Leu Ser Ile Ala			
130	135		140
Ala Ile Cys Ser Leu Val Trp Pro Ser Ser Arg Leu Val Val Gln Val			
145	150		155
Val Asp Asp Ser Thr Asp Pro Ala Val Arg Glu Gly Val Asp Val Glu			
165	170		175
Ile Ala Lys Trp Gln Ser Gln Gly Ile Asn Ile Arg Cys Glu Arg Arg			
180	185		190
Asp Asn Arg Asn Gly Tyr Lys Ala Gly Ala Met Lys Glu Ala Leu Thr			
195	200		205
Gln Ser Tyr Val Lys Gln Cys Asp Phe Val Ala Val Phe Asp Ala Asp			
210	215		220
Phe Gln Pro Glu Pro Asp Tyr Leu Ile Arg Ala Val Pro Phe Leu Val			
225	230		235
His Asn Pro Asp Val Ala Leu Val Gln Ala Arg Trp Ile Phe Val Asn			
245	250		255
Ala Asn Lys Cys Leu Met Thr Arg Met Gln Glu Met Ser Leu Asn Tyr			
260	265		270
His Phe Lys Val Glu Gln Glu Ser Gly Ser Thr Arg His Ala Phe Phe			
275	280		285
Gly Phe Asn Gly Thr Ala Gly Val Trp Arg Ile Ser Ala Met Glu Ala			
290	295		300
Ala Gly Gly Trp Lys Ser Arg Thr Thr Val Glu Asp Met Asp Leu Ala			
305	310		315
Val Arg Val Gly Leu His Gly Trp Lys Phe Val Tyr Leu Asn Asp Leu			
325	330		335
Thr Val Arg Asn Glu Leu Pro Ser Lys Phe Lys Ala Tyr Arg Phe Gln			
340	345		350
Gln His Arg Trp Ser Cys Gly Pro Ala Asn Leu Phe Arg Lys Met Thr			
355	360		365
Met Glu Ile Ile Phe Asn Lys Arg Val Ser Ile Trp Lys Lys Phe Tyr			
370	375		380
Val Ile Tyr Ser Phe Phe Phe Val Arg Lys Val Ala Val His Phe Leu			
385	390		395
Thr Phe Phe Phe Tyr Cys Ile Ile Val Pro Thr Ser Val Phe Phe Pro			
405	410		415
Glu Ile His Ile Pro Ser Trp Ser Thr Ile Tyr Val Pro Ser Leu Ile			
420	425		430
Ser Ile Phe His Thr Leu Ala Thr Pro Arg Ser Phe Tyr Leu Val Ile			
435	440		445
Phe Trp Val Leu Phe Glu Asn Val Met Ala Met His Arg Thr Lys Gly			
450	455		460
Thr Cys Ile Gly Leu Leu Glu Gly Gly Arg Val Asn Glu Trp Val Val			
465	470		475
Thr Glu Lys Leu Gly Asp Ala Leu Lys Ser Lys Leu Ser Arg Val			
485	490		495

Val Gln Arg Lys Ser Cys Tyr Gln Arg Val Asn Ser Lys Glu Val Met
500 505 510
Val Gly Val Tyr Ile Leu Gly Cys Ala Leu Tyr Gly Leu Ile Tyr Gly
515 520 525
His Thr Trp Leu His Phe Tyr Leu Phe Leu Gln Ala Thr Ala Phe Phe
530 535 540
Val Ser Gly Phe Gly Phe Val Gly Thr Ala
545 550

(2) INFORMATION FOR SEQ ID NO:678:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 481 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..481

(D) OTHER INFORMATION: / Ceres Seq. ID 1498826

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:678:

Met Cys Leu Val Leu Ser Ile Ile Val Phe Phe Glu Ser Phe Tyr Met
1 5 10 15
Asn Phe Val Ile Leu Phe Val Lys Leu Phe Lys Arg Lys Pro His Lys
20 25 30
Val Tyr Lys Trp Glu Ala Met Gln Glu Asp Val Glu Val Gly Pro Asp
35 40 45
Asn Tyr Pro Met Val Leu Ile Gln Ile Pro Met Tyr Asn Glu Lys Glu
50 55 60
Val Phe Gln Leu Ser Ile Ala Ala Ile Cys Ser Leu Val Trp Pro Ser
65 70 75 80
Ser Arg Leu Val Val Gln Val Val Asp Asp Ser Thr Asp Pro Ala Val
85 90 95
Arg Glu Gly Val Asp Val Glu Ile Ala Lys Trp Gln Ser Gln Gly Ile
100 105 110
Asn Ile Arg Cys Glu Arg Arg Asp Asn Arg Asn Gly Tyr Lys Ala Gly
115 120 125
Ala Met Lys Glu Ala Leu Thr Gln Ser Tyr Val Lys Gln Cys Asp Phe
130 135 140
Val Ala Val Phe Asp Ala Asp Phe Gln Pro Glu Pro Asp Tyr Leu Ile
145 150 155 160
Arg Ala Val Pro Phe Leu Val His Asn Pro Asp Val Ala Leu Val Gln
165 170 175
Ala Arg Trp Ile Phe Val Asn Ala Asn Lys Cys Leu Met Thr Arg Met
180 185 190
Gln Glu Met Ser Leu Asn Tyr His Phe Lys Val Glu Gln Glu Ser Gly
195 200 205
Ser Thr Arg His Ala Phe Phe Gly Phe Asn Gly Thr Ala Gly Val Trp
210 215 220
Arg Ile Ser Ala Met Glu Ala Ala Gly Gly Trp Lys Ser Arg Thr Thr
225 230 235 240
Val Glu Asp Met Asp Leu Ala Val Arg Val Gly Leu His Gly Trp Lys
245 250 255
Phe Val Tyr Leu Asn Asp Leu Thr Val Arg Asn Glu Leu Pro Ser Lys
260 265 270
Phe Lys Ala Tyr Arg Phe Gln Gln His Arg Trp Ser Cys Gly Pro Ala
275 280 285
Asn Leu Phe Arg Lys Met Thr Met Glu Ile Ile Phe Asn Lys Arg Val
290 295 300
Ser Ile Trp Lys Lys Phe Tyr Val Ile Tyr Ser Phe Phe Phe Val Arg
305 310 315 320
Lys Val Ala Val His Phe Leu Thr Phe Phe Phe Tyr Cys Ile Ile Val

325										330										335																											
Pro	Thr	Ser	Val	Phe	Phe	Pro	Glu	Ile	His	Ile	Pro	Ser	Trp	Ser	Thr	Pro	Thr	Ser	Val	Phe	Phe	Pro	Glu	Ile	His	Ile	Pro	Ser	Trp	Ser	Thr	Pro	Thr	Ser	Val	Phe	Phe	Pro	Glu	Ile	His	Ile	Pro	Ser	Trp	Ser	Thr
340										345										350																											
Ile	Tyr	Val	Pro	Ser	Leu	Ile	Ser	Ile	Phe	His	Thr	Leu	Ala	Thr	Pro	Ile	Tyr	Val	Pro	Ser	Leu	Ile	Ser	Ile	Phe	His	Thr	Leu	Ala	Thr	Pro	Ile	Tyr	Val	Pro	Ser	Leu	Ile	Ser	Ile	Phe	His	Thr	Leu	Ala	Thr	Pro
355										360										365																											
Arg	Ser	Phe	Tyr	Leu	Val	Ile	Phe	Trp	Val	Leu	Phe	Glu	Asn	Val	Met	Arg	Ser	Phe	Tyr	Leu	Val	Ile	Phe	Trp	Val	Leu	Phe	Glu	Asn	Val	Met	Arg	Ser	Phe	Tyr	Leu	Val	Ile	Phe	Trp	Val	Leu	Phe	Glu	Asn	Val	Met
370										375										380																											
Ala	Met	His	Arg	Thr	Lys	Gly	Thr	Cys	Ile	Gly	Leu	Leu	Glu	Gly	Gly	Ala	Met	His	Arg	Thr	Lys	Gly	Thr	Cys	Ile	Gly	Leu	Leu	Glu	Gly	Gly	Ala	Met	His	Arg	Thr	Lys	Gly	Thr	Cys	Ile	Gly	Leu	Leu	Glu	Gly	Gly
385										390										395																											
Arg	Val	Asn	Glu	Trp	Val	Val	Thr	Glu	Lys	Leu	Gly	Asp	Ala	Leu	Lys	Arg	Val	Asn	Glu	Trp	Val	Val	Thr	Glu	Lys	Leu	Gly	Asp	Ala	Leu	Lys	Arg	Val	Asn	Glu	Trp	Val	Val	Thr	Glu	Lys	Leu	Gly	Asp	Ala	Leu	Lys
405										410										415																											
Ser	Lys	Leu	Leu	Ser	Arg	Val	Val	Gln	Arg	Lys	Ser	Cys	Tyr	Gln	Arg	Ser	Lys	Leu	Leu	Ser	Arg	Val	Val	Gln	Arg	Lys	Ser	Cys	Tyr	Gln	Arg	Ser	Lys	Leu	Leu	Ser	Arg	Val	Val	Gln	Arg	Lys	Ser	Cys	Tyr	Gln	Arg
420										425										430																											
Val	Asn	Ser	Lys	Glu	Val	Met	Val	Gly	Val	Tyr	Ile	Leu	Gly	Cys	Ala	Val	Asn	Ser	Lys	Glu	Val	Met	Val	Gly	Val	Tyr	Ile	Leu	Gly	Cys	Ala	Val	Asn	Ser	Lys	Glu	Val	Met	Val	Gly	Val	Tyr	Ile	Leu	Gly	Cys	Ala
435										440										445																											
Leu	Tyr	Gly	Leu	Ile	Tyr	Gly	His	Thr	Trp	Leu	His	Phe	Tyr	Leu	Phe	Leu	Tyr	Gly	Leu	Ile	Tyr	Gly	His	Thr	Trp	Leu	His	Phe	Tyr	Leu	Phe	Leu	Tyr	Gly	Leu	Ile	Tyr	Gly	His	Thr	Trp	Leu	His	Phe	Tyr	Leu	Phe
450										455										460																											
Leu	Gln	Ala	Thr	Ala	Phe	Phe	Val	Ser	Gly	Phe	Gly	Phe	Val	Gly	Thr	Leu	Gln	Ala	Thr	Ala	Phe	Phe	Val	Ser	Gly	Phe	Gly	Phe	Val	Gly	Thr	Leu	Gln	Ala	Thr	Ala	Phe	Phe	Val	Ser	Gly	Phe	Gly	Phe	Val	Gly	Thr
465										470										475																											
Ala																				480																											

(2) INFORMATION FOR SEQ ID NO:679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..518

(D) OTHER INFORMATION: / Ceres Seq. ID 1498829

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:679:

ttccaaggaa	aaaaaaaaagtc	tttacccgta	aacatttttt	ctccatcttc	ttgatatcaa	60
caaaacacac	ctcaacaaaa	aaaaaaaaaa	aacttcattc	ctctcagatt	tcgaaattga	120
cccgctcggtg	attcttaatc	tctcctctct	gtctctctcc	gatcaaacct	cattccaaag	180
aaacaaaacca	tggatctcca	accagaagag	cttcaattct	tgacaataacc	tcaactactt	240
caagaatcaa	tctcaatcaa	gaacagatct	ccaagaacct	tctacctcat	aacctctccc	300
ttcatcttcc	ctctctcctt	cgctatcctc	gtcactcac	tcttcaactca	accaatetta	360
gccaaactcg	acaaatccga	cccaccaaac	tcagatcggt	cacgtcatga	ttggaactgtt	420
cttctaactc	tccagttcag	ttacttgatc	ttctctttg	ccttctctct	tctctcaacc	480
gctgcwgtwg	tcttaccctg	cgcttctctt	tacaccgg			

(2) INFORMATION FOR SEQ ID NO:680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..109

(D) OTHER INFORMATION: / Ceres Seq. ID 1498830

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:680:

Met	Asp	Leu	Gln	Pro	Glu	Glu	Leu	Gln	Phe	Leu	Thr	Ile	Pro	Gln	Leu
1		5						10					15		
Leu	Gln	Glu	Ser	Ile	Ser	Ile	Lys	Lys	Arg	Ser	Pro	Arg	Thr	Phe	Tyr
		20					25					30			
Leu	Ile	Thr	Leu	Ser	Phe	Ile	Phe	Pro	Leu	Ser	Phe	Ala	Ile	Leu	Ala
		35					40					45			
His	Ser	Leu	Phe	Thr	Gln	Pro	Ile	Leu	Ala	Lys	Leu	Asp	Lys	Ser	Asp

50 55 60
Pro Pro Asn Ser Asp Arg Ser Arg His Asp Trp Thr Val Leu Leu Ile
65 70 75 80
Phe Gln Phe Ser Tyr Leu Ile Phe Leu Phe Ala Phe Ser Leu Leu Ser
85 90 95
Thr Ala Xaa Xaa Val Phe Thr Val Ala Ser Leu Tyr Thr
100 105

(2) INFORMATION FOR SEQ ID NO:681:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 598 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..598
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:681:

aactttcaat ctacgcta atcaagtaac gtggaaagga ttgtttccgt caaagggttg 60
tgattataca gagactgagt tccgataaag ttggattgag ctgtttttca attgcggatc 120
tttgagaaaa aagtttgcaa ctttatggct ctggaacaac aacatgtttg tgaanaagcgg 180
cttcaagcca agaccttttc taccacaagag ttccagttga ctctcaattg ggatgattta 240
actgtgccca ttgttttggg ttccctcacc aatgtgtgac ttctccagtg ttcttcttac 300
ggaaacgggt gccgtgcttt tgctgtcaat actgatcacc ttcaactctaa ctgtttggat 360
cgtttcatta gcgcctgtgg tactgaatca cctcctgtct ctgatgagcc tcgtctctaa 420
gttttagaag agagttgcaa acctgtgtgt ccactgtgta gaggagaagt tactggctgg 480
cttggtgtag aagaagctcg ttctgtcttt gatgagaaaa aacgttgtct tgaggaagac 540
gatgcaggtt tatgggtact ttacttggag ctccgcaaac atgctcagtc agagcatc

(2) INFORMATION FOR SEQ ID NO:682:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498832

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:682:

Met Ala Leu Glu Gln Gln His Val Cys Glu Lys Arg Leu Gln Ala Lys
1 5 10 15
Thr Phe Ser Thr Gln Glu Phe Gln Leu Thr Leu Asn Trp Asp Asp Leu
20 25 30
Thr Cys Pro Ile Cys Leu Asp Phe Pro His Asn Gly Val Leu Leu Gln
35 40 45
Cys Ser Ser Tyr Gly Asn Gly Cys Arg Ala Phe Val Cys Asn Thr Asp
50 55 60
His Leu His Ser Asn Cys Leu Asp Arg Phe Ile Ser Ala Cys Gly Thr
65 70 75 80
Glu Ser Pro Pro Ala Pro Asp Glu Pro Arg Ser Lys Val Leu Glu Glu
85 90 95
Ser Cys Lys Pro Val Cys Pro Leu Cys Arg Gly Glu Val Thr Gly Trp
100 105 110
Leu Val Val Glu Glu Ala Arg Leu Arg Leu Asp Glu Lys Lys Arg Cys
115 120 125
Cys Glu Glu Asp Asp Ala Gly Leu Trp Val Leu Tyr Leu Glu Leu Arg
130 135 140
Lys His Ala Gln Ser Glu His
145 150

(2) INFORMATION FOR SEQ ID NO:683:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..487
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498841

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:683:

aatttaaatt	tctctttcta	tctactataa	aaagtgaact	tctaagaact	ccaaagatta	60
gaacattgaa	ttgaatttagc	catggagaag	aatactttctc	aaaccatctt	ctccaacttt	120
tttctttctc	ttctcctttc	ttcatgtgtc	tctgtctcagc	tccggacagg	tttctaccag	180
aactcatgtc	cgaacgtgga	aaccattgta	cgtaacgctg	tccgtcagaa	attccagcag	240
actttcggtta	cgcctccggc	cactcttctgc	ctcttcttcc	acgattgtct	cgttcgtgga	300
tgtgatcgct	caataatgat	agcatcacca	tccggagagag	accatccaga	tgacatgtca	360
ttggccggag	acggatttga	cacgggtggtg	aaggcggaaca	agccgttgat	agcaatccca	420
attgcgcgca	caaagtctca	tgtgctgaca	ttttggctct	cgccactcgt	gaagtcgtcg	480
ttttgac						

(2) INFORMATION FOR SEQ ID NO:684:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498842

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:684:

Met	Glu	Lys	Asn	Thr	Ser	Gln	Thr	Ile	Phe	Ser	Asn	Phe	Phe	Leu	Leu
1			5				10						15		
Leu	Leu	Leu	Ser	Ser	Cys	Val	Ser	Ala	Gln	Leu	Arg	Thr	Gly	Phe	Tyr
			20				25						30		
Gln	Asn	Ser	Cys	Pro	Asn	Val	Glu	Thr	Ile	Val	Arg	Asn	Ala	Val	Arg
			35				40					45			
Gln	Lys	Phe	Gln	Gln	Thr	Phe	Val	Thr	Ala	Pro	Ala	Thr	Leu	Arg	Leu
			50				55				60				
Phe	Phe	His	Asp	Cys	Phe	Val	Arg	Gly	Cys	Asp	Ala	Ser	Ile	Met	Ile
			65				70				75				80
Ala	Ser	Pro	Ser	Glu	Arg	Asp	His	Pro	Asp	Asp	Met	Ser	Leu	Ala	Gly
			85				90				95				
Asp	Gly	Phe	Asp	Thr	Val	Val	Lys	Ala	Asn	Lys	Pro	Leu	Ile	Ala	Ile
			100				105				110				
Pro	Ile	Ala	Ala	Thr	Lys	Ser	His	Val	Leu	Thr	Phe	Trp	Leu	Ser	Pro
			115				120				125				
Leu	Val	Lys	Ser	Ser	Phe										
			130												

(2) INFORMATION FOR SEQ ID NO:685:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 527 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..527

(D) OTHER INFORMATION: / Ceres Seq. ID 1498843
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:685:
aaaatccgaa aaagaccaat caatcctttc tcctgaaat ggcggcggt ctgcagacga 60
atatccggac ggtcaaggtt ccggctactgt tcagagctgt aagtaaacag tcaatggcac 120
ccttttagagt aagatgtgct gttgcttccc ctgggaaaaa acgatacacc atcactctcc 180
ttcccgagaga cggcatcggt ccggaggttg tctccattgc caaaaatgtg cttcagcaag 240
ctggatcttt ggaaggtgtg gaatttaact tccgtgagat gcccatgtga ggagctgctt 300
tggatttggt cggagtgccc ttgccggagg agactatctc agctgcaaaa gaatcagatg 360
cagtgtcttc tggagccatt ggagggtaca aatgggataa caatgaaaaa catctgaggc 420
ctgagaaggg gttacttcag attcgtgcag ctctcaaaat ctttgcaaat ctgagacctg 480
ctacagtctc cccacagtta gtgagtgctt ccaccttaaa gagagag

(2) INFORMATION FOR SEQ ID NO:686:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175

(D) OTHER INFORMATION: / Ceres Seq. ID 1498844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:686:

Asn Pro Lys Lys Thr Asn Gln Ser Phe Leu Pro Glu Met Ala Ala Ala
1 5 10 15
Leu Gln Thr Asn Ile Arg Thr Val Lys Val Pro Ala Thr Phe Arg Ala
20 25 30
Val Ser Lys Gln Ser Leu Ala Pro Phe Arg Val Arg Cys Ala Val Ala
35 40 45
Ser Pro Gly Lys Lys Arg Tyr Thr Ile Thr Leu Leu Pro Gly Asp Gly
50 55 60
Ile Gly Pro Glu Val Val Ser Ile Ala Lys Asn Val Leu Gln Gln Ala
65 70 75 80
Gly Ser Leu Glu Gly Val Glu Phe Asn Phe Arg Glu Met Pro Ile Gly
85 90 95
Gly Ala Ala Leu Asp Leu Val Gly Val Pro Leu Pro Glu Thr Ile
100 105 110
Ser Ala Ala Lys Glu Ser Asp Ala Val Leu Leu Gly Ala Ile Gly Gly
115 120 125
Tyr Lys Trp Asp Asn Asn Glu Lys His Leu Arg Pro Glu Lys Gly Leu
130 135 140
Leu Gln Ile Arg Ala Ala Leu Lys Val Phe Ala Asn Leu Arg Pro Ala
145 150 155 160
Thr Val Leu Pro Gln Leu Val Asp Ala Ser Thr Leu Lys Arg Glu
165 170 175

(2) INFORMATION FOR SEQ ID NO:687:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..163

(D) OTHER INFORMATION: / Ceres Seq. ID 1498845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:687:

Met Ala Ala Ala Leu Gln Thr Asn Ile Arg Thr Val Lys Val Pro Ala
1 5 10 15
Thr Phe Arg Ala Val Ser Lys Gln Ser Leu Ala Pro Phe Arg Val Arg
20 25 30

Cys Ala Val Ala Ser Pro Gly Lys Lys Arg Tyr Thr Ile Thr Leu Leu
35 40 45
Pro Gly Asp Gly Ile Gly Pro Glu Val Val Ser Ile Ala Lys Asn Val
50 55 60
Leu Gln Gln Ala Gly Ser Leu Glu Gly Val Glu Phe Asn Phe Arg Glu
65 70 75 80
Met. Pro Ile Gly Gly Ala Ala Leu Asp Leu Val Gly Val Pro Leu Pro
85 90 95
Glu Glu Thr Ile Ser Ala Ala Lys Glu Ser Asp Ala Val Leu Leu Gly
100 105 110
Ala Ile Gly Gly Tyr Lys Trp Asp Asn Asn Glu Lys His Leu Arg Pro
115 120 125
Glu Lys Gly Leu Leu Gln Ile Arg Ala Ala Leu Lys Val Phe Ala Asn
130 135 140
Leu Arg Pro Ala Thr Val Leu Pro Gln Leu Val Asp Ala Ser Thr Leu
145 150 155 160
Lys Arg Glu

(2) INFORMATION FOR SEQ ID NO:688:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1356 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1356

(D) OTHER INFORMATION: / Ceres Seq. ID 1498846

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:688:

aaacccaaac atttttcgat ttccccgcac ttctccgcac gatgcgatgg cgatagcgat 60
gggtattccg gtgacttatg ctccgacgat tgacacgatac atttgaggca gtctcccttg 120
tccagatttt ctctctcaac ctctttctct tgcttaccac ccaaatattc catctttgaa 180
actgcttcac ccttttgcgt ttggtgatcc tgaagactcc gctttatacc cattttgatc 240
tggagaagga tatagatgaa gtgctacagt cgcatactgt ttattcfaat gtttcgaaag 300
gagttcttgc aaaatcgaaa gactttgatga agtcgtttgg atcagatgat catacgaaaa 360
tatgcatacga tattttggag aaaggagagc ttcaagttgc tggaaaaaaa agagaattcac 420
agttctcaag ccagtttcgg gatatagcac cgattgttat gcagaaaact atcaacctgc 480
aaacacacag acctatatac atcagcatgg tagagcgctc aatgcataaa attcattttg 540
ctgttgatcc tcatagtaat tccaagaagc aggcacttga tgtcatccgt gagctgcata 600
agcacttccc tataaagcgt tctccaatga gactgcgtct tactgttctc gtccaaaatt 660
tcccctgcct tctggagaag ctaaaagaat gggatggtat ttgtgtctcc aaagacgaat 720
ctggaacaca gatgtccaat gtctgcgaga tggaaacggg cctattccga gagtgtgatt 780
cccattgtgag gagtatccag ggaagactag aaatactcgc tgtatcagtt catcgagaag 840
gtgacacaaag catgatgatc tacgatgagc atgatgatc gccattgcac acccacaagc 900
cgttgttacc tgcgtgagact gagactaagg atttgaccga tcccgtcgtt gaacttagca 960
agaaactgca gaagcaagag ataagtacta cagataaacat aaagcaagaa ggtggagaag 1020
aaaagaaggg gaccaagtcg agcacttgca acacgcttgc tggagagcct aagcaatata 1080
gagagcactg taagagtgat tggcacaaac acaaccttaa gcgtaagact cggaaactcc 1140
ctctattatg tgcgtgacga tgcattgtct agattgacat ggacgactct agagcagatt 1200
tgaaagacta ctctttctga aactacaatt ttctcctttt gtgcttttaa ttttgtcaat 1260
tgtgtaaact tctgtatcat atgtgagtat gaatacacaa aacttgtgga atgaaatttt 1320
gcgcaaacct taagagtaaa aacttgtgtt taagag

(2) INFORMATION FOR SEQ ID NO:689:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 297 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..297

(D) OTHER INFORMATION: / Ceres Seq. ID 1498847

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:689:

Met Lys Ser Phe Gly Ser Asp Asp His Thr Lys Ile Cys Ile Asp Ile
1 5 10 15
Leu Glu Lys Gly Glu Leu Gln Val Ala Gly Lys Glu Arg Glu Ser Gln
20 25 30
Phe Ser Ser Gln Phe Arg Asp Ile Ala Thr Ile Val Met Gln Lys Thr
35 40 45
Ile Asn Pro Glu Thr Gln Arg Pro Tyr Thr Ile Ser Met Val Glu Arg
50 55 60
Leu Met His Glu Ile His Phe Ala Val Asp Pro His Ser Asn Ser Lys
65 70 75 80
Lys Gln Ala Leu Asp Val Ile Arg Glu Leu Gln Lys His Phe Pro Ile
85 90 95
Lys Arg Ser Pro Met Arg Leu Arg Leu Thr Val Pro Val Gln Asn Phe
100 105 110
Pro Ser Leu Leu Glu Lys Leu Lys Glu Trp Asp Gly Ser Val Val Ser
115 120 125
Lys Asp Glu Ser Gly Thr Gln Met Ser Thr Val Cys Glu Met Glu Pro
130 135 140
Gly Leu Phe Arg Glu Cys Asp Ser His Val Arg Ser Ile Gln Gly Arg
145 150 155 160
Leu Glu Ile Leu Ala Val Ser Val His Ala Glu Gly Asp Thr Ser Met
165 170 175
Asp His Tyr Asp Glu His Asp Asp Met Ala Leu Gln Thr His Lys Pro
180 185 190
Leu Leu Pro Ala Glu Thr Glu Thr Lys Asp Leu Thr Asp Pro Val Val
195 200 205
Glu Leu Ser Lys Lys Leu Gln Lys Gln Glu Ile Ser Thr Thr Asp Asn
210 215 220
Ile Lys Gln Glu Gly Gly Glu Glu Lys Lys Gly Thr Lys Cys Ser Thr
225 230 235 240
Cys Asn Thr Phe Val Gly Glu Ala Lys Gln Tyr Arg Glu His Cys Lys
245 250 255
Ser Asp Trp His Lys His Asn Leu Lys Arg Lys Thr Arg Lys Leu Pro
260 265 270
Pro Ile Ser Ala Asp Glu Cys Met Ser Glu Ile Asp Met Asp Asp Ser
275 280 285
Arg Ala Asp Leu Lys Asp Tyr Ser Phe
290 295

(2) INFORMATION FOR SEQ ID NO:690:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 253 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..253

(D) OTHER INFORMATION: / Ceres Seq. ID 1498848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:690:

Met Gln Lys Thr Ile Asn Pro Glu Thr Gln Arg Pro Tyr Thr Ile Ser
1 5 10 15
Met Val Glu Arg Glu Leu Met His Glu Ile His Phe Ala Val Asp Pro His
20 25 30
Ser Asn Ser Lys Lys Gln Ala Leu Asp Val Ile Arg Glu Leu Gln Lys
35 40 45
His Phe Pro Ile Lys Arg Ser Pro Met Arg Leu Arg Leu Thr Val Pro

50	55	60
Val Gln Asn Phe Pro Ser	Leu Leu Glu Lys	Leu Lys Glu Trp Asp Gly
65	70	75
Ser Val Val Ser Lys Asp	Glu Ser Gly Thr	Gln Met Ser Thr Val Cys
85	90	95
Glu Met Glu Pro Gly Leu	Phe Arg Glu Cys	Asp Ser His Val Arg Ser
100	105	110
Ile Gln Gly Arg Leu Glu	Ile Leu Ala Val Ser	Val His Ala Glu Gly
115	120	125
Asp Thr Ser Met Asp His	Tyr Asp Glu His	Asp Asp Met Ala Leu Gln
130	135	140
Thr His Lys Pro Leu Leu	Pro Ala Glu Thr	Glu Thr Lys Asp Leu Thr
145	150	155
Asp Pro Val Val Glu Leu	Ser Lys Lys Leu	Gln Lys Glu Ile Ser
165	170	175
Thr Thr Asp Asn Ile Lys	Gln Glu Gly Glu	Glu Lys Lys Gly Thr
180	185	190
Lys Cys Ser Thr Cys Asn	Thr Phe Val Gly	Glu Ala Lys Lys Gln Tyr Arg
195	200	205
Glu His Cys Lys Ser Asp	Trp His Lys His	Asn Leu Lys Arg Lys Thr
210	215	220
Arg Lys Leu Pro Pro Ile	Ser Ala Asp Glu	Cys Met Ser Glu Ile Asp
225	230	235
Met Asp Asp Ser Arg Ala	Asp Leu Lys Asp	Tyr Ser Phe
245	250	

(2) INFORMATION FOR SEQ ID NO:691:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..237
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498849

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:691:

Met Val Glu Arg Leu Met	His Glu Ile His	Phe Ala Val Asp Pro His
1	5	10
Ser Asn Ser Ser Lys	Gln Ala Leu Asp	Val Ile Arg Glu Leu Gln Lys
20	25	30
His Phe Pro Ile Lys	Arg Ser Pro Met	Arg Leu Arg Leu Thr Val Pro
35	40	45
Val Gln Asn Phe Pro	Ser Leu Leu Glu Lys	Leu Lys Glu Trp Asp Gly
50	55	60
Ser Val Val Ser Lys	Asp Glu Ser Gly Thr	Gln Met Ser Thr Val Cys
65	70	75
Glu Met Glu Pro Gly	Leu Phe Arg Glu Cys	Asp Ser His Val Arg Ser
85	90	95
Ile Gln Gly Arg Leu	Glu Ile Leu Ala Val	Ser Val His Ala Glu Gly
100	105	110
Asp Thr Ser Met Asp	His Tyr Asp Glu His	Asp Asp Met Ala Leu Gln
115	120	125
Thr His Lys Pro Leu	Leu Pro Ala Glu Thr	Glu Thr Lys Asp Leu Thr
130	135	140
Asp Pro Val Val Glu	Leu Ser Lys Lys Leu	Gln Lys Gln Glu Ile Ser
145	150	155
Thr Thr Asp Asn Ile	Lys Gln Glu Gly Glu	Glu Lys Lys Gly Thr
165	170	175
Lys Cys Ser Thr Cys	Asn Thr Phe Val Gly	Glu Ala Lys Gln Tyr Arg
180	185	190

Glu His Cys Lys Ser Asp Trp His Lys His Asn Leu Lys Arg Lys Thr
195 200 205
Arg Lys Leu Pro Pro Ile Ser Ala Asp Glu Cys Met Ser Glu Ile Asp
210 215 220
Met Asp Asp Ser Arg Ala Asp Leu Lys Asp Tyr Ser Phe
225 230 235

(2) INFORMATION FOR SEQ ID NO:692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1337
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498854

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:692:

atatgaacat	aaccacatct	gaagatcaat	cataacctta	aacctatctct	cataattttta	60
gtattttctat	tctcaccacc	aaaactcggt	gatacatcac	accccaactg	ttgttactca	120
tgctctacag	atcgattttac	cgcactcttc	gacgggtact	atcatctctcg	gtacaatcct	180
ccgggttttag	aattgggagga	ttcaggggac	atctcattag	ccacttgcgc	aatgttcggc	240
tattgagctc	tgacacgtca	tctccggtaa	gtgggaataa	ccagccagaa	aatcctatcc	300
gaacgggcga	tggttaaagt	atatccactt	attggggat	acctctact	aagatcacta	360
aaccggacgg	ttcagcttgg	aagtgggaat	gttttcagcc	tattcaacgg	tacaaacccg	420
atgtgtccact	tgatgtaact	aaacatcata	aacctccaa	tttactgac	aaattcgcat	480
attggacgct	tcaaaactctg	aaaataccgg	ttcaactatt	ttttcagagg	aagcacatgt	540
gccatgcgat	gttctagag	acggtggctg	cggtgcggg	aatggctggg	tggtatgctt	600
tgcaacttgaa	attcttccgg	aggttcgaac	atagcggggg	atggatcaaa	gctttgctgc	660
aagagcgctga	gaacgagcgt	atgcattctc	tgactttcat	cgaactttca	caacccaaat	720
ggtaacgaacg	agcgattgtg	ttcaccgtcc	aaggcgtttt	cttcaacgca	tatttctctg	780
cttatgtaat	ttcaccacaa	cttgctcatc	gtatcactgg	atacttagaa	gaagaggctg	840
taaattotta	cactgaattt	ctcaaaagaca	ttgatccgg	aaaattcgaa	aactcgccag	900
ctccagccat	cgcaatcgat	tactggcggt	tgccataaaga	tgcaacgctt	agggatgtgg	960
tttatgttat	acgagctgac	gaagctcacc	accgtgatat	taaccactat	gcttcgggata	1020
tacaattcaa	aggacatgaa	ctcaaggaag	ctccggctcc	tattggatat	cattaaagat	1080
tatgtgacaa	agtcacaaag	ctgtgtatac	atctatgaac	atatgttgtt	gtggatctcc	1140
atgatatttt	tattttatgt	tttcgattta	tttaaaactg	ttatctgttt	ttattagctc	1200
aatatggata	tttaaacact	attattttgt	tacgattttat	gaacatagta	ctactcatgt	1260
gtgtgtaaaa	gatcatactg	cctggacacg	aagcggatat	ccggaaaaat	tataatatatt	1320
gttttttgat	tcgttttc					

(2) INFORMATION FOR SEQ ID NO:693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..318

(D) OTHER INFORMATION: / Ceres Seq. ID 1498855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:693:

Met	Ser	Tyr	Arg	Ser	Ile	Tyr	Arg	Thr	Leu	Arg	Pro	Val	Leu	Ser	Ser
1				5				10					15		
Ser	Val	Gln	Ser	Ser	Gly	Leu	Gly	Ile	Gly	Gly	Phe	Arg	Gly	His	Leu
				20				25					30		
Ile	Ser	His	Leu	Pro	Asn	Val	Arg	Leu	Leu	Ser	Ser	Asp	Thr	Ser	Ser
				35				40					45		
Pro	Val	Ser	Gly	Asn	Asn	Gln	Pro	Glu	Asn	Pro	Ile	Arg	Thr	Ala	Asp
				50				55					60		

Gly Lys Val Ile Ser Thr Tyr Trp Gly Ile Pro Pro Thr Lys Ile Thr
65 70 75 80
Lys Pro Asp Gly Ser Ala Trp Lys Trp Asn Cys Phe Gln Pro Trp Asp
85 90 95
Ser Tyr Lys Pro Asp Val Ser Ile Asp Val Thr Lys His His Lys Pro
100 105 110
Ser Asn Phe Thr Asp Lys Phe Ala Tyr Trp Thr Val Gln Thr Leu Lys
115 120 125
Ile Pro Val Gln Leu Phe Phe Gln Arg Lys His Met Cys His Ala Met
130 135 140
Leu Leu Glu Thr Val Ala Ala Val Pro Gly Met Val Gly Trp Met Leu
145 150 155 160
Leu His Leu Lys Ser Leu Arg Arg Phe Glu His Ser Gly Gly Trp Ile
165 170 175
Lys Ala Leu Leu Glu Glu Ala Glu Asn Glu Arg Met His Leu Met Thr
180 185 190
Phe Ile Glu Leu Ser Gln Pro Lys Trp Tyr Glu Arg Ala Ile Val Phe
195 200 205
Thr Val Gln Gly Val Phe Phe Asn Ala Tyr Phe Leu Ala Tyr Val Ile
210 215 220
Ser Pro Lys Leu Ala His Arg Ile Thr Gly Tyr Leu Glu Glu Ala
225 230 235 240
Val Asn Ser Tyr Thr Glu Phe Leu Lys Asp Ile Asp Ala Gly Lys Phe
245 250 255
Glu Asn Ser Pro Ala Pro Ala Ile Ala Ile Asp Tyr Trp Arg Leu Pro
260 265 270
Lys Asp Ala Thr Leu Arg Asp Val Val Tyr Val Ile Arg Ala Asp Glu
275 280 285
Ala His His Arg Asp Ile Asn His Tyr Ala Ser Asp Ile Gln Phe Lys
290 295 300
Gly His Glu Leu Lys Glu Ala Pro Ala Pro Ile Gly Tyr His
305 310 315

(2) INFORMATION FOR SEQ ID NO:694:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 179 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..179
(D) OTHER INFORMATION: / Ceres Seq. ID 1498856
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:694:
Met Cys His Ala Met Leu Leu Glu Thr Val Ala Ala Val Pro Gly Met
1 5 10 15
Val Gly Trp Met Leu Leu His Leu Lys Ser Leu Arg Arg Phe Glu His
20 25 30
Ser Gly Gly Trp Ile Lys Ala Leu Leu Glu Glu Ala Glu Asn Glu Arg
35 40 45
Met His Leu Met Thr Phe Ile Glu Leu Ser Gln Pro Lys Trp Tyr Glu
50 55 60
Arg Ala Ile Val Phe Thr Val Gln Gly Val Phe Phe Asn Ala Tyr Phe
65 70 75 80
Leu Ala Tyr Val Ile Ser Pro Lys Leu Ala His Arg Ile Thr Gly Tyr
85 90 95
Leu Glu Glu Glu Ala Val Asn Ser Tyr Thr Glu Phe Leu Lys Asp Ile
100 105 110
Asp Ala Gly Lys Phe Glu Asn Ser Pro Ala Pro Ala Ile Ala Ile Asp
115 120 125
Tyr Trp Arg Leu Pro Lys Asp Ala Thr Leu Arg Asp Val Tyr Val

```

      130                      135                      140
Ile Arg Ala Asp Glu Ala His His Arg Asp Ile Asn His Tyr Ala Ser
145                      150                      155                      160
Asp Ile Gln Phe Lys Gly His Glu Leu Lys Glu Ala Pro Ala Pro Ile
      165                      170                      175
Gly Tyr His
```

(2) INFORMATION FOR SEQ ID NO:695:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498857

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:695:

```

Met Leu Leu Glu Thr Val Ala Ala Val Pro Gly Met Val Gly Trp Met
1      5      10      15
Leu Leu His Leu Lys Ser Leu Arg Arg Phe Glu His Ser Gly Gly Trp
      20      25      30
Ile Lys Ala Leu Leu Glu Glu Ala Glu Asn Glu Arg Met His Leu Met
35      40      45
Thr Phe Ile Glu Leu Ser Gln Pro Lys Trp Tyr Glu Arg Ala Ile Val
50      55      60
Phe Thr Val Gln Gly Val Phe Phe Asn Ala Tyr Phe Leu Ala Tyr Val
65      70      75      80
Ile Ser Pro Lys Leu Ala His Arg Ile Thr Gly Tyr Leu Glu Glu Glu
85      90      95
Ala Val Asn Ser Tyr Thr Glu Phe Leu Lys Asp Ile Asp Ala Gly Lys
100      105      110
Phe Glu Asn Ser Pro Ala Pro Ala Ile Ala Ile Asp Tyr Trp Arg Leu
115      120      125
Pro Lys Asp Ala Thr Leu Arg Asp Val Val Tyr Val Ile Arg Ala Asp
130      135      140
Glu Ala His His Arg Asp Ile Asn His Tyr Ala Ser Asp Ile Gln Phe
145      150      155      160
Lys Gly His Glu Leu Lys Glu Ala Pro Ala Pro Ile Gly Tyr His
165      170      175
```

(2) INFORMATION FOR SEQ ID NO:696:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1159
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498858

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:696:

```

atagtttggt actttagtgt tgactgttga ccgcgacgaa tccgtcgcaa accggaatca      60
ccatggattt tctctcgacg aagcttgatt atcatgtaga catgttcaat cttcagttct      120
attccagatt tctctcctta tttaaggcgc aagatggacg catagctcta atactagaat      180
caacggtgtt tcattccaaa ggtggtggcc agccgtcaga caccggttta attgtttct      240
ccggttcgga ttgaaattt tccgttcaag atgttcgatc gaaagacgga attgttctcc      300
attacggagt ttctgaaggt tcgaatccgt aaagtggaaat tgatagtgag aaaggggaaag      360
aagtttactt aactgttgat gaatcaaggc gtaaaactcaa ttccaggttg cactcagctg      420
gacacttgct agatatgtgt atgcagaaag ttgggttagg acatttggag cctggaaaag      480
```

```

ggtaccattt tctcgacggt ccttttgtgg aatacaaaag aagcgtccca caggaggagt 540
ttcagggtgaa gcagaaaagag ttggaggcag aagctaacga actgatatcc aaaggaggaa 600
agggttatgc tgcctatattg ccctatgaag aggcactctgt gctctgtggt ggcagctcttc 660
ctgattatat ttccaaggcg agcactcccc ggatcataaa attaggtgac agccccgggt 720
gtccatgtgg tggaaacccat gtctccaatt tatctgatat cataagcatg aagatcacac 780
agatgagaac aaagaaaagga atgcagaaag ttttctacac cattgcatct tgaaactctt 840
atgggttcca gtttctatac ggtagatata caataagtca aggaaggaa tgatagttag 900
gacgactgtt ttcatcagtt cccttcaaca gcaagcagct tctcctgtgc ctcaacagcc 960
acaaatcagt atttgtgggt atttatcaat ctcttaaacg actctctcta ttattgataa 1020
gtcgtatatg atatatgata ttgatgtgat atttcttccc actcagcctc ttaattagta 1080
ttaatatatt gactcttggt attttagaat cgtaccggctc atttggctct agatttttat 1140
tcattgcatcg gtttgattt

```

(2) INFORMATION FOR SEQ ID NO:697:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..256
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498859

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:697:

```

Met Asp Phe Pro Thr Lys Leu Asp Tyr His Val Asp Met Phe Asn
1 5 10 15
Leu Gln Ser His Ser Arg Phe Leu Ser Leu Phe Lys Ala Gln Asp Gly
20 25 30
Arg Ile Ala Leu Ile Leu Glu Ser Thr Val Phe His Pro Gln Gly Gly
35 40 45
Gly Gln Pro Ser Asp Thr Gly Leu Ile Val Phe Ser Gly Ser Asp Leu
50 55 60
Lys Phe Ser Val Gln Asp Val Arg Ser Lys Asp Gly Ile Val Leu His
65 70 75 80
Tyr Gly Val Phe Glu Gly Ser Asn Pro Glu Ser Gly Ile Asp Ser Glu
85 90 95
Lys Gly Lys Glu Val Tyr Leu Thr Val Asp Glu Ser Arg Arg Lys Leu
100 105 110
Asn Ser Arg Leu His Ser Ala Gly His Leu Leu Asp Met Cys Met Gln
115 120 125
Lys Val Gly Leu Gly His Leu Glu Pro Gly Lys Gly Tyr His Phe Pro
130 135 140
Asp Gly Pro Phe Val Glu Tyr Lys Gly Ser Val Pro Gln Glu Glu Phe
145 150 155 160
Gln Val Lys Gln Lys Glu Leu Glu Ala Glu Asn Glu Leu Ile Ser
165 170 175
Lys Gly Gly Lys Val Tyr Ala Ala Ile Leu Pro Tyr Glu Glu Ala Ser
180 185 190
Val Leu Cys Gly Gly Ser Leu Pro Asp Tyr Ile Ser Lys Gly Ser Thr
195 200 205
Pro Arg Ile Ile Lys Leu Gly Asp Ser Pro Gly Cys Pro Cys Gly Gly
210 215 220
Thr His Val Ser Asn Leu Ser Asp Ile Ile Ser Met Lys Ile Thr Gln
225 230 235 240
Met Arg Thr Lys Lys Gly Met Thr Lys Val Phe Tyr Thr Ile Ala Ser
245 250 255

```

(2) INFORMATION FOR SEQ ID NO:698:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..243
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498860
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:698:
Met Phe Asn Leu Gln Ser His Ser Arg Phe Leu Ser Leu Phe Lys Ala
1 5 10 15
Gln Asp Gly Arg Ile Ala Leu Ile Leu Glu Ser Thr Val Phe His Pro
 20 25 30
Gln Gly Gly Gly Gln Pro Ser Asp Thr Gly Leu Ile Val Phe Ser Gly
 35 40 45
Ser Asp Leu Lys Phe Ser Val Gln Asp Val Arg Ser Lys Asp Gly Ile
50 55 60
Val Leu His Tyr Gly Val Phe Glu Gly Ser Asn Pro Glu Ser Gly Ile
65 70 75 80
Asp Ser Glu Lys Gly Lys Glu Val Tyr Leu Thr Val Asp Glu Ser Arg
 85 90 95
Arg Lys Leu Asn Ser Arg Leu His Ser Ala Gly His Leu Leu Asp Met
 100 105 110
Cys Met Gln Lys Val Gly Leu Gly His Leu Glu Pro Gly Lys Gly Tyr
 115 120 125
His Phe Pro Asp Gly Pro Phe Val Glu Tyr Lys Gly Ser Val Pro Gln
130 135 140
Glu Glu Phe Gln Val Lys Gln Lys Glu Leu Glu Ala Glu Ala Asn Glu
145 150 155 160
Leu Ile Ser Lys Gly Gly Lys Val Tyr Ala Ala Ile Leu Pro Tyr Glu
 165 170 175
Glu Ala Ser Val Leu Cys Gly Gly Ser Leu Pro Asp Tyr Ile Ser Lys
180 185 190
Gly Ser Thr Pro Arg Ile Ile Lys Leu Gly Asp Ser Pro Gly Cys Pro
195 200 205
Cys Gly Gly Thr His Val Ser Asn Leu Ser Asp Ile Ile Ser Met Lys
210 215 220
Ile Thr Gln Met Arg Thr Lys Lys Gly Met Thr Lys Val Phe Tyr Thr
225 230 235 240
Ile Ala Ser

(2) INFORMATION FOR SEQ ID NO:699:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1498861

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:699:

Met Cys Met Gln Lys Val Gly Leu Gly His Leu Glu Pro Gly Lys Gly
1 5 10 15
Tyr His Phe Pro Asp Gly Pro Phe Val Glu Tyr Lys Gly Ser Val Pro
 20 25 30
Gln Glu Glu Phe Gln Val Lys Gln Lys Glu Leu Glu Ala Glu Ala Asn
35 40 45
Glu Leu Ile Ser Lys Gly Gly Lys Val Tyr Ala Ala Ile Leu Pro Tyr
50 55 60

Glu Glu Ala Ser Val Leu Cys Gly Gly Ser Leu Pro Asp Tyr Ile Ser
65 70 75 80
Lys Gly Ser Thr Pro Arg Ile Ile Lys Leu Gly Asp Ser Pro Gly Cys
85 90 95
Pro Cys Gly Gly Thr His Val Ser Asn Leu Ser Asp Ile Ile Ser Met
100 105 110
Lys Ile Thr Gln Met Arg Thr Lys Lys Gly Met Thr Lys Val Phe Tyr
115 120 125
Thr Ile Ala Ser
130

(2) INFORMATION FOR SEQ ID NO:700:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1308 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1308

(D) OTHER INFORMATION: / Ceres Seq. ID 1498874

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:700:

cttcttcgta	cgtaaataaa	aatctgaaga	aacaaaatcg	tgaatcgcg	ctctttaagc	60
atcatctagg	gttcatcact	gaaatacaaaa	atgcaataaa	atctctacaa	aatctctcag	120
atctaataccc	agatcgttgt	tggtttcttc	tccgtaaac	aatccacat	atgaataaaa	180
gattcgatct	cgaatcggtt	ggcttttgtt	gttgttgcat	tcttcggtga	tggtcccgac	240
tcggattcta	accagagacg	aagagcttgg	tggtatttca	gacgatgatg	attctccatc	300
gggtaaaaaa	tctaaacttg	atcgcttccc	tcttagccgt	tggaactcgc	ccgtttctct	360
cggtgtcttc	ctcgtctctt	cctctggact	ctgttgtatc	tacatgacca	tgctctgtgc	420
tgaatttggc	aaactcaaac	ttccaagaaa	gcctcgctga	tctccgtttg	ctcaaaagata	480
atctagcvaa	ttatgcgrat	gagtatcccg	cgcagttttg	ttttagggta	ttgtgcaacg	540
tacattttta	tgacagacct	tatgattcca	gggaactatc	tcatgtcact	attagctgga	600
gctctctttg	gagtattcaa	aggtgttgtc	ttgtgtgttt	tcaatgcaac	agcaggagct	660
acctcgttgt	tctttttgtc	gaaattgatt	ggcgcaccgt	tgattacttg	gctatggcct	720
gacaaaattaa	gattctttca	agcagagatt	agtaagcgta	gagataagct	tctgaactat	780
atgtgtgttt	tgaggataac	accaaactctg	ccaaatcttt	ttatcaatct	tgcatctctt	840
atagtcgatg	tacctttcca	tgtcttcttt	ttggcgacat	tgattggtct	cattctctga	900
gcttatataa	ctgtcagagc	tggtccttgt	acttgagat	ctcaaatcgg	tgaaagatct	960
gtatgatttc	aagacattgt	cagtgtcttt	cctcatcggt	tttatctcta	ttcttccaac	1020
gatactgaaa	agaaaaga	ttgttgaata	gccagggaga	agcatcttta	caatacacat	1080
ggcctaatac	tcaatgccat	acagagaaaca	agaatacac	taactgtttt	agaggacaca	1140
acagaaacaa	actctctgatt	cgtttacttg	tcacttgctc	taacgattcg	ttgatagtgt	1200
ttttttgtgc	atattttctt	actatttgcc	aagttagagt	tgagaagaaa	ttcacagaaa	1260
aatacaattt	ttgttacaag	acgagagacc	atgaaatatt	ttgtgtct		

(2) INFORMATION FOR SEQ ID NO:701:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..157

(D) OTHER INFORMATION: / Ceres Seq. ID 1498875

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:701:

Met	Xaa	Met	Ser	Ile	Arg	Arg	Ser	Phe	Val	Leu	Gly	Tyr	Cys	Ala	Thr
1		5		10		15		20		25		30			
Tyr	Ile	Phe	Met	Gln	Thr	Phe	Met	Ile	Pro	Gly	Thr	Ile	Phe	Met	Ser
Leu	Leu	Ala	Gly	Ala	Leu	Phe	Gly	Val	Phe	Lys	Gly	Val	Val	Leu	Val

35 40 45
Val Phe Asn Ala Thr Ala Gly Ala Thr Ser Cys Phe Phe Leu Ser Lys
50 55 60
Leu Ile Gly Arg Pro Leu Ile Thr Trp Leu Trp Pro Asp Lys Leu Arg
65 70 75 80
Phe Phe Gln Ala Glu Ile Ser Lys Arg Arg Asp Lys Leu Leu Asn Tyr
85 90 95
Met Leu Phe Leu Arg Ile Thr Pro Thr Leu Pro Asn Leu Phe Ile Asn
100 105 110
Leu Ala Ser Pro Ile Val Asp Val Pro Phe His Val Phe Phe Leu Ala
115 120 125
Thr Leu Ile Gly Leu Ile Pro Ala Ala Tyr Ile Thr Val Arg Ala Gly
130 135 140
Leu Ala Thr Trp Arg Ser Gln Ile Gly Glu Arg Ser Val
145 150 155

(2) INFORMATION FOR SEQ ID NO:702:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..155

(D) OTHER INFORMATION: / Ceres Seq. ID 1498876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:702:

Met Ser Ile Arg Arg Ser Phe Val Leu Gly Tyr Cys Ala Thr Tyr Ile
1 5 10 15
Phe Met Gln Thr Phe Met Ile Pro Gly Thr Ile Phe Met Ser Leu Leu
20 25 30
Ala Gly Ala Leu Phe Gly Val Phe Lys Gly Val Val Leu Val Val Phe
35 40 45
Asn Ala Thr Ala Gly Ala Thr Ser Cys Phe Phe Leu Ser Lys Leu Ile
50 55 60
Gly Arg Pro Leu Ile Thr Trp Leu Trp Pro Asp Lys Leu Arg Phe Phe
65 70 75 80
Gln Ala Glu Ile Ser Lys Arg Arg Asp Lys Leu Leu Asn Tyr Met Leu
85 90 95
Phe Leu Arg Ile Thr Pro Thr Leu Pro Asn Leu Phe Ile Asn Leu Ala
100 105 110
Ser Pro Ile Val Asp Val Pro Phe His Val Phe Phe Leu Ala Thr Leu
115 120 125
Ile Gly Leu Ile Pro Ala Ala Tyr Ile Thr Val Arg Ala Gly Leu Ala
130 135 140
Thr Trp Arg Ser Gln Ile Gly Glu Arg Ser Val
145 150 155

(2) INFORMATION FOR SEQ ID NO:703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1498877

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:703:

Met Gln Thr Phe Met Ile Pro Gly Thr Ile Phe Met Ser Leu Leu Ala
1 5 10 15

Gly Ala Leu Phe Gly Val Phe Lys Gly Val Val Leu Val Val Phe Asn
20 25 30
Ala Thr Ala Gly Ala Thr Ser Cys Phe Phe Leu Ser Lys Leu Ile Gly
35 40 45
Arg Pro Leu Ile Thr Trp Leu Trp Pro Asp Lys Leu Arg Phe Phe Gln
50 55 60
Ala Glu Ile Ser Lys Arg Arg Asp Lys Leu Leu Asn Tyr Met Leu Phe
65 70 75 80
Leu Arg Ile Thr Pro Thr Leu Pro Asn Leu Phe Ile Asn Leu Ala Ser
85 90 95
Pro Ile Val Asp Val Pro Phe His Val Phe Phe Leu Ala Thr Leu Ile
100 105 110
Gly Leu Ile Pro Ala Ala Tyr Ile Thr Val Arg Ala Gly Leu Ala Thr
115 120 125
Trp Arg Ser Gln Ile Gly Glu Arg Ser Val
130 135

(2) INFORMATION FOR SEQ ID NO:704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1603
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498878

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:704:

ctttttgcga	tcaatcgaaa	gaaaacaaaa	aatggggaaa	gttccgctgt	cgtttcgtag	60
tataccggcg	aatttatgtg	tcagaaaaac	aacaccatct	ctccagcgcg	cgccgcgaga	120
ttttcgcgaac	agaaccggcg	tgggaggaga	ttcagccaaa	cttccccaca	atactcaaacg	180
ccctcgcgag	ccctcccttga	ggaatccatt	caagtcacca	aatctctcag	acgctaaaaag	240
ccctctccaat	tcaatcgccg	ccaattccacg	aatcccactc	gatctcaaat	tccacaaactc	300
tggtctccaa	tccatagctt	caatcgccgt	cgtcgacgat	acggtgaaat	tctttcagca	360
tattatgaaa	tcgcagccta	atttcaggcc	gggacgttca	acgttctctta	tcttgcttct	420
acatgcttgt	agagctcctg	attcgtcgat	ttcgaatgtt	catagagttc	ttaactctcat	480
ggttaataat	gggttagagc	ctgatcaagt	aactaccgat	attgcgggtga	gggtctctttg	540
cgaaacgggt	cgggttgatg	aagctaagga	tttgatgaag	gagctcactg	agaaacactc	600
tcctccggat	acataatact	ataactttct	actgaagcat	ttgtgcaaat	gcaaatgatct	660
tcattgttgt	tatgattgtt	ttgatgagat	gagagatgat	ttcagtggtta	agccgggatct	720
tggttagcttc	actatcttga	ttgataatgt	ttgttaactct	aagaacttga	ggaggagcaat	780
gtatctagtt	agtaaggtag	gtaatgctgg	gtttaagccg	gattgtttcc	tctataaacac	840
gattatgaaa	ggtttttgca	cactgagtaa	agggagtgag	cgggttggtg	tgataaagaa	900
aatgaaggaa	gaaggtgttg	agccagatca	gattacttac	aatactttga	tatttggaact	960
gtcgaaagct	ggtagagttg	aggaaagctg	gatgtatttg	aaaactatgg	ttgatgcggg	1020
gtatgagccg	gatactgcta	cttacacatc	actgatgaat	ggaatgtgta	gaaaagggtga	1080
gtcttttaggt	gcggttgagtt	ttgtagaaga	aatggaaagca	agagggtgtg	ctccaaatga	1140
ttgtagcttat	aatactttgc	ttcatggatt	gtgtaaaagca	aggttgatag	ataaagggat	1200
ggagttatat	gaatgatgta	aatacaagtgg	tgtaaaagctt	gagagttaag	gttatgtact	1260
actgttgagg	tctctggtta	aaagtggcaa	ggtcgcagag	gcttatgaa	gtgttgatta	1320
tgcaagttag	agcaagagtt	tgctcagatgc	ttctgcgtac	tctacacttg	aaactacatt	1380
gaaatgggtg	aaaaaagcta	aagaacaagg	cttggttcca	taaatgtgat	ccctagactg	1440
agctttaccg	actttctctt	ttatgcaagt	ccatatttca	ttttgaagt	agtggttactc	1500
caaaagcaat	gaatttggtt	cgaaatatgc	tggttcgattc	ttaagggacc	agcagtgatt	1560
tataatagta	actttgttgg	taattatttt	gtcacttgag	att		

(2) INFORMATION FOR SEQ ID NO:705:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..473

SEQUENCE DESCRIPTION: SEQ ID NO:705:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:705:

[illegible]

435 440 445
Asp Ala Ser Ala Tyr Ser Thr Leu Glu Thr Thr Leu Lys Trp Leu Lys
450 455 460
Lys Ala Lys Glu Gln Gly Leu Val Pro
465 470

(2) INFORMATION FOR SEQ ID NO:706:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..463
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498880

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:706:

Met	Gly	Lys	Val	Pro	Ser	Ser	Phe	Arg	Ser	Ile	Pro	Ala	Asn	Leu	Leu
1															
			5						10					15	
Val	Arg	Lys	Thr	Thr	Pro	Ser	Pro	Pro	Ala	Pro	Pro	Arg	Asp	Phe	Arg
			20					25					30		
Asn	Arg	Thr	Ala	Val	Gly	Gly	Asp	Ser	Ala	Lys	Leu	Pro	His	Asn	Thr
			35				40					45			
Gln	Ala	Pro	Arg	Glu	Pro	Ser	Leu	Arg	Asn	Pro	Phe	Lys	Ser	Pro	Asn
			50				55				60				
Leu	Ser	Asp	Ala	Lys	Ser	Leu	Phe	Asn	Ser	Ile	Ala	Ala	Thr	Ser	Arg
			65			70				75				80	
Ile	Pro	Leu	Asp	Leu	Lys	Phe	His	Asn	Ser	Val	Leu	Gln	Ser	Tyr	Ala
			85						90				95		
Ser	Ile	Ala	Val	Val	Asp	Asp	Thr	Val	Lys	Phe	Phe	Gln	His	Ile	Met
			100					105					110		
Lys	Ser	Gln	Pro	Asn	Phe	Arg	Pro	Gly	Arg	Ser	Thr	Phe	Leu	Ile	Leu
			115				120					125			
Leu	Ser	His	Ala	Cys	Arg	Ala	Pro	Asp	Ser	Ser	Ile	Ser	Asn	Val	His
			130			135					140				
Arg	Val	Leu	Asn	Leu	Met	Val	Asn	Asn	Gly	Leu	Glu	Pro	Asp	Gln	Val
			145			150				155					160
Thr	Thr	Asp	Ile	Ala	Val	Arg	Ser	Leu	Cys	Glu	Thr	Gly	Arg	Val	Asp
			165						170					175	
Glu	Ala	Lys	Asp	Leu	Met	Lys	Glu	Leu	Thr	Glu	Lys	His	Ser	Pro	Pro
			180				185						190		
Asp	Thr	Tyr	Thr	Tyr	Asn	Phe	Leu	Leu	Lys	His	Leu	Cys	Lys	Cys	Lys
			195				200					205			
Asp	Leu	His	Val	Val	Tyr	Glu	Phe	Val	Asp	Glu	Met	Arg	Asp	Asp	Phe
			210				215				220				
Asp	Val	Lys	Pro	Asp	Leu	Val	Ser	Phe	Thr	Ile	Leu	Ile	Asp	Asn	Val
			225			230				235					240
Cys	Asn	Ser	Lys	Asn	Leu	Arg	Glu	Ala	Met	Tyr	Leu	Val	Ser	Lys	Leu
			245						250					255	
Gly	Asn	Ala	Gly	Phe	Lys	Pro	Asp	Cys	Phe	Leu	Tyr	Asn	Thr	Ile	Met
			260					265					270		
Lys	Gly	Phe	Cys	Thr	Leu	Ser	Lys	Gly	Ser	Glu	Ala	Val	Gly	Val	Tyr
			275				280					285			
Lys	Lys	Met	Lys	Glu	Glu	Gly	Val	Glu	Pro	Asp	Gln	Ile	Thr	Tyr	Asn
			290			295					300				
Thr	Leu	Ile	Phe	Gly	Leu	Ser	Lys	Ala	Gly	Arg	Val	Glu	Glu	Ala	Arg
			305			310				315					320
Met	Tyr	Leu	Lys	Thr	Met	Val	Asp	Ala	Gly	Tyr	Glu	Pro	Asp	Thr	Ala
			325						330					335	
Thr	Thr	Thr	Ser	Leu	Met	Asn	Gly	Met	Cys	Arg	Lys	Gly	Glu	Ser	Leu
			340				345						350		

Gly Ala Leu Ser Leu Leu Glu Glu Met Glu Ala Arg Gly Cys Ala Pro
355 360 365
Asn Asp Cys Thr Tyr Asn Thr Leu Leu His Gly Leu Cys Lys Ala Arg
370 375 380
Leu Met Asp Lys Gly Met Glu Leu Tyr Glu Met Met Lys Ser Ser Gly
385 390 395 400
Val Lys Leu Glu Ser Asn Gly Tyr Ala Thr Leu Val Arg Ser Leu Val
405 410 415
Lys Ser Gly Lys Val Ala Glu Ala Tyr Glu Val Phe Asp Tyr Ala Val
420 425 430
Asp Ser Lys Ser Leu Ser Asp Ala Ser Ala Tyr Ser Thr Leu Glu Thr
435 440 445
Thr Leu Lys Trp Leu Lys Lys Ala Lys Glu Gln Gly Leu Val Pro
450 455 460

(2) INFORMATION FOR SEQ ID NO:707:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..352
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498881

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:707:

Met Lys Ser Gln Pro Asn Phe Arg Pro Gly Arg Ser Thr Phe Leu Ile
1 5 10 15
Leu Leu Ser His Ala Cys Arg Ala Pro Asp Ser Ser Ile Ser Asn Val
20 25 30
His Arg Val Leu Asn Leu Met Val Asn Asn Gly Leu Glu Pro Asp Gln
35 40 45
Val Thr Thr Asp Ile Ala Val Arg Ser Leu Cys Glu Thr Gly Arg Val
50 55 60
Asp Glu Ala Lys Asp Leu Met Lys Glu Leu Thr Glu Lys His Ser Pro
65 70 75 80
Pro Asp Thr Tyr Thr Tyr Asn Phe Leu Leu Lys His Leu Cys Lys Cys
85 90 95
Lys Asp Leu His Val Val Tyr Glu Phe Val Asp Glu Met Arg Asp Asp
100 105 110
Phe Asp Val Lys Pro Asp Leu Val Ser Phe Thr Ile Leu Ile Asp Asn
115 120 125
Val Cys Asn Ser Lys Asn Leu Arg Glu Ala Met Tyr Leu Val Ser Lys
130 135 140
Leu Gly Asn Ala Gly Phe Lys Pro Asp Cys Phe Leu Tyr Asn Thr Ile
145 150 155 160
Met Lys Gly Phe Cys Thr Leu Ser Lys Gly Ser Glu Ala Val Gly Val
165 170 175
Tyr Lys Lys Met Lys Glu Glu Gly Val Glu Pro Asp Gln Ile Thr Tyr
180 185 190
Asn Thr Leu Ile Phe Gly Leu Ser Lys Ala Gly Arg Val Glu Glu Ala
195 200 205
Arg Met Tyr Leu Lys Thr Met Val Asp Ala Gly Tyr Glu Pro Asp Thr
210 215 220
Ala Thr Tyr Thr Ser Leu Met Asn Gly Met Cys Arg Lys Gly Glu Ser
225 230 235 240
Leu Gly Ala Leu Ser Leu Leu Glu Glu Met Glu Ala Arg Gly Cys Ala
245 250 255
Pro Asn Asp Cys Thr Tyr Asn Thr Leu Leu His Gly Leu Cys Lys Ala
260 265 270
Arg Leu Met Asp Lys Gly Met Glu Leu Tyr Glu Met Met Lys Ser Ser

(2) INFORMATION FOR SEQ ID NO:708:

(A) LENGTH: 823 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (g

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..823

(D) OTHER INFORMATION: / Ceres Seq. ID 1498882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:708:

(X1) SEQUENCE BASE						
taacctctgc	aaaaaaatca	atcccgatgc	cgatcaagtt	tatttttcgc	attcgcttc	60
aagttcaatt	caatttcaac	cctaattttg	ttgggaaga	ttaagccatg	ggagctgcacg	120
ctgtgtttgaa	tattcttcca	caagaagaggt	ggaacgttta	caactctggac	agctcgaaag	180
gatgaagaag	ctcgcggctg	agaagagcag	atcaaacccg	aggagcgtag	aaaaagagat	240
ctggaacttc	gtctcgcaagt	ctgcgtctga	ctcgcgtggt	tgcacctctc	caccggacga	300
agagaaggggt	aagaatgata	cggttggtggt	ggcggcggct	gtgtgttaaa	ccacgcgatgt	360
tgttgtgagc	agttgtgaat	cgaaaaatgt	atagatggg	atactgagtt	ctgtgtaaag	420
gttctgagacg	tccttgagaa	acgtataacg	gaaaatgata	gtgttcgag	tgaagggtgat	480
gactggtgat	ctgtgtggtta	tgaagctaat	aagaagaaga	tgagctggaa	gaagagctta	540
aaggatgata	agagggagag	gggttgagaa	gaagaagaga	tgagcccttt	catgaaacag	600
agccaaagag	ccggttggttt	ttcccggagc	tgagtttttg	tgatgaataa	tcaagtattt	660
cgattgggtg	tgtaacaagt	atgtagtaac	tggtgttaac	tgattcaat	ccacgtatt	720
ggtttattaa	cgctactcga	ctcttagtgc	tgatgaaac	attgatcatg	tttgagagtg	780
catgatagtt	tattcacggc	aatacagtc	tattcaggtc	ctc		

(2) INFORMATION FOR SEQ ID NO:709:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..33

(D) OTHER INFORMATION: / Ceres Seq. ID 1498883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709:

Thr	Ser	Ala	Lys	Lys	Ser	Ile	Pro	Ile	Pro	Ile	Lys	Phe	Tyr	Phe	Pro
1				5					10					15	
Ile	Arg	Phe	Gln	Val	Gln	Phe	Asn	Phe	Asn	Pro	Asn	Phe	Val	Trp	Lys
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:710:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..40
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498884
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:710:
Met Arg Arg Trp Trp Arg Arg Leu Leu Asn Pro Arg Met Leu
1 5 10 15
Leu Trp Arg Val Leu Asn Arg Lys Met Tyr Arg Leu Gly Tyr Gly Val
 20 25 30
Ala Gly Lys Gly Val Lys Arg Pro
 35 40
(2) INFORMATION FOR SEQ ID NO:711:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..37
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498885
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711:
Met Ser Gly Lys Lys Ser Leu Lys Glu Leu Lys Arg Glu Arg Val Glu
1 5 10 15
Lys Glu Arg Glu Arg Ala Leu Phe Met Lys Gln Ser Gln Arg Ala Gly
 20 25 30
Gly Phe Ser Arg Arg
 35
(2) INFORMATION FOR SEQ ID NO:712:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1517 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..1517
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498886
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:712:
aaactaagaa acacccaaga aaacaaacaa actttttaaa aaatgtccgt ttcaacacat 60
caccaccacg tggctcctct cccctacatg tcaaaaggcc acatcatccc tctcctccaa 120
ttcggtcgtc tccctcctccg taccacccgc aaagaaccaa ccatcacccg caccgttttc 180
accactccca agaaccaaac ttctcatcca gacttctctc cggacacgcc ggagatcaaa 240
gtcatctctc tccctttccc ggaaaaacatc accggaatcc ctcccggcgt cgagaacacc 300
gaaaaggctcc catccatgac acttttctgc cccctcacac gcgccacgaa gcttctccaa 360
cctttcttcg aagaacactc caagactctt ccaaaagtgt cgttcagtgt tctctcttac 420
ttcctctggt ggacatcgga gtctgcagct gctctgaaga ttccaagatt cctctgatga 480
ggcatgaaat cttactccgc cgctgtctcc atctctgttt tcaaacacga actctttacc 540
gaaccggaaa gtaaatctga tacccaaccc gtcactgtac cagactttcc atggatcaag 600
atcaagaagt gtgatttcca ccatggcact accgagccgg aagaatcagg tgcagccctc 660
gaactatcta tggaccaaat caagtgcacc accacaagcc atgggttttt tgcataatagc 720
ttctacgagc tcgagtcagc attgtttgat tacaacaaca actctgttga taaaccaaag 780
tcgtggtgtg ttgggcactc gtgtttgaca gatcctccta aacaggggag tgctaaaccg 840
gcttggtattc attgtgttga tcagaagcga gaggaaggcg gtccggtttt gtacgtggcg 900
tttgaaacgc aggcagagat atcgaaacaag cagcttatgg aactagcttt cggcttggaa 960
gattcaaaag tgaactttct gtgggtcaca agaaaagatg tggaggagat tatttgagaa 1020
ggattcaacg atagaataag agagagtggg atgatagtga gagattgggt ggaccaatgg 1080
gagatatattg cacatgaaag tgtcaaaagg tttttgagcc attgtgggtg gaactcagca 1140

caagagagca tatgtgtcgg ggtcccatgt ttggcttggc cgatgatggc cgagcaaccg 1200
ctcaatgcga agatggttgt ggaggagata aaggtgggag taagagtgtg aacggaagat 1260
gggagtgtaa aaggttttgt gacaagagag gaactaagtg gaaagattaa agaactgatg 1320
gaaggagaaa cggggaaaaa cgcaagaaa aatgtgaaa aatactcgaa aatggcaaaa 1380
gcggctttgg tcgaaggagc tggttcgtca tggaagaatt tagatatgat tcttaaggac 1440
ttatgtaaga gtagagattc aaacggtgct agtgagtaga gtgattaaga attgaataac 1500
tgaaccggtc tacgttt

(2) INFORMATION FOR SEQ ID NO:713:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..478
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498887

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:713:

Met	Ser	Val	Ser	Thr	His	His	His	His	Val	Val	Leu	Phe	Pro	Tyr	Met
1			5					10					15		
Ser	Lys	Gly	His	Ile	Ile	Pro	Leu	Leu	Gln	Phe	Gly	Arg	Leu	Leu	Leu
			20				25					30			
Arg	His	His	Arg	Lys	Glu	Pro	Thr	Ile	Thr	Val	Thr	Val	Phe	Thr	Thr
			35				40				45				
Pro	Lys	Asn	Gln	Pro	Phe	Ile	Ser	Asp	Phe	Leu	Ser	Asp	Thr	Pro	Glu
			50				55				60				
Ile	Lys	Val	Ile	Ser	Leu	Pro	Phe	Pro	Glu	Asn	Ile	Thr	Gly	Ile	Pro
			65				70				75			80	
Pro	Gly	Val	Glu	Asn	Thr	Glu	Arg	Leu	Pro	Ser	Met	Ser	Leu	Phe	Val
			85					90					95		
Pro	Phe	Thr	Arg	Ala	Thr	Lys	Leu	Leu	Gln	Pro	Phe	Phe	Glu	Glu	Thr
			100				105						110		
Leu	Lys	Thr	Leu	Pro	Lys	Val	Ser	Phe	Met	Val	Ser	Asp	Gly	Phe	Leu
			115				120					125			
Trp	Trp	Thr	Ser	Glu	Ser	Ala	Ala	Lys	Phe	Asn	Ile	Pro	Arg	Phe	Val
			130				135					140			
Ser	Tyr	Gly	Met	Asn	Ser	Tyr	Ser	Ala	Ala	Val	Ser	Ile	Ser	Val	Phe
			145				150					155			160
Lys	His	Glu	Leu	Phe	Thr	Glu	Pro	Glu	Ser	Lys	Ser	Asp	Thr	Glu	Pro
			165							170				175	
Val	Thr	Val	Pro	Asp	Phe	Pro	Trp	Ile	Lys	Ile	Lys	Lys	Cys	Asp	Phe
			180					185					190		
Asp	His	Gly	Thr	Thr	Glu	Pro	Glu	Glu	Ser	Gly	Ala	Ala	Leu	Glu	Leu
			195				200					205			
Ser	Met	Asp	Gln	Ile	Lys	Ser	Thr	Thr	Thr	Ser	His	Gly	Phe	Leu	Val
			210				215					220			
Asn	Ser	Phe	Tyr	Glu	Leu	Glu	Ser	Ala	Phe	Val	Asp	Tyr	Asn	Asn	Asn
			225				230				235				240
Ser	Gly	Asp	Lys	Pro	Lys	Ser	Trp	Cys	Val	Gly	Pro	Leu	Cys	Leu	Thr
			245						250				255		
Asp	Pro	Pro	Lys	Gln	Gly	Ser	Ala	Lys	Pro	Ala	Trp	Ile	His	Trp	Leu
			260					265					270		
Asp	Gln	Lys	Arg	Glu	Glu	Gly	Arg	Pro	Val	Leu	Tyr	Val	Ala	Phe	Gly
			275				280					285			
Thr	Gln	Ala	Glu	Ile	Ser	Asn	Lys	Gln	Leu	Met	Glu	Leu	Ala	Phe	Gly
			290				295					300			
Leu	Glu	Asp	Ser	Lys	Val	Asn	Phe	Leu	Trp	Val	Thr	Arg	Lys	Asp	Val
			305				310				315				320
Glu	Glu	Ile	Ile	Gly	Glu	Gly	Phe	Asn	Asp	Arg	Ile	Arg	Glu	Ser	Gly
			325					330					335		

Met Ile Val Arg Asp Trp Val Asp Gln Trp Glu Ile Leu Ser His Glu
340 345 350
Ser Val Lys Gly Phe Leu Ser His Cys Gly Trp Asn Ser Ala Gln Glu
355 360 365
Ser Ile Cys Val Gly Val Pro Leu Leu Ala Trp Pro Met Met Ala Glu
370 375 380
Gln Pro Leu Asn Ala Lys Met Val Val Glu Glu Ile Lys Val Gly Val
385 390 395 400
Arg Val Glu Thr Glu Asp Gly Ser Val Lys Gly Phe Val Thr Arg Glu
405 410 415
Glu Leu Ser Gly Lys Ile Lys Glu Leu Met Glu Gly Glu Thr Gly Lys
420 425 430
Thr Ala Arg Lys Asn Val Lys Glu Tyr Ser Lys Met Ala Lys Ala Ala
435 440 445
Leu Val Glu Gly Thr Gly Ser Ser Trp Lys Asn Leu Asp Met Ile Leu
450 455 460
Lys Asp Leu Cys Lys Ser Arg Asp Ser Asn Gly Ala Ser Glu
465 470 475

(2) INFORMATION FOR SEQ ID NO:714:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 463 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..463

(D) OTHER INFORMATION: / Ceres Seq. ID 1498888

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:714:

Met Ser Lys Gly His Ile Ile Pro Leu Leu Gln Phe Gly Arg Leu Leu
1 5 10 15
Leu Arg His His Arg Lys Glu Pro Thr Ile Thr Val Thr Val Phe Thr
20 25 30
Thr Pro Lys Asn Gln Pro Phe Ile Ser Asp Phe Leu Ser Asp Thr Pro
35 40 45
Glu Ile Lys Val Ile Ser Leu Pro Phe Pro Glu Asn Ile Thr Gly Ile
50 55 60
Pro Pro Gly Val Glu Asn Thr Glu Arg Leu Pro Ser Met Ser Leu Phe
65 70 75 80
Val Pro Phe Thr Arg Ala Thr Lys Leu Leu Gln Pro Phe Phe Glu Glu
85 90 95
Thr Leu Lys Thr Leu Pro Lys Val Ser Phe Met Val Ser Asp Gly Phe
100 105 110
Leu Trp Trp Thr Ser Glu Ser Ala Ala Lys Phe Asn Ile Pro Arg Phe
115 120 125
Val Ser Tyr Gly Met Asn Ser Tyr Ser Ala Ala Val Ser Ile Ser Val
130 135 140
Phe Lys His Glu Leu Phe Thr Glu Pro Glu Ser Lys Ser Asp Thr Glu
145 150 155 160
Pro Val Thr Val Pro Asp Phe Pro Trp Ile Lys Ile Lys Lys Cys Asp
165 170 175
Phe Asp His Gly Thr Thr Glu Pro Glu Glu Ser Gly Ala Ala Leu Glu
180 185 190
Leu Ser Met Asp Gln Ile Lys Ser Thr Thr Thr Ser His Gly Phe Leu
195 200 205
Val Asn Ser Phe Tyr Glu Leu Glu Ser Ala Phe Val Asp Tyr Asn Asn
210 215 220
Asn Ser Gly Asp Lys Pro Lys Ser Trp Cys Val Gly Pro Leu Cys Leu
225 230 235 240
Thr Asp Pro Pro Lys Gln Gly Ser Ala Lys Pro Ala Trp Ile His Trp

245	250	255
Leu Asp Gln Lys Arg Glu Glu Gly Arg Pro Val Leu Tyr Val Ala Phe		
260	265	270
Gly Thr Gln Ala Glu Ile Ser Asn Lys Gln Leu Met Glu Leu Ala Phe		
275	280	285
Gly Leu Glu Asp Ser Lys Val Asn Phe Leu Trp Val Thr Arg Lys Asp		
290	295	300
Val Glu Glu Ile Ile Gly Glu Gly Phe Asn Asp Arg Ile Arg Glu Ser		
305	310	315
Gly Met Ile Val Arg Asp Trp Val Asp Gln Trp Glu Ile Leu Ser His		
325	330	335
Glu Ser Val Lys Gly Phe Leu Ser His Cys Gly Trp Asn Ser Ala Gln		
340	345	350
Glu Ser Ile Cys Val Gly Val Pro Leu Leu Ala Trp Pro Met Met Ala		
355	360	365
Glu Gln Pro Leu Asn Ala Lys Met Val Val Glu Glu Ile Lys Val Gly		
370	375	380
Val Arg Val Glu Thr Glu Asp Gly Ser Val Lys Gly Phe Val Thr Arg		
385	390	395
Glu Glu Leu Ser Gly Lys Ile Lys Glu Leu Met Glu Gly Glu Thr Gly		
405	410	415
Lys Thr Ala Arg Lys Asn Val Lys Glu Tyr Ser Lys Met Ala Lys Ala		
420	425	430
Ala Leu Val Glu Gly Thr Gly Ser Ser Trp Lys Asn Leu Asp Met Ile		
435	440	445
Leu Lys Asp Leu Cys Lys Ser Arg Asp Ser Asn Gly Ala Ser Glu		
450	455	460

(2) INFORMATION FOR SEQ ID NO:715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..387
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498889

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:715:

Met Ser Leu Phe Val Pro Phe Thr Arg Ala Thr Lys Leu Leu Gln Pro	
1 5 10 15	
Phe Phe Glu Glu Thr Leu Lys Thr Leu Pro Lys Val Ser Phe Met Val	
20 25 30	
Ser Asp Gly Phe Leu Trp Trp Thr Ser Glu Ser Ala Ala Lys Phe Asn	
35 40 45	
Ile Pro Arg Phe Val Ser Tyr Gly Met Asn Ser Tyr Ser Ala Ala Val	
50 55 60	
Ser Ile Ser Val Phe Lys His Glu Leu Phe Thr Glu Pro Glu Ser Lys	
65 70 75 80	
Ser Asp Thr Glu Pro Val Thr Val Pro Asp Phe Pro Trp Ile Lys Ile	
85 90 95	
Lys Lys Cys Asp Phe Asp His Gly Thr Thr Glu Pro Glu Glu Ser Gly	
100 105 110	
Ala Ala Leu Glu Leu Ser Met Asp Gln Ile Lys Ser Thr Thr Thr Ser	
115 120 125	
His Gly Phe Leu Val Asn Ser Phe Tyr Glu Leu Glu Ser Ala Phe Val	
130 135 140	
Asp Tyr Asn Asn Asn Ser Gly Asp Lys Pro Lys Ser Trp Cys Val Gly	
145 150 155 160	
Pro Leu Cys Leu Thr Asp Pro Pro Lys Gln Gly Ser Ala Lys Pro Ala	
165 170 175	

Trp Ile His Trp Leu Asp Gln Lys Arg Glu Glu Gly Arg Pro Val Leu
180 185 190
Tyr Val Ala Phe Gly Thr Gln Ala Glu Ile Ser Asn Lys Gln Leu Met
195 200 205
Glu Leu Ala Phe Gly Leu Glu Asp Ser Lys Val Asn Phe Leu Trp Val
210 215 220
Thr Arg Lys Asp Val Glu Glu Ile Ile Gly Glu Phe Asn Asp Arg
225 230 235 240
Ile Arg Glu Ser Gly Met Ile Val Arg Asp Trp Val Asp Gln Trp Glu
245 250 255
Ile Leu Ser His Glu Ser Val Lys Gly Phe Leu Ser His Cys Gly Trp
260 265 270
Asn Ser Ala Gln Glu Ser Ile Cys Val Gly Val Pro Leu Leu Ala Trp
275 280 285
Pro Met Met Ala Glu Gln Pro Leu Asn Ala Lys Met Val Val Glu Glu
290 295 300
Ile Lys Val Gly Val Arg Val Glu Thr Glu Asp Gly Ser Val Lys Gly
305 310 315 320
Phe Val Thr Arg Glu Glu Leu Ser Gly Lys Ile Lys Glu Leu Met Glu
325 330 335
Gly Glu Thr Gly Lys Thr Ala Arg Lys Asn Val Lys Glu Tyr Ser Lys
340 345 350
Met Ala Lys Ala Ala Leu Val Glu Gly Thr Gly Ser Ser Trp Lys Asn
355 360 365
Leu Asp Met Ile Leu Lys Asp Leu Cys Lys Ser Arg Asp Ser Asn Gly
370 375 380
Ala Ser Glu
385

(2) INFORMATION FOR SEQ ID NO:716:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1689 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1689
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498890

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:716:

atttgctct	ttatcttgct	ttgtctgat	cagtagtcac	tacatttggt	tctttcacaa	60
tctttctttt	ttgcttcata	ttgaactgca	agaccaatcc	atgaatgcac	atataaaata	120
ttgtcttaacg	gttaaccatc	tctaagtggt	tgtagtcac	gaattgtgaa	attgtttcgc	180
ttcaaacata	gaattagttg	atttggaaa	gtagacatga	atgcttatct	aaatacaata	240
aaactgtgtc	ttgtttcagt	tgtgtatcag	agatgagacc	ttgactggta	atttcaatgg	300
agcataaatta	aatgctaata	atacttattt	tctggttaat	gcaggagggt	tgagagtttg	360
aagaaacatc	ttacgccacc	cagggaagtg	catgttccaa	tcttgcaact	catgccacct	420
caaaaagatcg	agatcttcaa	atctatggaa	aaactggccg	aggagaacct	tctgattcac	480
ctcaaggatg	tggagaagtc	ttggcaaccc	caggatttct	tgccctgacc	tgcatcagat	540
gggtttgaag	atcaggtaag	agagttaaga	gagaggggta	gagagctccc	tgatgattac	600
tttgtttgtt	tggtggggga	catgatcaca	gaagaagcac	ttccgacctc	tcaaacatgt	660
ttgaacactt	ttgatggagt	tagggatgaa	acaggtgcta	gtcctacttc	atgggctatt	720
tggaaccagag	cttggtactgc	agaagaaaac	cgacatggcg	atctttctga	taaataacct	780
tacttgtctg	gtcgtgttga	catgaggcag	atcgaaaaga	ccattccagta	cttgattgga	840
tctggaatgg	atccgcggac	agagaataac	ccctaccttg	gcttcatcta	tacgtcaatc	900
caagaaaagag	cgacattcat	ctctcacgga	aacacagccc	gccaaagcca	agagcaccgg	960
gacatacaac	tagccccaat	atgtggcaca	atagctcgag	acgagaagcg	tcatgaacaa	1020
gcatacacca	agatagtgtg	aaagctcttt	gagattgtac	ctgatggtag	tgctatggct	1080
tttgacagca	tgatgagaaa	gaaaatctca	attgcctgctc	acttgatgta	tgatggggcg	1140
aacgacaacc	tctttgacaa	cttctcttcc	gtggctcaga	ggctcggtgt	ttacaccggc	1200
aaagactatg	cagacattct	tgagtttctg	gttggttaggt	ggaaaatcca	ggacttaacc	1260

gggctttcag gtgaaggaaa caaagcacaa gactatttat gcgggttgge toccaaggate 1320
aagagattgg atgagagagc tcaagcaaga gcccaagaaag gacccaagat tccctttcagt 1380
tggatacacg acagagaagt gcagctcttaa aaggacaaaag acaaaaaacaa aaacctatcc 1440
tcccggttcc tcatttccatc tgtctgctct taaaattggt gtagattact atggttttct 1500
gataatgttg gtgggtctag ttacaaagt ggagatgcagt gatttagtag ctttgttttt 1560
cccagtcact atattgtttg tctttgtgcc gttagcacac ttgtagtagt taaaacagtt 1620
taagtattgt ctgtgtctag tcttctctct ctctgtggag tttgttttaa gttcaggtta 1680
gtttgttt

(2) INFORMATION FOR SEQ ID NO:717:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..332
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:717:

Met	Pro	Pro	Gln	Lys	Ile	Glu	Ile	Phe	Lys	Ser	Met	Glu	Asn	Trp	Ala
1					5				10					15	
Glu	Glu	Asn	Leu	Ile	His	Leu	Lys	Asp	Val	Glu	Lys	Ser	Trp	Gln	
			20				25					30			
Pro	Gln	Asp	Phe	Leu	Pro	Asp	Pro	Ala	Ser	Asp	Gly	Phe	Glu	Asp	Gln
			35				40					45			
Val	Arg	Glu	Leu	Arg	Glu	Arg	Ala	Arg	Glu	Leu	Pro	Asp	Asp	Tyr	Phe
			50				55				60				
Val	Val	Leu	Val	Gly	Asp	Met	Ile	Thr	Glu	Glu	Ala	Leu	Pro	Thr	Tyr
			65				70				75				80
Gln	Thr	Met	Leu	Asn	Thr	Leu	Asp	Gly	Val	Arg	Asp	Glu	Thr	Gly	Ala
			85						90					95	
Ser	Pro	Thr	Ser	Trp	Ala	Ile	Trp	Thr	Arg	Ala	Trp	Thr	Ala	Glu	Glu
			100						105				110		
Asn	Arg	His	Gly	Asp	Leu	Leu	Asn	Lys	Tyr	Leu	Tyr	Leu	Ser	Gly	Arg
			115						120				125		
Val	Asp	Met	Arg	Gln	Ile	Glu	Lys	Thr	Ile	Gln	Tyr	Leu	Ile	Gly	Ser
			130				135					140			
Gly	Met	Asp	Pro	Arg	Thr	Glu	Asn	Asn	Pro	Tyr	Leu	Gly	Phe	Ile	Tyr
					150					155				160	
Thr	Ser	Phe	Gln	Glu	Arg	Ala	Thr	Phe	Ile	Ser	His	Gly	Asn	Thr	Ala
					165				170					175	
Arg	Gln	Ala	Lys	Glu	His	Gly	Asp	Ile	Lys	Leu	Ala	Gln	Ile	Cys	Gly
			180						185					190	
Thr	Ile	Ala	Ala	Asp	Glu	Lys	Arg	His	Glu	Thr	Ala	Tyr	Thr	Lys	Ile
			195						200				205		
Val	Glu	Lys	Leu	Phe	Glu	Ile	Asp	Pro	Asp	Gly	Thr	Val	Met	Ala	Phe
			210				215					220			
Ala	Asp	Met	Met	Arg	Lys	Lys	Ile	Ser	Met	Pro	Ala	His	Leu	Met	Tyr
			225				230				235				240
Asp	Gly	Arg	Asn	Asp	Asn	Leu	Phe	Asp	Asn	Phe	Ser	Ser	Val	Ala	Gln
					245					250				255	
Arg	Leu	Gly	Val	Tyr	Thr	Ala	Lys	Asp	Tyr	Ala	Asp	Ile	Leu	Glu	Phe
			260						265				270		
Leu	Val	Gly	Arg	Trp	Lys	Ile	Gln	Asp	Leu	Thr	Gly	Leu	Ser	Gly	Glu
			275						280				285		
Gly	Asn	Lys	Ala	Gln	Asp	Tyr	Leu	Cys	Gly	Leu	Ala	Pro	Arg	Ile	Lys
			290				295						300		
Arg	Leu	Asp	Glu	Arg	Ala	Gln	Ala	Arg	Ala	Lys	Lys	Gly	Pro	Lys	Ile
					310					315					320
Pro	Phe	Ser	Trp	Ile	His	Asp	Arg	Glu	Val	Gln	Leu				

325

330

(2) INFORMATION FOR SEQ ID NO:718:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..321

(D) OTHER INFORMATION: / Ceres Seq. ID 1498892

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:718:

Met	Glu	Asn	Trp	Ala	Glu	Glu	Asn	Leu	Leu	Ile	His	Leu	Lys	Asp	Val	
1				5					10					15		
Glu	Lys	Ser	Trp	Gln	Pro	Gln	Asp	Phe	Leu	Pro	Asp	Pro	Ala	Ser	Asp	
			20				25						30			
Gly	Phe	Glu	Asp	Gln	Val	Arg	Glu	Leu	Arg	Glu	Arg	Ala	Arg	Glu	Leu	
		35					40					45				
Pro	Asp	Asp	Tyr	Phe	Val	Val	Leu	Val	Gly	Asp	Met	Ile	Thr	Glu	Glu	
		50				55				60						
Ala	Leu	Pro	Thr	Tyr	Gln	Thr	Met	Leu	Asn	Thr	Leu	Asp	Gly	Val	Arg	
65					70				75					80		
Asp	Glu	Thr	Gly	Ala	Ser	Pro	Thr	Ser	Trp	Ala	Ile	Trp	Thr	Arg	Ala	
			85						90					95		
Trp	Thr	Ala	Glu	Glu	Asn	Arg	His	Gly	Asp	Leu	Leu	Asn	Lys	Tyr	Leu	
			100					105					110			
Tyr	Leu	Ser	Gly	Arg	Val	Asp	Met	Arg	Gln	Ile	Glu	Lys	Thr	Ile	Gln	
			115				120					125				
Tyr	Leu	Ile	Gly	Ser	Gly	Met	Asp	Pro	Arg	Thr	Glu	Asn	Asn	Pro	Tyr	
			130			135					140					
Leu	Gly	Phe	Ile	Tyr	Thr	Ser	Phe	Gln	Glu	Arg	Ala	Thr	Phe	Ile	Ser	
145					150				155					160		
His	Gly	Asn	Thr	Ala	Arg	Gln	Ala	Lys	Glu	His	Gly	Asp	Ile	Lys	Leu	
			165						170					175		
Ala	Gln	Ile	Cys	Gly	Thr	Ile	Ala	Ala	Asp	Glu	Lys	Arg	His	Glu	Thr	
			180				185						190			
Ala	Tyr	Thr	Lys	Ile	Val	Glu	Lys	Leu	Phe	Glu	Ile	Asp	Pro	Asp	Gly	
			195				200					205				
Thr	Val	Met	Ala	Phe	Ala	Asp	Met	Met	Arg	Lys	Lys	Ile	Ser	Met	Pro	
			210			215						220				
Ala	His	Leu	Met	Tyr	Asp	Gly	Arg	Asn	Asp	Asn	Leu	Phe	Asp	Asn	Phe	
225					230					235				240		
Ser	Ser	Val	Ala	Gln	Arg	Leu	Gly	Val	Tyr	Thr	Ala	Lys	Asp	Tyr	Ala	
			245						250					255		
Asp	Ile	Leu	Glu	Phe	Leu	Val	Gly	Arg	Trp	Lys	Ile	Gln	Asp	Leu	Thr	
			260					265					270			
Gly	Leu	Ser	Gly	Glu	Gly	Asn	Lys	Ala	Gln	Asp	Tyr	Leu	Cys	Gly	Leu	
			275				280						285			
Ala	Pro	Arg	Ile	Lys	Arg	Leu	Asp	Glu	Arg	Ala	Gln	Ala	Arg	Ala	Lys	
			290			295					300					
Lys	Gly	Pro	Lys	Ile	Pro	Phe	Ser	Trp	Ile	His	Asp	Arg	Glu	Val	Gln	
305					310					315					320	
Leu																

(2) INFORMATION FOR SEQ ID NO:719:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..262

(D) OTHER INFORMATION: / Ceres Seq. ID 1498893

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:719:

```
Met Ile Thr Glu Ala Leu Pro Thr Tyr Gln Thr Met Leu Asn Thr
1      5      10      15
Leu Asp Gly Val Arg Asp Glu Thr Gly Ala Ser Pro Thr Ser Trp Ala
20      25      30
Ile Trp Thr Arg Ala Trp Thr Ala Glu Glu Asn Arg His Gly Asp Leu
35      40      45
Leu Asn Lys Tyr Leu Tyr Leu Ser Gly Arg Val Asp Met Arg Gln Ile
50      55      60
Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser Gly Met Asp Pro Arg Thr
65      70      75      80
Glu Asn Asn Pro Tyr Leu Gly Phe Ile Tyr Thr Ser Phe Gln Glu Arg
85      90      95
Ala Thr Phe Ile Ser His Gly Asn Thr Ala Arg Gln Ala Lys Glu His
100     105     110
Gly Asp Ile Lys Leu Ala Gln Ile Cys Gly Thr Ile Ala Ala Asp Glu
115     120     125
Lys Arg His Glu Thr Ala Tyr Thr Lys Ile Val Glu Lys Leu Phe Glu
130     135     140
Ile Asp Pro Asp Gly Thr Val Met Ala Phe Ala Asp Met Met Arg Lys
145     150     155     160
Lys Ile Ser Met Pro Ala His Leu Met Tyr Asp Gly Arg Asn Asp Asn
165     170     175
Leu Phe Asp Asn Phe Ser Ser Val Ala Gln Arg Leu Gly Val Tyr Thr
180     185     190
Ala Lys Asp Tyr Ala Asp Ile Leu Glu Phe Leu Val Gly Arg Trp Lys
195     200     205
Ile Gln Asp Leu Thr Gly Leu Ser Gly Glu Gly Asn Lys Ala Gln Asp
210     215     220
Tyr Leu Cys Gly Leu Ala Pro Arg Ile Lys Arg Leu Asp Glu Arg Ala
225     230     235     240
Gln Ala Arg Ala Lys Lys Gly Pro Lys Ile Pro Phe Ser Trp Ile His
245     250     255
Asp Arg Glu Val Gln Leu
260
```

(2) INFORMATION FOR SEQ ID NO:720:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1029 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1029

(D) OTHER INFORMATION: / Ceres Seq. ID 1498905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:720:

```
aacaaagtgt gttcttaaat tatcttctct gataaccaaa aaagccctat ttcccgagat
60
gaatacccta gaagaagtag atgaatccac tcatacttc aacgctttga tgagtctaat
120
gaggaaattt ttgttcagag ttctatgcgt cggtccaatc cctactaaca ttctattcat
180
catggatgga aaccgcaggt tcgctaagaa acacaatcct ataggcctag atgcaggaca
240
tagagctggg ttcatatccg tgaaatatat tcttcaatac tgcaaaagaa ttggtgtacc
300
gtacgtcaca ctccacgcgt ttggtatgga taatttcaag agagagacctg aagaagtcaa
360
gtgtgtgtag gatctaatgc ttgagaaaagt cgcagctgcg atcgatacaag ctgtatcagg
420
gaatatgaac ggcgtgagaa taatctttgc cgtgtgattg gattcgttaa acgagcattt
480
tagagctgcg acaagaagaa tgatggagct tacgaggagg aatagagatc tgatttgtgt
540
```


gggttgcggt	gcttacacga	caagtctcga	gattgttcac	gctgttcgaa	aatcttgtgt	600
tagaaaatgt	acgaatggag	atgatcttgt	acttttgag	ttgagtgatg	ttgaagatgt	660
tatgtataca	tcgattgtgc	cggttcocga	tcttgtgata	agaaccggag	gaggagatcg	720
gctgagtaac	ttcatgacgt	ggcaacttc	gaggtctctt	cttcacagaa	cggaggctct	780
ttggccggag	ttagggtctt	ggcatttggt	ttgggcaatt	cttaaattcc	aaagaatgca	840
agattacttg	acgaagaaga	aaaagctcga	ttagatagtt	tctaaagtta	aacctgcag	900
gaaagaactt	ttaaactctt	attacgttta	attacgtgtt	ttctatgact	ggaacgaga	960
aagctcacaa	gcaaatcttt	tttattatgt	attggatccg	tataacaac	acgaatatac	1020
aaaacatcg						

(2) INFORMATION FOR SEQ ID NO:721:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 290 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..290

(D) OTHER INFORMATION: / Ceres Seq. ID 1498906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:721:

Thr	Lys	Cys	Val	Leu	Lys	Leu	Ser	Ser	Leu	Ile	Thr	Lys	Lys	Ala	Leu	
1			5						10					15		
Phe	Ser	Glu	Met	Asn	Thr	Leu	Glu	Glu	Val	Asp	Glu	Ser	Thr	His	Ile	
			20					25					30			
Phe	Asn	Ala	Leu	Met	Ser	Leu	Met	Arg	Lys	Phe	Leu	Phe	Arg	Val	Leu	
		35					40					45				
Cys	Val	Gly	Pro	Ile	Pro	Thr	Asn	Ile	Ser	Phe	Ile	Met	Asp	Gly	Asn	
	50					55					60					
Arg	Arg	Phe	Ala	Lys	Lys	His	Asn	Leu	Ile	Gly	Leu	Asp	Ala	Gly	His	
	65				70					75				80		
Arg	Ala	Gly	Phe	Ile	Ser	Val	Lys	Tyr	Ile	Leu	Gln	Tyr	Cys	Lys	Glu	
		85							90				95			
Ile	Gly	Val	Pro	Tyr	Val	Thr	Leu	His	Ala	Phe	Gly	Met	Asp	Asn	Phe	
	100						105						110			
Lys	Arg	Gly	Pro	Glu	Glu	Val	Lys	Cys	Val	Met	Asp	Leu	Met	Leu	Glu	
	115					120					125					
Lys	Val	Glu	Leu	Ala	Ile	Asp	Gln	Ala	Val	Ser	Gly	Asn	Met	Asn	Gly	
	130				135						140					
Val	Arg	Ile	Ile	Phe	Ala	Gly	Asp	Leu	Asp	Ser	Leu	Asn	Glu	His	Phe	
	145				150				155					160		
Arg	Ala	Ala	Thr	Lys	Lys	Leu	Met	Glu	Leu	Thr	Glu	Glu	Asn	Arg	Asp	
			165						170					175		
Leu	Ile	Val	Val	Val	Cys	Val	Ala	Tyr	Ser	Thr	Ser	Leu	Glu	Ile	Val	
	180							185					190			
His	Ala	Val	Arg	Lys	Ser	Cys	Val	Arg	Lys	Cys	Thr	Asn	Gly	Asp	Asp	
	195					200						205				
Leu	Val	Leu	Leu	Glu	Leu	Ser	Asp	Val	Glu	Glu	Cys	Met	Tyr	Thr	Ser	
	210				215						220					
Ile	Val	Pro	Val	Pro	Asp	Leu	Val	Ile	Arg	Thr	Gly	Gly	Asp	Arg		
	225				230				235				240			
Leu	Ser	Asn	Phe	Met	Thr	Trp	Gln	Thr	Ser	Arg	Ser	Leu	Leu	His	Arg	
		245						250					255			
Thr	Glu	Ala	Leu	Trp	Pro	Glu	Leu	Gly	Leu	Trp	His	Leu	Val	Trp	Ala	
	260					265						270				
Ile	Leu	Lys	Phe	Gln	Arg	Met	Gln	Asp	Tyr	Leu	Thr	Lys	Lys	Lys		
	275					280						285				

Leu Asp
290

(2) INFORMATION FOR SEQ ID NO:722:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 271 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..271
(D) OTHER INFORMATION: / Ceres Seq. ID 1498907
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:722:
Met Asn Thr Leu Glu Val Asp Glu Ser Thr His Ile Phe Asn Ala
1 5 10 15
Leu Met Ser Leu Met Arg Lys Phe Leu Phe Arg Val Leu Cys Val Gly
20 25 30
Pro Ile Pro Thr Asn Ile Ser Phe Ile Met Asp Gly Asn Arg Arg Phe
35 40 45
Ala Lys Lys His Asn Leu Ile Gly Leu Asp Ala Gly His Arg Ala Gly
50 55 60
Phe Ile Ser Val Lys Tyr Ile Leu Gln Tyr Cys Lys Glu Ile Gly Val
65 70 75 80
Pro Tyr Val Thr Leu His Ala Phe Gly Met Asp Asn Phe Lys Arg Gly
85 90 95
Pro Glu Glu Val Lys Cys Val Met Asp Leu Met Leu Glu Lys Val Glu
100 105 110
Leu Ala Ile Asp Gln Ala Val Ser Gly Asn Met Asn Gly Val Arg Ile
115 120 125
Ile Phe Ala Gly Asp Leu Asp Ser Leu Asn Glu His Phe Arg Ala Ala
130 135 140
Thr Lys Lys Leu Met Glu Leu Thr Glu Glu Asn Arg Asp Leu Ile Val
145 150 155 160
Val Val Cys Val Ala Tyr Ser Thr Ser Leu Glu Ile Val His Ala Val
165 170 175
Arg Lys Ser Cys Val Arg Lys Cys Thr Asn Gly Asp Asp Leu Val Leu
180 185 190
Leu Glu Leu Ser Asp Val Glu Glu Cys Met Tyr Thr Ser Ile Val Pro
195 200 205
Val Pro Asp Leu Val Ile Arg Thr Gly Gly Gly Asp Arg Leu Ser Asn
210 215 220
Phe Met Thr Trp Gln Thr Ser Arg Ser Leu Leu His Arg Thr Glu Ala
225 230 235 240
Leu Trp Pro Glu Leu Gly Leu Trp His Leu Val Trp Ala Ile Leu Lys
245 250 255
Phe Gln Arg Met Gln Asp Tyr Leu Thr Lys Lys Lys Leu Asp
260 265 270
(2) INFORMATION FOR SEQ ID NO:723:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 254 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..254
(D) OTHER INFORMATION: / Ceres Seq. ID 1498908
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:723:
Met Ser Leu Met Arg Lys Phe Leu Phe Arg Val Leu Cys Val Gly Pro
1 5 10 15
Ile Pro Thr Asn Ile Ser Phe Ile Met Asp Gly Asn Arg Arg Phe Ala
20 25 30
Lys Lys His Asn Leu Ile Gly Leu Asp Ala Gly His Arg Ala Gly Phe

[illegible]

(2) INFORMATION FOR SEQ ID NO:724:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1358 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1358
(D) OTHER INFORMATION

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:724:

(X1) SEQUENCE DESCRIPTION: SEQ ID:10712						
aaggaaacac	ttaaccaagc	aaacacacaa	tggctctctt	aatgctgtctt	cttccctcca	60
ttctctattc	cataccagct	tttctcagtt	cggtttttgc	cgtttcacca	ctccaaaactg	120
atacgttaaa	accggggcag	cagctcagag	actgggagca	tgtgatctct	gcggagggta	180
ttctctactc	cggattcttt	accactaaag	actcatctac	ttccgaactc	gggtcagctg	240
gtcttagata	ttctgtgatt	tggtctcaaa	tatttccaat	aaatctagtt	tggtgtggta	300
accocacgga	atacgttttt	gattcatctg	gtttctctatc	catgtgacac	aatgggggttc	360
taagataaac	acaggcctac	gctattccaa	ttctgtgtga	ccaaagacca	gcgcgcagc	420
tttcatggct	cgggatagtg	ttgtccattt	tactgatata	cgggaacttt	gtgtgtccag	480
atacaggcgt	aggaggaatt	ccgggtgtgt	ttctatggca	aagctttgac	catccccaaa	540
acacattact	tcccgggatg	aagattgggt	ttaacctaaag	accagaagaa	gaagatcatg	600
ttacgtctgt	gataactgac	caagtccagc	tcccagatgc	atccagacta	gagagacc	660
atcaggagct	aaccagttac	tgtcttggtg	ccgcggggaa	atctactggt	ccagtggaa	720
cttgacgaac	atcgggaagt	ctcatgtgaa	cttagaagta	ttccagactc	acattgatta	780
tgaattcaag	tttgattcaa	ataagttacat	gaagtacttc	agctactcaa	tcgaagaagc	840
taaatgattg	gtgttttcca	gtctgtcttc	ggataactct	ggccaaaata	ctgaacctt	900
ttctctcag	agtaaacata	cgagcacctg	gatttcogaa	acagatgaac	cctgcgaagc	960
ggattttaag	accagttcac	caattctcat	cacgggagaa	ccoaacgggt	gtaggaaaag	1020
gtcagatgat	tctgaaccca	gaagagagta	catgatggaa	ataataacog	gtttattacc	1080
attttactat	gacgatagtt	tgagcgcgtg	ttctagccag	tgtcatggaa	cctgcgtgag	1140
aaactgttgt	tgcatagctt	tccaagcctt	ttcttagtga	tgccaatatg	gggaaaaagc	1200
atcaaaagtt	gtctcttagt	atagcttcaa	ctccaattat	gtaacctatg	ttcttgatcc	1260
gttaaaagta	tgtgtgtgtg	taacttgaa	gacgaattat	gtaaccagag	tagtatcagt	1320

aaaggggtttt attaagaaac taaagaatca agcagttc

(2) INFORMATION FOR SEQ ID NO:725:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..231

(D) OTHER INFORMATION: / Ceres Seq. ID 1498913

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:725:

Met	Ala	Leu	Ser	Ile	Val	Leu	Leu	Pro	Phe	Ile	Leu	Ile	Leu	Ile	Pro	
1				5					10						15	
Thr	Phe	Leu	Ser	Ser	Val	Phe	Ala	Val	Ser	Pro	Leu	Lys	Thr	Asp	Thr	
				20					25						30	
Leu	Lys	Pro	Gly	Gln	Gln	Leu	Arg	Asp	Trp	Glu	Gln	Leu	Ile	Ser	Ala	
				35					40						45	
Asp	Gly	Ile	Phe	Thr	Leu	Gly	Phe	Phe	Thr	Pro	Lys	Asp	Ser	Ser	Thr	
				50					55						60	
Ser	Glu	Leu	Gly	Ser	Ala	Gly	Leu	Arg	Tyr	Leu	Gly	Ile	Trp	Pro	Gln	
65									70						80	
Ser	Ile	Pro	Ile	Asn	Leu	Val	Trp	Val	Gly	Asn	Pro	Thr	Glu	Ser	Val	
				85					90						95	
Ser	Asp	Ser	Ser	Gly	Ser	Leu	Ser	Ile	Asp	Thr	Asn	Gly	Val	Leu	Lys	
				100					105						110	
Ile	Thr	Gln	Ala	Asn	Ala	Ile	Pro	Ile	Leu	Val	Asn	Gln	Arg	Pro	Ala	
				115					120						125	
Ala	Gln	Leu	Ser	Leu	Val	Gly	Asn	Val	Ser	Ala	Ile	Leu	Leu	Asp	Thr	
				130					135						140	
Gly	Asn	Phe	Val	Val	Arg	Glu	Ile	Arg	Pro	Gly	Gly	Val	Pro	Gly	Arg	
145									150						155	
Val	Leu	Trp	Gln	Ser	Phe	Asp	His	Pro	Thr	Asn	Thr	Leu	Leu	Pro	Gly	
				165					170						175	
Met	Lys	Ile	Gly	Phe	Asn	Leu	Arg	Thr	Lys	Lys	Glu	Val	Ser	Val	Thr	
				180					185						190	
Ser	Trp	Ile	Thr	Asp	Gln	Val	Pro	Val	Pro	Gly	Ala	Phe	Arg	Leu	Gly	
				195					200						205	
Glu	Thr	His	Gln	Glu	Leu	Thr	Ser	Tyr	Ser	Ser	Gly	Ala	Ala	Gly	Lys	
				210					215						220	
Ser	Thr	Gly	Pro	Val	Glu	Ser										
225									230							

(2) INFORMATION FOR SEQ ID NO:726:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1498914

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:726:

Met	Lys	Tyr	Phe	Ser	Tyr	Ser	Ile	Lys	Lys	Ala	Asn	Ser	Ser	Val	Phe	
1									10						15	
Ser	Ser	Trp	Phe	Leu	Asp	Thr	Leu	Gly	Gln	Ile	Thr	Val	Thr	Phe	Ser	
				20					25						30	
Leu	Ser	Ser	Asn	Asn	Ser	Ser	Thr	Trp	Ile	Ser	Glu	Ser	Ser	Glu	Pro	
				35					40						45	

Cys Lys Thr Asp Leu Lys Asn Ser Ser Ala Ile Cys Ile Thr Glu Lys
50 55 60
Pro Thr Ala Cys Arg Lys Gly Ser Glu Tyr Phe Glu Pro Arg Arg Gly
65 70 75 80
Tyr Met Met Glu Asn Asn Thr Gly Tyr Tyr Pro Phe Tyr Tyr Asp Asp
85 90 95
Ser Leu Ser Ala Gly Leu Ser Asp Cys His Gly Thr Cys Trp Arg Asn
100 105 110
Cys Ser Cys Ile Ala Phe Gln Ala Phe Pro Asp Gly Cys Gln Tyr Trp
115 120 125
Glu Lys Gly Ser Lys Phe Val Pro Tyr Asp Ser Phe Asn Ser Asn Leu
130 135 140
Val Thr Tyr Val Leu Asp Ser Val Lys
145 150

(2) INFORMATION FOR SEQ ID NO:727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1153

(D) OTHER INFORMATION: / Ceres Seq. ID 1498918

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:727:

gacataacct	gcaagctgtt	gagatcttcc	atcctcaata	actttattct	tccatatctc	60
tcctcttcgc	ctctctattt	cacatcccca	tataacataa	tatacaatca	cacatatcat	120
ttctatatag	tatttaattg	ggagacagcc	atgctgtgac	aagctagggg	tgaagaaagg	180
gccgtggacg	gtggaggaag	ataagaagct	tataaacttc	atactaacca	atggccattg	240
ttgctggcgt	gottttccga	agctggccgg	tctccgtcgc	tgtggaaaga	gctgccgcct	300
ccggtggact	aactatctcc	ggcctgaact	aaaacgagcg	cttctctcgc	atgatgaaga	360
acaactgtgc	atagatcttc	atgctaactc	cggaataaag	tggtctaaga	tagcttcaag	420
attacctgga	agaacagata	acgaataaaa	aaaccattgg	aataactcata	tcaagaagaa	480
acttcttaag	atgggaatcg	atcctatgac	ccatcaacc	ctaatcaag	aaccttctaa	540
tatcgataat	tccaaaacca	ttccgtccaa	tccagacgat	gtctcagtg	aaccaagac	600
aactaacacg	aaatacgtgg	agataagtgt	cacgacaaca	gaagaagaaa	gtagtagcac	660
ggttactgat	caaaacagtt	cgatggataa	tgaataatcat	ctaatgaca	acatttatga	720
tgatgatgaa	ttgttttagtt	acttatggtc	cgacgaaact	acgaaagatg	aggcctcttg	780
gagtgatagt	aacttttggt	ttggtggaac	attatatgac	cacaatatct	ccggcgccga	840
tcgagatttt	ccgatattgt	accggaaag	aatcaatgac	gagaagatgt	ttttggatta	900
ttgtcaagac	ttttgtgttc	atgatatttg	gttttgactg	ttcacattatg	acatatattggc	960
aactcttatgg	agatgaacac	aagcattgag	ttgtcatgtt	tatacatacg	tgccatatcac	1020
atatatatat	atgtacatta	tatgtaaaaca	tatacacgca	tacaaatcat	aaacatgttaa	1080
ggataataaa	tccatgtaaa	tcagtaaggg	tgccaccatg	ttttcaagta	ttattaatta	1140
gggttggtga	ggt					

(2) INFORMATION FOR SEQ ID NO:728:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..266

(D) OTHER INFORMATION: / Ceres Seq. ID 1498919

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:728:

Met Gly Arg Gln Pro Cys Cys Asp Lys Leu Gly Val Lys Lys Gly Pro
1 5 10 15
Trp Thr Val Glu Glu Asp Lys Lys Leu Ile Asn Phe Ile Leu Thr Asn

Met	Gly	Ile	Asp	Pro	Met	Thr	His	Gln	Pro	Leu	Asn	Gln	Glu	Pro	Ser
1			5					10					15		
Asn	Ile	Asp	Asn	Ser	Lys	Thr	Ile	Pro	Ser	Asn	Pro	Asp	Asp	Val	Ser
		20						25					30		
Val	Glu	Pro	Lys	Thr	Thr	Asn	Thr	Lys	Tyr	Val	Glu	Ile	Ser	Val	Thr
		35					40					45			
Thr	Thr	Glu	Glu	Glu	Ser	Ser	Ser	Thr	Val	Thr	Asp	Gln	Asn	Ser	Ser
		50				55					60				
Met	Asp	Asn	Glu	Asn	His	Leu	Ile	Asp	Asn	Ile	Tyr	Asp	Asp	Asp	Glu
65					70					75					80
Leu	Phe	Ser	Tyr	Leu	Trp	Ser	Asp	Glu	Thr	Thr	Lys	Asp	Glu	Ala	Ser
				85				90						95	
Trp	Ser	Asp	Ser	Asn	Phe	Gly	Val	Gly	Gly	Thr	Leu	Tyr	Asp	His	Asn
		100						105					110		
Ile	Ser	Gly	Ala	Asp	Ala	Asp	Phe	Pro	Ile	Trp	Ser	Pro	Glu	Arg	Ile
		115				120						125			
Asn	Asp	Glu	Lys	Met	Phe	Leu	Asp	Tyr	Cys	Gln	Asp	Phe	Gly	Val	His
	130					135					140				

Asp Phe Gly Phe
145

(2) INFORMATION FOR SEQ ID NO:730:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..143
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498921

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:730:

Met	Thr	His	Gln	Pro	Leu	Asn	Gln	Glu	Pro	Ser	Asn	Ile	Asp	Asn	Ser	
1				5					10						15	
Lys	Thr	Ile	Pro	Ser	Asn	Pro	Asp	Asp	Val	Ser	Val	Glu	Pro	Lys	Thr	
			20					25					30			
Thr	Asn	Thr	Lys	Tyr	Val	Glu	Ile	Ser	Val	Thr	Thr	Thr	Glu	Glu	Glu	
			35				40					45				
Ser	Ser	Ser	Thr	Val	Thr	Asp	Gln	Asn	Ser	Ser	Met	Asp	Asn	Glu	Asn	
						55					60					
His	Leu	Ile	Asp	Asn	Ile	Tyr	Asp	Asp	Asp	Glu	Phe	Ser	Tyr	Leu		
65					70					75				80		
Trp	Ser	Asp	Glu	Thr	Thr	Lys	Asp	Glu	Ala	Ser	Trp	Ser	Asp	Ser	Asn	
					85					90				95		
Phe	Gly	Val	Gly	Gly	Thr	Leu	Tyr	Asp	His	Asn	Ile	Ser	Gly	Ala	Asp	
			100					105					110			
Ala	Asp	Phe	Pro	Ile	Trp	Ser	Pro	Glu	Arg	Ile	Asn	Asp	Glu	Lys	Met	
			115					120					125			
Phe	Leu	Asp	Tyr	Cys	Gln	Asp	Phe	Gly	Val	His	Asp	Phe	Gly	Phe		
			130				135									

(2) INFORMATION FOR SEQ ID NO:731:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1202
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498922

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:731:

gaaacgtctt	cggaacacat	ctcagtcgca	cgctctttca	cgcgcccttt	cgatttcaca	60
ttcggatccg	atttgtttac	ccgcggaaga	tccaccggca	tcttctctaa	acggctctgt	120
cgagaaggat	cgcgctatt	attgctggag	gacgattggg	tgtttacttt	ttactagtaa	180
acggagtaat	ttcccaagcg	aaaggtttca	ttttgagct	ccacgttgaa	cgaactaagc	240
ggtttctcgg	agttctcttg	cttcctctcc	acccagcgca	atggagaaaa	cagacgaaga	300
gaggaagaag	gctcagatgc	tggaagctcg	ggccagaaaac	attagccaca	atgttcgctg	360
cactgagtgt	ggaagttagt	ccattgaaga	ctcgcaggga	gatatcgcta	ttctccttag	420
acagctgac	cgtaatgaga	taggagctgg	aaaaactgac	aaagagatct	acagtaagct	480
ggaggatgaa	tttggggaga	cagtgcctta	tgccccaata	tttgatttgc	agaccgcagc	540
cttgttgctc	acaccgggta	taattgctgg	aggtaccgct	cgaggataag	tttaccagaa	600
gcacaggcta	aggaaaaatg	tagacatcat	ggcgttgaac	cttattagag	gtgtaccatt	660
gactccaaaa	gagagagtta	ccattcttga	tggtcttatt	ccaccttccc	ctctcctca	720
gggagtgtgt	tcccgattga	ggagatggct	caaccggtag	ttccctgttc	tccttagctc	780
tcttgcttct	ggctcgaaac	ttgtgtgtgt	aacaagttaa	caatgtgtgt	aaaagagtga	840
gtacactctg	attgtcttgg	agaaacagat	agggactgct	ttgcattcat	tacaaacaaa	900
tggattcttc	tgtagaagat	cttgggatga	gatattgatc	gagaaagcat	tattgaaagt	960
gtgatacttg	ttgtaccttt	ctgtgtgtat	tgaatacaga	gagcgggtcg	atagttatat	1020

tacttttcggc acaaagattt atttctttcc aaatagtttt tgtgctaaat gagctttttt 1080
ccacatctttt attcttaataa gccgaagctc acaaaatgta ttgacctgcy tattgtatat 1140
acaagaagca atgagtaaac aagaagaat agtcttgctc acaagaatga gactgtatgt 1200
tg

(2) INFORMATION FOR SEQ ID NO:732:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..159
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498923

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:732:

Met	Glu	Lys	Thr	Asp	Glu	Glu	Arg	Lys	Lys	Ala	Gln	Met	Leu	Asp	Ala
1				5					10					15	
Arg	Ala	Arg	Asn	Ile	Ser	His	Asn	Val	Arg	Cys	Thr	Glu	Cys	Gly	Ser
			20					25					30		
Gln	Ser	Ile	Glu	Asp	Ser	Gln	Ala	Asp	Ile	Ala	Ile	Leu	Leu	Arg	Gln
		35					40					45			
Leu	Ile	Arg	Asn	Glu	Ile	Gly	Ala	Gly	Lys	Thr	Asp	Lys	Glu	Ile	Tyr
	50					55					60				
Ser	Lys	Leu	Glu	Asp	Glu	Phe	Gly	Glu	Thr	Val	Leu	Tyr	Ala	Pro	Lys
	65				70					75				80	
Phe	Asp	Leu	Gln	Thr	Ala	Ala	Leu	Trp	Leu	Thr	Pro	Val	Ile	Ile	Ala
			85					90						95	
Gly	Gly	Thr	Ala	Ala	Gly	Ile	Val	Tyr	Gln	Lys	His	Arg	Leu	Arg	Lys
			100					105						110	
Asn	Val	Asp	Ile	Met	Ala	Leu	Asn	Leu	Ile	Arg	Gly	Val	Pro	Leu	Thr
			115				120						125		
Pro	Lys	Glu	Arg	Val	Thr	Ile	Leu	Asp	Val	Leu	Ile	Pro	Pro	Ser	Pro
	130						135				140				
Pro	Pro	Gln	Gly	Val	Val	Ser	Arg	Leu	Arg	Arg	Trp	Leu	Asn	Arg	
	145				150				155						

(2) INFORMATION FOR SEQ ID NO:733:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:733:

Met	Leu	Asp	Ala	Arg	Ala	Arg	Asn	Ile	Ser	His	Asn	Val	Arg	Cys	Thr
1					5					10				15	
Glu	Cys	Gly	Ser	Gln	Ser	Ile	Glu	Asp	Ser	Gln	Ala	Asp	Ile	Ala	Ile
			20					25					30		
Leu	Leu	Arg	Gln	Leu	Ile	Arg	Asn	Glu	Ile	Gly	Ala	Gly	Lys	Thr	Asp
		35					40					45			
Lys	Glu	Ile	Tyr	Ser	Lys	Leu	Glu	Asp	Glu	Phe	Gly	Gly	Thr	Val	Leu
	50					55					60				
Tyr	Ala	Pro	Lys	Phe	Asp	Leu	Gln	Thr	Ala	Ala	Leu	Trp	Leu	Thr	Pro
	65				70					75				80	
Val	Ile	Ile	Ala	Gly	Gly	Thr	Ala	Ala	Gly	Ile	Val	Tyr	Gln	Lys	His
			85					90						95	
Arg	Leu	Arg	Lys	Asn	Val	Asp	Ile	Met	Ala	Leu	Asn	Leu	Ile	Arg	Gly

100 105 110
Val Pro Leu Thr Pro Lys Glu Arg Val Thr Ile Leu Asp Val Leu Ile
115 120 125
Pro Pro Ser Pro Pro Pro Gln Gly Val Val Ser Arg Leu Arg Arg Trp
130 135 140
Leu Asn Arg
145

(2) INFORMATION FOR SEQ ID NO:734:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1931 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1931
(D) OTHER INFORMATION: / Ceres Seq. ID 1498925

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:734:

aattttttcac tttctatctc tctatatcta tttttttata gatatatatt ttgtcttgggt 60
tggatttttgt tctcgtgggt tacttacttg agagaacctc gagacctgtc ttgtctttat 120
gcttcagaag caaatcaaa catctctcca agatttgaag ctccatctat ggctggccctt 180
cttctccttt tccttttctc cttcgcaagc tctgctctct ctcaagattc ttgtatcggt 240
gtgaattattg tgaactgaat gacaaacatg ccaagtccaa cacaagtagt agcactctc 300
aaatcacaga acatcaacccg cgtccgcctc tatgacgcag accgctcaat gcttctcgcg 360
tttctgcaca ccggggttca agttataact tccagtacctc acgaccagct tctcgtgtac 420
agccaatcaa atgcaaccgc agccaattgg gtgactagaa atgtagctgc atattaccct 480
gcgaccaaca ttaccacaat tgcgtgcgga tcagaagtcc taaccagcct aacaaaacgca 540
gcttctgtcc ttgctcagc cctcaaatca atacaagctg ctctcgtcac ggccaatctc 600
gaccgtgaca tcaaaagtac gacacgcgac tcttcaacca tcattcttga ttctttccct 660
ccttcgcaag ctttcttcaa caagacttgg gatccagtta ttgtccctct cctcaaatc 720
ctacagtcga cggatgcgcc attgtcgtc aacggtttacc cgtatttcca ctatgttcc 780
tccaattggag ttataccgct tgaactacgc cttttccagc ctctccaagc caacaaagaa 840
gctgtagacg ccaacacatt gttacattac acaaacgttt ttgatgcaat cgtagacgt 900
gcttattttg caatgtctta tcttaacttc accaacattc caatcgtggt cacagaatct 960
ggatggccat ctaaaggagg ccctctctgag cacgacgcga cggtagagaa tgcaaacact 1020
tacaatagca atttgcacca gcatgtgata acaagactg gaacgccaaa acacccggga 1080
actgcagtta ctacatacat ctacagactt tacaacgagg atacgaggcc aggaacggta 1140
tctgagaaga actgggggct gttttatata aacgggaact ccgtttacac attgcgttta 1200
cggggtgcag gggcgattct ggcaaatgat actacaaccc agacattttg tatagcgaa 1260
gaaaagggtg atagaaagat gcttcaagca gctcttgact gggtctgcgg tccaggggaa 1320
gtcgtattct cggcactgat gcaggagag tcattgttat aaccgcagca tgggtgtgca 1380
cattctacct atgcgtttaa tgccttattc cagaagatgg gaaaagcttc aggaagctgt 1440
gatttcaaaag gattgtctac agtcaccacc actgatccaa gtgcaggaaac atgcgtgttc 1500
ctcgggaagt caaaaagcaa tcagacactt ggaaacaaca cctgcgcgtt gcccctcttc 1560
cgcgaactcta caacctctgg atgtatccca aagtaactat atcaccctca cgtactcttc 1620
ggtagacttaa cattactctc ccttctactg atcattgct tagtattctt gtgaaaactc 1680
tgaaaaagac aacaactctc aattcttggt tctctaaatt ttaactctct tctttgcaac 1740
acttgagaca aaagagctcg gtgggtttgt tctctctgtg tctagtgttc tccccagttt 1800
tgttgatcat ctcccttttaa catggagtcc attgagggta gcatgttggt taogcttcaa 1860
ctgcatggat gattgtaact aatttctcgt gttgaaagct tgattctcttc ttttttatgg 1920
ctgaatattt c

(2) INFORMATION FOR SEQ ID NO:735:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 557 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(D) OTHER INFORMATION: / Ceres Seq. ID 1498926

(X1) SEQUENCE DESCRIPTION: UG															
Asn	Phe	Ser	Leu	Ser	Ile	Ser	Leu	Tyr	Leu	Phe	Phe	Tyr	Arg	Tyr	Ile
1				5					10					15	
Phe	Cys	Leu	Gly	Trp	Ile	Leu	Phe	Ser	Trp	Val	Thr	Tyr	Leu	Arg	Glu
		20						25					30		
Pro	Arg	Asp	Leu	Ser	Cys	Leu	Tyr	Ala	Ser	Glu	Ala	Asn	Gln	Ser	Ile
		35					40					45			
Ser	Pro	Arg	Phe	Glu	Ala	Pro	Ser	Met	Ala	Ala	Leu	Leu	Leu	Phe	
		50				55					60				
Leu	Phe	Leu	Phe	Ala	Ser	Ser	Ala	Leu	Ser	Gln	Asp	Ser	Leu	Ile	Gly
65				70						75				80	
Val	Asn	Ile	Gly	Thr	Glu	Val	Thr	Asn	Met	Pro	Ser	Pro	Thr	Gln	Val
				85				90					95		
Val	Ala	Leu	Leu	Lys	Ser	Gln	Asn	Ile	Asn	Arg	Val	Arg	Leu	Tyr	Asp
		100						105					110		
Ala	Asp	Arg	Ser	Met	Leu	Leu	Ala	Phe	Ala	His	Thr	Gly	Val	Gln	Val
		115					120					125			
Ile	Ile	Ser	Val	Pro	Asn	Asp	Gln	Leu	Leu	Gly	Ile	Ser	Gln	Ser	Asn
		130				135					140				
Ala	Thr	Ala	Ala	Asn	Trp	Val	Thr	Arg	Asn	Val	Ala	Ala	Tyr	Tyr	Pro
145				150						155					160
Ala	Thr	Asn	Ile	Thr	Thr	Ile	Ala	Val	Gly	Ser	Glu	Val	Leu	Thr	Ser
				165					170					175	
Leu	Thr	Asn	Ala	Ala	Ser	Val	Leu	Val	Ser	Ala	Leu	Lys	Tyr	Ile	Gln
		180						185					190		
Ala	Ala	Leu	Val	Thr	Ala	Asn	Leu	Asp	Arg	Gln	Ile	Lys	Val	Ser	Thr
		195					200					205			
Pro	His	Ser	Ser	Thr	Ile	Ile	Leu	Asp	Ser	Phe	Pro	Pro	Ser	Gln	Ala
		210				215					220				
Phe	Phe	Asn	Lys	Thr	Trp	Asp	Pro	Val	Ile	Val	Pro	Leu	Leu	Lys	Phe
225				230						235					240
Leu	Gln	Ser	Thr	Gly	Ser	Pro	Leu	Leu	Asn	Val	Tyr	Pro	Tyr	Phe	
				245					250				255		
Asp	Trp	Val	Gln	Ser	Asn	Gly	Val	Ile	Pro	Leu	Asp	Tyr	Ala	Leu	Phe
		260						265					270		
Gln	Pro	Leu	Gln	Ala	Asn	Lys	Glu	Ala	Val	Asp	Ala	Asn	Thr	Leu	Leu
		275					280					285			
His	Tyr	Thr	Asn	Val	Phe	Asp	Ala	Ile	Val	Asp	Ala	Ala	Tyr	Phe	Ala
290						295					300				
Met	Ser	Tyr	Leu	Asn	Phe	Thr	Asn	Ile	Pro	Ile	Val	Val	Thr	Glu	Ser
305				310						315					320
Gly	Trp	Pro	Ser	Lys	Gly	Gly	Pro	Ser	Glu	His	Asp	Ala	Thr	Val	Glu
				325					330					335	
Asn	Ala	Asn	Thr	Tyr	Asn	Ser	Asn	Leu	I						

Ala Phe Asn Ala Tyr Tyr Gln Lys Met Gly Lys Ala Ser Gly Ser Cys
465 470 475 480
Asp Phe Lys Gly Val Ala Thr Val Thr Thr Asp Pro Ser Arg Gly
485 490 495
Thr Cys Val Phe Pro Gly Ser Ala Lys Ser Asn Gln Thr Leu Gly Asn
500 505 510
Asn Thr Ser Ala Leu Ala Pro Ser Ala Asn Ser Thr Thr Ser Gly Cys
515 520 525
Ile Pro Lys Tyr Tyr His His Pro His Ala Ser Phe Gly Asp Leu Thr
530 535 540
Leu Leu Ser Leu Leu Leu Ile Ile Ala Leu Val Phe Leu
545 550 555

(2) INFORMATION FOR SEQ ID NO:736:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..501

(D) OTHER INFORMATION: / Ceres Seq. ID 1498927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:736:

Met Ala Ala Leu Leu Leu Phe Leu Phe Ala Ser Ser Ala
1 5 10 15
Leu Ser Gln Asp Ser Leu Ile Gly Val Asn Ile Gly Thr Glu Val Thr
20 25 30
Asn Met Pro Ser Pro Thr Gln Val Val Ala Leu Leu Lys Ser Gln Asn
35 40 45
Ile Asn Arg Val Arg Leu Tyr Asp Ala Asp Arg Ser Met Leu Leu Ala
50 55 60
Phe Ala His Thr Gly Val Gln Val Ile Ile Ser Val Pro Asn Asp Gln
65 70 75 80
Leu Leu Gly Ile Ser Gln Ser Asn Ala Thr Ala Ala Asn Trp Val Thr
85 90 95
Arg Asn Val Ala Ala Tyr Tyr Pro Ala Thr Asn Ile Thr Thr Ile Ala
100 105 110
Val Gly Ser Glu Val Leu Thr Ser Leu Thr Asn Ala Ala Ser Val Leu
115 120 125
Val Ser Ala Leu Lys Tyr Ile Gln Ala Ala Leu Val Thr Ala Asn Leu
130 135 140
Asp Arg Gln Ile Lys Val Ser Thr Pro His Ser Ser Thr Ile Ile Leu
145 150 155 160
Asp Ser Phe Pro Pro Ser Gln Ala Phe Phe Asn Lys Thr Trp Asp Pro
165 170 175
Val Ile Val Pro Leu Leu Lys Phe Leu Gln Ser Thr Gly Ser Pro Leu
180 185 190
Leu Leu Asn Val Tyr Pro Tyr Phe Asp Tyr Val Gln Ser Asn Gly Val
195 200 205
Ile Pro Leu Asp Tyr Ala Leu Phe Gln Pro Leu Gln Ala Asn Lys Glu
210 215 220
Ala Val Asp Ala Asn Thr Leu Leu His Tyr Thr Asn Val Phe Asp Ala
225 230 235 240
Ile Val Asp Ala Ala Tyr Phe Ala Met Ser Tyr Leu Asn Phe Thr Asn
245 250 255
Ile Pro Ile Val Val Thr Glu Ser Gly Trp Pro Ser Lys Gly Gly Pro
260 265 270
Ser Glu His Asp Ala Thr Val Glu Asn Ala Asn Thr Tyr Asn Ser Asn
275 280 285
Leu Ile Gln His Val Ile Asn Lys Thr Gly Thr Pro Lys His Pro Gly

290	295	300
Thr Ala Val Thr Thr Tyr Ile Tyr Glu Leu Tyr Asn Glu Asp Thr Arg		
305	310	315
Pro Gly Pro Val Ser Glu Lys Asn Trp Gly Leu Phe Tyr Thr Asn Gly		
	325	330
Thr Pro Val Tyr Thr Leu Arg Leu Ala Gly Ala Ile Leu Ala		
	340	345
Asn Asp Thr Thr Asn Gln Thr Phe Cys Ile Ala Lys Glu Lys Val Asp		
	355	360
Arg Lys Met Leu Gln Ala Ala Leu Asp Trp Ala Cys Gly Pro Gly Lys		
	370	375
Val Asp Cys Ser Ala Leu Met Gln Gly Glu Ser Cys Tyr Glu Pro Asp		
	385	390
Asp Val Val Ala His Ser Thr Tyr Ala Phe Asn Ala Tyr Tyr Gln Lys		
		405
Met Gly Lys Ala Ser Gly Ser Cys Asp Phe Lys Gly Val Ala Thr Val		
	420	425
Thr Thr Thr Asp Pro Ser Arg Gly Thr Cys Val Phe Pro Gly Ser Ala		
	435	440
Lys Ser Asn Gln Thr Leu Gly Asn Asn Thr Ser Ala Leu Ala Pro Ser		
	450	455
Ala Asn Ser Thr Thr Ser Gly Cys Ile Pro Lys Tyr Tyr His His Pro		
	465	470
His Ala Ser Phe Gly Asp Leu Thr Leu Leu Ser Leu Leu Leu Ile Ile		
	485	490
Ala Leu Val Phe Leu		495
	500	

(2) INFORMATION FOR SEQ ID NO:737:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 468 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..468

(D) OTHER INFORMATION: / Ceres Seq. ID 1498928

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:737:

Met	Pro	Ser	Pro	Thr	Gln	Val	Val	Ala	Leu	Leu	Lys	Ser	Gln	Asn	Ile
1			5						10				15		
Asn	Arg	Val	Arg	Leu	Tyr	Asp	Ala	Asp	Arg	Ser	Met	Leu	Leu	Ala	Phe
			20					25					30		
Ala	His	Thr	Gly	Val	Gln	Val	Ile	Ile	Ser	Val	Pro	Asn	Asp	Gln	Leu
			35				40					45			
Leu	Gly	Ile	Ser	Gln	Ser	Asn	Ala	Thr	Ala	Ala	Asn	Trp	Val	Thr	Arg
			50				55					60			
Asn	Val	Ala	Ala	Tyr	Tyr	Pro	Ala	Thr	Asn	Ile	Thr	Thr	Ile	Ala	Val
			65				70			75			80		
Gly	Ser	Glu	Val	Leu	Thr	Ser	Leu	Thr	Asn	Ala	Ala	Ser	Val	Leu	Val
				85					90				95		
Ser	Ala	Leu	Lys	Tyr	Ile	Gln	Ala	Ala	Leu	Val	Thr	Ala	Asn	Leu	Asp
			100					105					110		
Arg	Gln	Ile	Lys	Val	Ser	Thr	Pro	His	Ser	Ser	Thr	Ile	Ile	Leu	Asp
			115					120				125			
Ser	Phe	Pro	Pro	Ser	Gln	Ala	Phe	Phe	Asn	Lys	Thr	Trp	Asp	Pro	Val
			130				135				140				
Ile	Val	Pro	Leu	Leu	Lys	Phe	Leu	Gln	Ser	Thr	Gly	Ser	Pro	Leu	Leu
			145				150			155				160	
Leu	Asn	Val	Tyr	Pro	Tyr	Phe	Asp	Tyr	Val	Gln	Ser	Asn	Gly	Val	Ile
			165						170					175	

Pro Leu Asp Tyr Ala Leu Phe Gln Pro Leu Gln Ala Asn Lys Glu Ala
180 185 190
Val Asp Ala Asn Thr Leu Leu His Tyr Thr Asn Val Phe Asp Ala Ile
195 200 205
Val Asp Ala Ala Tyr Phe Ala Met Ser Tyr Leu Asn Phe Thr Asn Ile
210 215 220
Pro Ile Val Val Thr Glu Ser Gly Trp Pro Ser Lys Gly Gly Pro Ser
225 230 235 240
Glu His Asp Ala Thr Val Glu Asn Ala Asn Thr Tyr Asn Ser Asn Leu
245 250 255
Ile Gln His Val Ile Asn Lys Thr Gly Thr Pro Lys His Pro Gly Thr
260 265 270
Ala Val Thr Thr Tyr Ile Tyr Glu Leu Tyr Asn Glu Asp Thr Arg Pro
275 280 285
Gly Pro Val Ser Glu Lys Asn Trp Gly Leu Phe Tyr Thr Asn Gly Thr
290 295 300
Pro Val Tyr Thr Leu Arg Leu Ala Gly Ala Gly Ala Ile Leu Ala Asn
305 310 315 320
Asp Thr Thr Asn Gln Thr Phe Cys Ile Ala Lys Glu Lys Val Asp Arg
325 330 335
Lys Met Leu Gln Ala Ala Leu Asp Trp Ala Cys Gly Pro Gly Lys Val
340 345 350
Asp Cys Ser Ala Leu Met Gln Gly Glu Ser Cys Tyr Glu Pro Asp Asp
355 360 365
Val Val Ala His Ser Thr Tyr Ala Phe Asn Ala Tyr Tyr Gln Lys Met
370 375 380
Gly Lys Ala Ser Gly Ser Cys Asp Phe Lys Gly Val Ala Thr Val Thr
385 390 395 400
Thr Thr Asp Pro Ser Arg Gly Thr Cys Val Phe Pro Gly Ser Ala Lys
405 410 415
Ser Asn Gln Thr Leu Gly Asn Asn Thr Ser Ala Leu Ala Pro Ser Ala
420 425 430
Asn Ser Thr Thr Ser Gly Cys Ile Pro Lys Tyr Tyr His His Pro His
435 440 445
Ala Ser Phe Gly Asp Leu Thr Leu Leu Ser Leu Leu Leu Ile Ile Ala
450 455 460
Leu Val Phe Leu
465

(2) INFORMATION FOR SEQ ID NO:738:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 673 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..673
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498929

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:738:

gcctataaag	tgatccttgt	gatgccttca	actatgagct	tagagagaag	aatcattctg	60
agggcactag	gtgcagacct	tcatcwmctg	gaccagcgca	taggccttaa	aggaatgttg	120
gagaaaaactg	aagcgatttt	aagcaaaact	cctgggtggtt	acattccaca	acaatttgaa	180
aatcctgcaa	accocgagat	tcattaccga	accacgggac	cggaaatatg	gagagattca	240
gccgggaaag	tagatatatt	ggctgcgtgc	gtagggactg	gtggaaactgc	tactggagta	300
gggaagttcc	tcaaggagca	gaacaaagac	atcaagggtt	gtgtggtgga	accagtagaa	360
agtcgggtac	ttagcggagg	tcaaccaggt	ccacatttga	ttcagggaat	tggtcttggt	420
atcgctccat	tcaatttggg	cttaaccatt	gttgatgaaa	tattcaagt	ggcagggtgaa	480
gaggctattg	aaacagccaa	gcttcttgcc	ctcaaaagag	gattactggt	gggaatatcc	540
ctctgagccg	cagcagcgcg	tgcgttaaag	gttgcaaaag	ggccagaaaa	cgcggggaaa	600
ctcattgkgg	tggtttttcc	tagtggagga	gaacgttatt	tatcgactaa	actgttcgat	660

tcgattagat atg

(2) INFORMATION FOR SEQ ID NO:739:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..224

(D) OTHER INFORMATION: / Ceres Seq. ID 1498930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:739:

Ala	Tyr	Lys	Val	Ile	Leu	Val	Met	Pro	Ser	Thr	Met	Ser	Leu	Glu	Arg	
1				5					10					15		
Arg	Ile	Ile	Leu	Arg	Ala	Leu	Gly	Ala	Asp	Leu	His	Xaa	Ser	Asp	Gln	
			20				25						30			
Arg	Ile	Gly	Leu	Lys	Gly	Met	Leu	Glu	Lys	Thr	Glu	Ala	Ile	Leu	Ser	
		35				40					45					
Lys	Thr	Pro	Gly	Gly	Tyr	Ile	Pro	Gln	Gln	Phe	Glu	Asn	Pro	Ala	Asn	
		50			55					60						
Pro	Glu	Ile	His	Tyr	Arg	Thr	Thr	Gly	Pro	Glu	Ile	Trp	Arg	Asp	Ser	
65				70					75					80		
Ala	Gly	Lys	Val	Asp	Ile	Leu	Val	Ala	Gly	Val	Gly	Thr	Gly	Gly	Thr	
			85						90					95		
Ala	Thr	Gly	Val	Gly	Lys	Phe	Leu	Lys	Glu	Gln	Asn	Lys	Asp	Ile	Lys	
			100					105					110			
Val	Cys	Val	Val	Glu	Pro	Val	Glu	Ser	Pro	Val	Leu	Ser	Gly	Gly	Gln	
			115				120						125			
Pro	Gly	Pro	His	Leu	Ile	Gln	Gly	Ile	Gly	Ser	Gly	Ile	Val	Pro	Phe	
			130			135					140					
Asn	Leu	Asp	Leu	Thr	Ile	Val	Asp	Glu	Ile	Ile	Gln	Val	Ala	Gly	Glu	
145				150					155					160		
Glu	Ala	Ile	Glu	Thr	Ala	Lys	Leu	Leu	Ala	Leu	Lys	Glu	Gly	Leu	Leu	
			165					170						175		
Val	Gly	Ile	Ser	Gly	Ala	Ala	Ala	Ala	Ala	Ala	Leu	Lys	Val	Ala		
			180				185						190			
Lys	Arg	Pro	Glu	Asn	Ala	Gly	Lys	Leu	Ile	Xaa	Val	Val	Phe	Pro	Ser	
			195				200						205			
Gly	Gly	Glu	Arg	Tyr	Leu	Ser	Thr	Lys	Leu	Phe	Asp	Ser	Ile	Arg	Tyr	
			210				215						220			

(2) INFORMATION FOR SEQ ID NO:740:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..217

(D) OTHER INFORMATION: / Ceres Seq. ID 1498931

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:740:

Met	Pro	Ser	Thr	Met	Ser	Leu	Glu	Arg	Arg	Ile	Ile	Leu	Arg	Ala	Leu	
1				5					10					15		
Gly	Ala	Asp	Leu	His	Xaa	Ser	Asp	Gln	Arg	Ile	Gly	Leu	Lys	Gly	Met	
			20					25					30			
Leu	Glu	Lys	Thr	Glu	Ala	Ile	Leu	Ser	Lys	Thr	Pro	Gly	Gly	Tyr	Ile	
			35				40						45			

[illegible]

210

(2) INFORMATION FOR SEQ ID NO:742:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1334

(D) OTHER INFORMATION: / Ceres Seq. ID 1498933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:742:

```
cccgggggaag agagagacta ttgaatatct tcttctcttc actttggtgt agagagcgac      60
gacgatggcg gaattctcgca gcaacagagc ggcgggttcag gctactaacg acgatgcatc      120
cgccagtaaa ttgtctttgtg tcaaaaaagg atatatgaaa gacgactatg ttcactcttt      180
tgtgaaaaaga cctgtttcgaa gatctcccat cattaatcga ggtaactttt cccgtttggg      240
tgcccttcga aagcttatgt ctgagtttct tctaagcggg acaagtctta agaaacagat      300
actgtcactc ggagctggct ttgatactac ctattttcag ttgctggatg aggggaatgg      360
gccaatctct tatgtggaac ttgattttta gtagggtgact agcaagaagg ctgctgttat      420
acaaaactcc agccaactca gggacaaact aggcgcgaat gcatctatct ctattgacga      480
aggaaaagtt ctgagtgatc attacaagtt acttccagtt gacctgcgcg atataccaaa      540
attaagagat gttatatcct ttgcagatat ggatctaagt ctgcgcgact ttattattgc      600
agaatgtggt ttgattttatc tggaccocga ttcaagccgt gccactgcga attggtgcgt      660
aaaaacgttt tcaactgcag tatttttctt atatgagcag atccatccag atgatgcatt      720
tgggcatcaa atgattagaa atttgagagc tcgggggatg gcaactotaa gcaatgatgc      780
atcaccactc ttacttgcaa aggagagatt gtttcttgat aatggatggc agagagctgt      840
tgccctggag atgctaaaag tgtatggtag ttttgttgat actcaagaaa aacgcaggat      900
cgagcgattg gagttgtttg acgaatttga agagtggcac atgatgcagg aacattactg      960
tgtcacatat gctgtcaagt atgcaatggg aatatttggg gatttcggtt tcacaagaga      1020
agggggcggt gaagaatga gctcatcagc gtcatacact tgaaaaggag gagggtgtgt      1080
attgcaatga atccccggaa cttgcaactg gaatgatgat tgattgcaca aagttagaaa      1140
ggcctttctc tgggtgtcga gcagaaaacg aaggaaacac gaacttgtct cggttatctg      1200
tgcttttgat ttagtttagg ctcatggctg agatatgtgg gccgggcctc ccctgtgttt      1260
atttttggtt gtattttcta ataattgtgc aaacacaaa aacctcacct cggtcgaaga      1320
acgctctgaa atct
```

(2) INFORMATION FOR SEQ ID NO:743:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1498934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:743:

```
Pro Gly Lys Arg Glu Thr Ile Glu Tyr Ser Ser Ser Phe Thr Leu Ala
1      5      10      15
Glu Arg Ala Thr Thr Met Ala Glu Ser Arg Ser Asn Arg Ala Ala Val
20      25      30
Gln Ala Thr Asn Asp Asp Ala Ser Ala Ser Lys Leu Ser Cys Val Lys
35      40      45
Lys Gly Tyr Met Lys Asp Asp Tyr Val His Leu Phe Val Lys Arg Pro
50      55      60
Val Arg Arg Ser Pro Ile Ile Asn Arg Gly Tyr Phe Ser Arg Trp Ala
65      70      75
Ala Phe Arg Lys Leu Met Ser Gln Phe Leu Leu Ser Gly Thr Ser Ser
85      90      95
Lys Lys Gln Ile Leu Ser Leu Gly Ala Gly Phe Asp Thr Thr Tyr Phe
```


100 105 110
Gln Leu Leu Asp Glu Gly Asn Gly Pro Asn Leu Tyr Val Glu Leu Asp
115 120 125
Phe Lys
130

(2) INFORMATION FOR SEQ ID NO:744:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..164

- (D) OTHER INFORMATION: / Ceres Seq. ID 1498935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:744:

Met Asp Leu Ser Leu Pro Thr Phe Ile Ile Ala Glu Cys Val Leu Ile
1 5 10 15
Tyr Leu Asp Pro Asp Ser Ser Arg Ala Ile Val Asn Trp Ser Ser Lys
20 25 30
Thr Phe Ser Thr Ala Val Phe Phe Leu Tyr Glu Gln Ile His Pro Asp
35 40 45
Asp Ala Phe Gly His Gln Met Ile Arg Asn Leu Glu Ser Arg Gly Cys
50 55 60
Ala Leu Leu Ser Ile Asp Ala Ser Pro Thr Leu Leu Ala Lys Glu Arg
65 70 75 80
Leu Phe Leu Asp Asn Gly Trp Gln Arg Ala Val Ala Trp Asp Met Leu
85 90 95
Lys Val Tyr Gly Ser Phe Val Asp Thr Gln Glu Lys Arg Arg Ile Glu
100 105 110
Arg Leu Glu Leu Phe Asp Glu Phe Glu Glu Trp His Met Met Gln Glu
115 120 125
His Tyr Cys Val Thr Tyr Ala Val Asn Asp Ala Met Gly Ile Phe Gly
130 135 140
Asp Phe Gly Phe Thr Arg Glu Gly Gly Gly Glu Arg Met Ser Ser Ser
145 150 155 160
Ala Ser Ser Pro

(2) INFORMATION FOR SEQ ID NO:745:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..110

- (D) OTHER INFORMATION: / Ceres Seq. ID 1498936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:745:

Met Ile Arg Asn Leu Glu Ser Arg Gly Cys Ala Leu Ser Ile Asp
1 5 10 15
Ala Ser Pro Thr Leu Leu Ala Lys Glu Arg Leu Phe Leu Asp Asn Gly
20 25 30
Trp Gln Arg Ala Val Ala Trp Asp Met Leu Lys Val Tyr Gly Ser Phe
35 40 45
Val Asp Thr Gln Glu Lys Arg Arg Ile Glu Arg Leu Glu Leu Phe Asp
50 55 60
Glu Phe Glu Glu Trp His Met Met Gln Glu His Tyr Cys Val Thr Tyr
65 70 75 80

Ala Val Asn Asp Ala Met Gly Ile Phe Gly Asp Phe Gly Phe Thr Arg
85 90 95
Glu Gly Gly Gly Glu Arg Met Ser Ser Ser Ala Ser Ser Pro
100 105 110

(2) INFORMATION FOR SEQ ID NO:746:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 855 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..855
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498937

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:746:

aaaaatcaag aaatatggcc acaagagctt ctacatctag cagagtctct ccagctttca 60
ctttcctcgt catctttctt ctcttatctc tcaactgctc agtagaagct gctggtcgtg 120
gagtttaacaa tgacaagaaa ggcggcggtat taggagcttc ttccatattc ggagattctc 180
tagtcgatgc cggaataaat aattatctat cgacgtttgt tagggctaat atgaagccta 240
atggtattga ttccaaagct tccggaggaa ctctaccgg ccggttcacc aatggacgga 300
ccatcggtga tatcgtttgg gaagaactcg gatcagcgaa ctacgcgatc ccgtttcttg 360
caccagacgc gaagggaaaa gctttattag cggagtgaa ctatgcattc ggaggaggag 420
gaatcatgaa tgcaccggg agaattcttg tgaatagatt aggtatggat gtacaagtgt 480
atttcttcaa cactacacgg aaacagtttg atgactctac tggaaaagag aaagcaaaag 540
attacatagc caagaaatcg atattctcaa tcactatagg agcaaatgat ttcctcaaca 600
attatctatt ccactactc toggtagcat tcatgattcc tctcctcgtt ccaatgcatt 660
agagagagaa aagaaaagtc ctcaaaagtc gaagacaaaag aaagatgttt aatctctctc 720
tttattcttc tagctctgt tttttaaagt ttggaacact tgcattgtgt tccaaaagat 780
gtttttttaa ggataaaacc atttgagaaa tgtattagaa gctcttgatt tctctatcta 840
tgtctctctc tcgcc

(2) INFORMATION FOR SEQ ID NO:747:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..219
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498938

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:747:

Lys Ser Arg Asn Met Ala Thr Arg Ala Ser Thr Ser Ser Arg Val Ser
1 5 10 15
Pro Ala Phe Thr Phe Leu Val Ile Phe Phe Leu Leu Ser Leu Thr Ala
20 25 30
Ser Val Glu Ala Ala Gly Arg Gly Val Asn Asn Asp Lys Lys Gly Gly
35 40 45
Gly Leu Gly Ala Ser Phe Ile Phe Gly Asp Ser Leu Val Asp Ala Gly
50 55 60
Asn Asn Asn Tyr Leu Ser Thr Leu Ser Arg Ala Asn Met Lys Pro Asn
65 70 75 80
Gly Ile Asp Phe Lys Ala Ser Gly Gly Thr Pro Thr Gly Arg Phe Thr
85 90 95
Asn Gly Arg Thr Ile Gly Asp Ile Val Gly Glu Glu Leu Gly Ser Ala
100 105 110
Asn Tyr Ala Ile Pro Phe Leu Ala Pro Asp Ala Lys Gly Lys Ala Leu
115 120 125
Leu Ala Gly Val Asn Tyr Ala Ser Gly Gly Gly Ile Met Asn Ala
130 135 140

Thr Gly Arg Ile Phe Val Asn Arg Leu Gly Met Asp Val Gln Val Asp
145 150 155 160
Phe Phe Asn Thr Thr Arg Lys Gln Phe Asp Asp Leu Leu Gly Lys Glu
165 170 175
Lys Ala Lys Asp Tyr Ile Ala Lys Lys Ser Ile Phe Ser Ile Thr Ile
180 185 190
Gly Ala Asn Asp Phe Leu Asn Asn Tyr Leu Phe Pro Leu Leu Ser Val
195 200 205
Ala Phe Met Ile Pro Pro Gly Pro Met His
210 215

(2) INFORMATION FOR SEQ ID NO:748:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..215
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498939

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:748:

Met Ala Thr Arg Ala Ser Thr Ser Ser Arg Val Ser Pro Ala Phe Thr
1 5 10 15
Phe Leu Val Ile Phe Phe Leu Leu Ser Leu Thr Ala Ser Val Glu Ala
20 25 30
Ala Gly Arg Gly Val Asn Asn Asp Lys Lys Gly Gly Leu Gly Ala
35 40 45
Ser Phe Ile Phe Gly Asp Ser Leu Val Asp Ala Gly Asn Asn Asn Tyr
50 55 60
Leu Ser Thr Leu Ser Arg Ala Asn Met Lys Pro Asn Gly Ile Asp Phe
65 70 75 80
Lys Ala Ser Gly Gly Thr Pro Thr Gly Arg Phe Thr Asn Gly Arg Thr
85 90 95
Ile Gly Asp Ile Val Gly Glu Glu Leu Gly Ser Ala Asn Tyr Ala Ile
100 105 110
Pro Phe Leu Ala Pro Asp Ala Lys Gly Lys Ala Leu Leu Ala Gly Val
115 120 125
Asn Tyr Ala Ser Gly Gly Gly Gly Ile Met Asn Ala Thr Gly Arg Ile
130 135 140
Phe Val Asn Arg Leu Gly Met Asp Val Gln Val Asp Phe Phe Asn Thr
145 150 155 160
Thr Arg Lys Gln Phe Asp Asp Leu Leu Gly Lys Glu Lys Ala Lys Asp
165 170 175
Tyr Ile Ala Lys Lys Ser Ile Phe Ser Ile Thr Ile Gly Ala Asn Asp
180 185 190
Phe Leu Asn Asn Tyr Leu Phe Pro Leu Leu Ser Val Ala Phe Met Ile
195 200 205
Pro Pro Pro Gly Pro Met His
210 215

(2) INFORMATION FOR SEQ ID NO:749:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..143
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498940

Met	Lys	Pro	Asn	Gly	Ile	Asp	Phe	Lys	Ala	Ser	Gly	Gly	Thr	Pro	Thr
1			5					10						15	
Gly	Arg	Phe	Thr	Asn	Gly	Arg	Thr	Ile	Gly	Asp	Ile	Val	Gly	Glu	Glu
			20				25					30			
Leu	Gly	Ser	Ala	Asn	Tyr	Ala	Ile	Pro	Phe	Leu	Ala	Pro	Asp	Ala	Lys
			35				40					45			
Gly	Lys	Ala	Leu			Gly	Val	Asn	Tyr	Ala	Ser	Gly	Gly	Gly	Gly
			50				55				60				
Ile	Met	Asn	Ala	Thr	Gly	Arg	Ile	Phe	Val	Asn	Arg	Leu	Gly	Met	Asp
65					70				75					80	
Val	Gln	Val	Asp	Phe	Phe	Asn	Thr	Arg	Lys	Gln	Phe	Asp	Asp	Leu	
					85			90					95		
Leu	Gly	Lys	Glu	Lys	Ala	Lys	Asp	Tyr	Ile	Ala	Lys	Lys	Ser	Ile	Phe
			100					105					110		
Ser	Ile	Thr	Ile	Gly	Ala	Asn	Asp	Phe	Leu	Asn	Asn	Tyr	Leu	Phe	Pro
			115				120					125			
Leu	Leu	Ser	Val	Ala	Phe	Met	Ile	Pro	Pro	Pro	Gly	Pro	Met	His	
			130				135				140				

(X1) SEQUENCE DESCRIPTION: SEQ ID: 100						
aaacttaata	aagcctcgta	ctcgagagtc	aaacaaaac	aaacaaaac	ccaaacacct	60
accaaaataa	tcaattatgc	agaattcttc	ctctcttaat	cctcaaaaaa	acacaaaacc	120
ttctctcacc	ctctctctct	gattcatctc	ctagggttaat	gggtgtgttc	tcgaattacc	180
gaggaccacg	agccggcgat	accacagatg	aattctccgc	gacaaattggc	tcctctctgt	240
ctctctcttc	tcacatcgta	tcaaatcaagc	gaaaattatc	gaatttggtta	ccactctgcg	300
ttgctctcgt	agtttatcgt	gagatcgggt	tctcgggtgc	gctcgataaa	gtcgtcttgg	360
ttgatcagtt	gactgatttc	taccaccagt	ctcgcgactc	ctcgcgagtc	ccaccggcgc	420
gtgcgcagtc	gaagaagatc	ggattattta	ctgtagaggg	ctcgcgaggg	gtgttgatga	480
gagaaagact	agtttactta	cttagagatt	ttaactaaga	tcacattttt	atctcttgtg	540
gtgaaaagga	ctttcaatgg	tgttctgtgg	atttgacatt	tggagatagt	tcaggggaaa	600
caccagatgc	tgcgcttgga	ttaggtcgaga	aaacctggaac	tcttagtata	atacgtctcca	660
tgcaatcagc	acagatttat	ccaaaataat	actttcgaca	ggcaccagcg	tgggagaggt	720
ctgatataag	tgatgaccac	tagctatcac	tcagatgctc	ctgttggtata	ttctctcgtg	780
cgcgagatgt	atatattgct	tcgggtacga	ccaaaactgc	agagacgcat	tgacgtctgt	840
ttattttcta	attgtggctg	tcggaatttt	cgctcacaga	cacttgaggc	attgatgaaa	900
actaacaatta	agattgattc	ttaatgttgt	tgctacgcag	accggtagtg	gaaggttgac	960
aaggttgaa	ctcttaagcg	atacaaatct	agttttgcgt	ttgagaatac	taacgaggaa	1020
gatttatgca	ccgagaagtt	ctttcaatcc	ttagtctgct	ggtcgcctcc	cgctgtgaat	1080
ggctctccaa	atatagaaga	attttgcgct	gcttggagct	cattctctca	cattaagact	1140
atggaagatg	tagagccagc	tgcaaaagaga	atgaattatc	tcgcagctaa	ccctcgtcgt	1200
tataactaga	cactaagatg	gaaaatcagag	tgactctcag	attctttcaa	ggcactgtgt	1260
gatatggctg	ctgtacactc	tctctgcgct	ctctcgattt	tctctggcac	gaggtgtcga	1320
gacaacagaa	aggaagaacc	taatttcaag	aaacgacgtg	gcaaatagtg	gaggggagaa	1380
tcagacacag	tttatcatgt	ttttgttgaa	gaagagagcc	gtgttgaaat	ggactcagtc	1440
tttttgaggg	gtaaaagttg	gactcaggaa	ctctcagaat	ctgcgattct	cgccaagttc	1500
aagctcttaa	acatagaggc	aggttggaag	aaggaaagcg	ctggaactct	aaaaggagac	1560
aaagagcgtg	aatatcacgt	gattttaccg	ctctggccctc	cgcaacgaca	ggctttgtac	1620
aactctaaat	tcaggggaaa	tgcagttcta	atgagtcaaa	tcaaaaaaaa	cccttgtgct	1680
aattttgagg	ttgtctctgt	ctagtttcat	tctctcgtag	ctgtcacagg	tatcatctca	1740
gctaagaaga	actttctctg	tgctagaatt	gcaaaattct	aaacaaaacc	attagatgaa	1800

acaaaaggtt aatagtcgatg agattggtga actcattttg tttaggcagt gtatctgttaa 1860
atcgttctga cattgcagac gatgtgttct tgatagctgg atgcataaat gtttgaagat 1920
ttagagcaat ttgatagttt tgaatctctt gagagtgtgt taattaatct ttaaattttt 1980
cc

(2) INFORMATION FOR SEQ ID NO:751:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..338
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498942

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:751:

Met	Ile	Leu	His	Arg	His	Asp	Gly	Gly	Arg	Gly	Tyr	Asp	Ile	Val	Met
1				5					10					15	
Thr	Thr	Ser	Leu	Ser	Ser	Asp	Val	Pro	Val	Gly	Tyr	Phe	Ser	Trp	Ala
			20					25					30		
Glu	Tyr	Asp	Ile	Met	Ser	Pro	Val	Gln	Pro	Lys	Thr	Glu	Arg	Ala	Ile
		35				40					45				
Ala	Ala	Ala	Phe	Ile	Ser	Asn	Cys	Gly	Ala	Arg	Asn	Phe	Arg	Leu	Gln
	50					55				60					
Ala	Leu	Glu	Ala	Leu	Met	Lys	Thr	Asn	Ile	Lys	Ile	Asp	Ser	Tyr	Gly
65				70					75					80	
Gly	Cys	His	Arg	Asn	Arg	Asp	Gly	Lys	Val	Asp	Lys	Val	Glu	Ala	Leu
			85					90					95		
Lys	Arg	Tyr	Lys	Phe	Ser	Leu	Ala	Phe	Glu	Asn	Thr	Asn	Glu	Glu	Asp
			100					105					110		
Tyr	Val	Thr	Glu	Lys	Phe	Phe	Gln	Ser	Leu	Val	Ala	Gly	Ser	Val	Pro
		115					120					125			
Val	Val	Val	Gly	Pro	Pro	Asn	Ile	Glu	Glu	Phe	Ala	Pro	Ala	Ser	Asp
		130				135					140				
Ser	Phe	Leu	His	Ile	Lys	Thr	Met	Glu	Asp	Val	Glu	Pro	Val	Ala	Lys
145				150					155					160	
Arg	Met	Lys	Tyr	Leu	Ala	Ala	Asn	Pro	Ala	Ala	Tyr	Asn	Gln	Thr	Leu
			165					170					175		
Arg	Trp	Lys	Tyr	Glu	Gly	Pro	Ser	Asp	Ser	Phe	Lys	Ala	Leu	Val	Asp
			180					185					190		
Met	Ala	Ala	Val	His	Ser	Ser	Cys	Arg	Leu	Cys	Ile	Phe	Leu	Ala	Thr
		195					200				205				
Arg	Val	Arg	Glu	Gln	Glu	Glu	Glu	Ser	Pro	Asn	Phe	Lys	Lys	Arg	Pro
		210				215				220					
Cys	Lys	Cys	Ser	Arg	Gly	Gly	Ser	Asp	Thr	Val	Tyr	His	Val	Phe	Val
225				230				235						240	
Arg	Glu	Arg	Gly	Arg	Phe	Glu	Met	Glu	Ser	Val	Phe	Leu	Arg	Gly	Lys
			245					250					255		
Ser	Val	Thr	Gln	Glu	Ala	Leu	Glu	Ser	Ala	Val	Leu	Ala	Lys	Phe	Lys
			260				265						270		
Ser	Leu	Lys	His	Glu	Ala	Val	Trp	Lys	Lys	Glu	Arg	Pro	Gly	Asn	Leu
		275					280					285			
Lys	Gly	Asp	Lys	Glu	Leu	Lys	Ile	His	Arg	Ile	Tyr	Pro	Leu	Gly	Leu
		290				295					300				
Thr	Gln	Arg	Gln	Ala	Leu	Tyr	Asn	Phe	Lys	Phe	Glu	Gly	Asn	Ser	Ser
305				310					315					320	
Leu	Ser	Ser	His	Ile	Gln	Asn	Asn	Pro	Cys	Ala	Lys	Phe	Glu	Val	Val
			325					330					335		

Phe Val

(2) INFORMATION FOR SEQ ID NO:752:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 323 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..323
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498943
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:752:

Met	Thr	Thr	Ser	Leu	Ser	Ser	Asp	Val	Pro	Val	Gly	Tyr	Phe	Ser	Trp	
1				5						10				15		
Ala	Glu	Tyr	Asp	Ile	Met	Ser	Pro	Val	Gln	Pro	Lys	Thr	Glu	Arg	Ala	
			20					25					30			
Ile	Ala	Ala	Ala	Phe	Ile	Ser	Asn	Cys	Gly	Ala	Arg	Asn	Phe	Arg	Leu	
			35				40					45				
Gln	Ala	Leu	Glu	Ala	Leu	Met	Lys	Thr	Asn	Ile	Lys	Ile	Asp	Ser	Tyr	
			50			55					60					
Gly	Gly	Cys	His	Arg	Asn	Arg	Asp	Gly	Lys	Val	Asp	Lys	Val	Glu	Ala	
65					70					75				80		
Leu	Lys	Arg	Tyr	Lys	Phe	Ser	Leu	Ala	Phe	Glu	Asn	Thr	Asn	Glu	Glu	
				85					90					95		
Asp	Tyr	Val	Thr	Glu	Lys	Phe	Phe	Gln	Ser	Leu	Val	Ala	Gly	Ser	Val	
			100					105						110		
Pro	Val	Val	Val	Gly	Pro	Pro	Asn	Ile	Glu	Glu	Phe	Ala	Pro	Ala	Ser	
			115				120						125			
Asp	Ser	Phe	Leu	His	Ile	Lys	Thr	Met	Glu	Asp	Val	Glu	Pro	Val	Ala	
			130			135					140					
Lys	Arg	Met	Lys	Tyr	Leu	Ala	Ala	Asn	Pro	Ala	Ala	Tyr	Asn	Gln	Thr	
145					150					155				160		
Leu	Arg	Trp	Lys	Tyr	Glu	Gly	Pro	Ser	Asp	Ser	Phe	Lys	Ala	Leu	Val	
			165						170					175		
Asp	Met	Ala	Ala	Val	His	Ser	Ser	Cys	Arg	Leu	Cys	Ile	Phe	Leu	Ala	
			180					185					190			
Thr	Arg	Val	Arg	Glu	Gln	Glu	Glu	Ser	Pro	Asn	Phe	Lys	Lys	Arg		
			195				200					205				
Pro	Cys	Lys	Cys	Ser	Arg	Gly	Gly	Ser	Asp	Thr	Val	Tyr	His	Val	Phe	
			210			215					220					
Val	Arg	Glu	Arg	Gly	Arg	Phe	Glu	Met	Glu	Ser	Val	Phe	Leu	Arg	Gly	
225					230					235				240		
Lys	Ser	Val	Thr	Gln	Glu	Ala	Leu	Glu	Ser	Ala	Val	Leu	Ala	Lys	Phe	
			245						250					255		
Lys	Ser	Leu	Lys	His	Glu	Ala	Val	Trp	Lys	Lys	Glu	Arg	Pro	Gly	Asn	
			260					265					270			
Leu	Lys	Gly	Asp	Lys	Glu	Leu	Lys	Ile	His	Arg	Ile	Tyr	Pro	Leu	Gly	
			275				280					285				
Leu	Thr	Gln	Arg	Gln	Ala	Leu	Tyr	Asn	Phe	Lys	Phe	Glu	Gly	Asn	Ser	
			290			295						300				
Ser	Leu	Ser	Ser	His	Ile	Gln	Asn	Asn	Pro	Cys	Ala	Lys	Phe	Glu	Val	
					310					315					320	
Val	Phe	Val														

- (2) INFORMATION FOR SEQ ID NO:753:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 302 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..302
(D) OTHER INFORMATION: / Ceres Seq. ID 1498944
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:753:

Met	Ser	Pro	Val	Gln	Pro	Lys	Thr	Glu	Arg	Ala	Ile	Ala	Ala	Ala	Phe
1				5				10					15		
Ile	Ser	Asn	Cys	Gly	Ala	Arg	Asn	Phe	Arg	Leu	Gln	Ala	Leu	Glu	Ala
			20				25					30			
Leu	Met	Lys	Thr	Asn	Ile	Lys	Ile	Asp	Ser	Tyr	Gly	Gly	Cys	His	Arg
		35				40					45				
Asn	Arg	Asp	Gly	Lys	Val	Asp	Lys	Val	Glu	Ala	Leu	Lys	Arg	Tyr	Lys
		50			55					60					
Phe	Ser	Leu	Ala	Phe	Glu	Asn	Thr	Asn	Glu	Glu	Asp	Tyr	Val	Thr	Glu
65				70					75					80	
Lys	Phe	Phe	Gln	Ser	Leu	Val	Ala	Gly	Ser	Val	Pro	Val	Val	Val	Gly
			85					90				95			
Pro	Pro	Asn	Ile	Glu	Glu	Phe	Ala	Pro	Ala	Ser	Asp	Ser	Phe	Leu	His
		100						105				110			
Ile	Lys	Thr	Met	Glu	Asp	Val	Glu	Pro	Val	Ala	Lys	Arg	Met	Lys	Tyr
		115					120					125			
Leu	Ala	Ala	Asn	Pro	Ala	Ala	Tyr	Asn	Gln	Thr	Leu	Arg	Trp	Lys	Tyr
		130				135					140				
Glu	Gly	Pro	Ser	Asp	Ser	Phe	Lys	Ala	Leu	Val	Asp	Met	Ala	Ala	Val
145					150				155					160	
His	Ser	Ser	Cys	Arg	Leu	Cys	Ile	Phe	Leu	Ala	Thr	Arg	Val	Arg	Glu
			165					170					175		
Gln	Glu	Glu	Glu	Ser	Pro	Asn	Phe	Lys	Lys	Arg	Pro	Cys	Lys	Cys	Ser
		180					185					190			
Arg	Gly	Gly	Ser	Asp	Thr	Val	Tyr	His	Val	Phe	Val	Arg	Glu	Arg	Gly
		195					200					205			
Arg	Phe	Glu	Met	Glu	Ser	Val	Phe	Leu	Arg	Gly	Lys	Ser	Val	Thr	Gln
		210				215					220				
Glu	Ala	Leu	Glu	Ser	Ala	Val	Leu	Ala	Lys	Phe	Lys	Ser	Leu	Lys	His
225					230				235					240	
Glu	Ala	Val	Trp	Lys	Lys	Glu	Arg	Pro	Gly	Asn	Leu	Lys	Gly	Asp	Lys
			245					250					255		
Glu	Leu	Lys	Ile	His	Arg	Ile	Tyr	Pro	Leu	Gly	Leu	Thr	Gln	Arg	Gln
		260					265						270		
Ala	Leu	Tyr	Asn	Phe	Lys	Phe	Glu	Gly	Asn	Ser	Ser	Leu	Ser	Ser	His
		275				280						285			
Ile	Gln	Asn	Asn	Pro	Cys	Ala	Lys	Phe	Glu	Val	Val	Phe	Val		
		290				295					300				

(2) INFORMATION FOR SEQ ID NO:754:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1299
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:754:

cttttagaca	aaactagtgg	cagactgaaa	aatgaacgca	gcgcttgcaa	caaccaccgc	60
cacaactccc	gcactccgcc	gtgagacgcc	tcttattcat	tattgttctc	tcacaacaaa	120
atcgccgggt	taccaaatca	acagagttag	attcggatct	tgcytgcaaa	cagtcagcaa	180
gaaattcttg	aaaatctcgg	cgagctctca	gagcgcttca	gcgcgcgtca	atatcacggc	240
ggatgcttcg	attccgaaag	agatgaagcg	gtgggtgtat	agtgaactacg	gcggagttga	300
tgttttgaaa	ctggagagta	acattgctgt	gcgcggagatt	aaagaagatc	aggttctgat	360
taaagtgtgt	gcggcgggct	ttaatcccg	cgatgctaag	agacggcgagg	ggaaatttaa	420

agccactgat	tcgectctcc	cgactgttcc	gggatacgac	gttgccggag	tggtgggtgaa	480
agtgggaagt	gcggtgaagg	atttcaaaga	aggagatgaa	gtttatgcta	acgtgagcga	540
gaaagcattg	gaaggtccaa	agcaattcgg	ttctttagcg	gagtagacgg	ccgtgggaaga	600
gaagttatta	gctttaaaac	ctaaaaacat	cgatttcgcg	caagctgcag	ggcttccggt	660
ggcgatagaa	accgctgatg	aagggttagt	taggactgaa	ttctcccgcc	gaaagtccat	720
ttctgttctt	aatggtgccg	gaggagtagg	gagttctatg	attcagttgg	cgaagcacgt	780
gtatggagct	tcaaaagtgg	ctgcaacagc	gagtagcagg	aagctggagc	tagtgagaag	840
cttaggtgct	gatttagcta	ttgattacac	aaaggagaat	atagaagact	tgccctgaca	900
gtacgatggt	gtctttgacg	ccattgggat	gtgtgataag	gcagtgaaag	tgattaagga	960
aggagggaag	gttgtggcat	tgactggagc	tgtaacgctt	ccgtgttttc	gattcggtgt	1020
tacatctaatt	ggcgatgttt	tgaagaaact	taaccatcat	attgagagtg	ggaaggtgaa	1080
gcctgtggtt	gatcccaaa	gaccgttccc	cttctcagcg	gttgctgatg	ctttttcata	1140
cttagaagac	aaccatgcca	cagggaaggt	cgttgtttat	cccatctcct	aaggggctg	1200
cttgagtgta	gtagccttta	tctatctatg	tgtataagca	tagcaagtgt	tatcttctct	1260
ttgtattaat	gaggtgggaa	ataaaagtaa	atgctctttt			

(2) INFORMATION FOR SEQ ID NO:755:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 386 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..386

(D) OTHER INFORMATION: / Ceres Seq. ID 1498950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:755:

Met	Asn	Ala	Ala	Leu	Ala	Thr	Thr	Thr	Ala	Thr	Thr	Pro	Ala	Leu	Arg
1				5					10					15	
Arg	Glu	Thr	Pro	Leu	Ile	His	Tyr	Cys	Ser	Leu	Thr	Thr	Lys	Ser	Pro
			20					25					30		
Val	Tyr	Gln	Ile	Asn	Arg	Val	Arg	Phe	Gly	Ser	Cys	Val	Gln	Thr	Val
			35				40				45				
Ser	Lys	Lys	Phe	Leu	Lys	Ile	Ser	Ala	Ser	Ser	Gln	Ser	Ala	Ser	Ala
			50				55				60				
Ala	Val	Asn	Ile	Thr	Ala	Asp	Ala	Ser	Ile	Pro	Lys	Glu	Met	Lys	Ala
			65				70			75				80	
Trp	Val	Tyr	Ser	Asp	Tyr	Gly	Gly	Val	Asp	Val	Leu	Lys	Leu	Glu	Ser
				85				90					95		
Asn	Ile	Ala	Val	Pro	Glu	Ile	Lys	Glu	Asp	Gln	Val	Leu	Ile	Lys	Val
			100					105					110		
Val	Ala	Ala	Gly	Leu	Asn	Pro	Val	Asp	Ala	Lys	Arg	Arg	Gln	Gly	Lys
			115				120					125			
Phe	Lys	Ala	Thr	Asp	Ser	Pro	Leu	Pro	Thr	Val	Pro	Gly	Tyr	Asp	Val
			130				135				140				
Ala	Gly	Val	Val	Val	Lys	Val	Gly	Ser	Ala	Val	Lys	Asp	Phe	Lys	Glu
			145				150			155				160	
Gly	Asp	Glu	Val	Tyr	Ala	Asn	Val	Ser	Glu	Lys	Ala	Leu	Glu	Gly	Pro
				165					170				175		
Lys	Gln	Phe	Gly	Ser	Leu	Ala	Glu	Tyr	Thr	Ala	Val	Glu	Glu	Lys	Leu
			180					185					190		
Leu	Ala	Leu	Lys	Pro	Lys	Asn	Ile	Asp	Phe	Ala	Gln	Ala	Ala	Gly	Leu
			195				200					205			
Pro	Leu	Ala	Ile	Glu	Thr	Ala	Asp	Glu	Gly	Leu	Val	Arg	Thr	Glu	Phe
			210				215				220				
Ser	Ala	Gly	Lys	Ser	Ile	Leu	Val	Leu	Asn	Gly	Ala	Gly	Gly	Val	Gly
			225				230			235				240	
Ser	Leu	Met	Ile	Gln	Leu	Ala	Lys	His	Val	Tyr	Gly	Ala	Ser	Lys	Val
				245				250					255		
Ala	Ala	Thr	Ala	Ser	Thr	Gly	Lys	Leu	Glu	Leu	Val	Arg	Ser	Leu	Gly
			260				265					270			

Ala Asp Leu Ala Ile Asp Tyr Thr Lys Glu Asn Ile Glu Asp Leu Pro
275 280 285
Asp Lys Tyr Asp Val Val Phe Asp Ala Ile Gly Met Cys Asp Lys Ala
290 295 300
Val Lys Val Ile Lys Glu Gly Gly Lys Val Val Ala Leu Thr Gly Ala
305 310 315 320
Val Thr Pro Pro Gly Phe Arg Phe Val Val Thr Ser Asn Gly Asp Val
325 330 335
Leu Lys Lys Leu Asn Pro Tyr Ile Glu Ser Gly Lys Val Lys Pro Val
340 345 350
Val Asp Pro Lys Gly Pro Phe Pro Phe Ser Arg Val Ala Asp Ala Phe
355 360 365
Ser Tyr Leu Glu Thr Asn His Ala Thr Gly Lys Val Val Tyr Pro
370 375 380
Ile Pro
385

(2) INFORMATION FOR SEQ ID NO:756:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..309
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498951

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:756:

Met Lys Ala Trp Val Tyr Ser Asp Tyr Gly Gly Val Asp Val Leu Lys
1 5 10 15
Leu Glu Ser Asn Ile Ala Val Pro Glu Ile Lys Glu Asp Gln Val Leu
20 25 30
Ile Lys Val Val Ala Ala Gly Leu Asn Pro Val Asp Ala Lys Arg Arg
35 40 45
Gln Gly Lys Phe Lys Ala Thr Asp Ser Pro Leu Pro Thr Val Pro Gly
50 55 60
Tyr Asp Val Ala Gly Val Val Val Lys Val Gly Ser Ala Val Lys Asp
65 70 75 80
Phe Lys Glu Gly Asp Glu Val Tyr Ala Asn Val Ser Glu Lys Ala Leu
85 90 95
Glu Gly Pro Lys Gln Phe Gly Ser Leu Ala Glu Tyr Thr Ala Val Glu
100 105 110
Glu Lys Leu Leu Ala Leu Lys Pro Lys Asn Ile Asp Phe Ala Gln Ala
115 120 125
Ala Gly Leu Pro Leu Ala Ile Glu Thr Ala Asp Glu Gly Leu Val Arg
130 135 140
Thr Glu Phe Ser Ala Gly Lys Ser Ile Leu Val Leu Asn Gly Ala Gly
145 150 155 160
Gly Val Gly Ser Leu Met Ile Gln Leu Ala Lys His Val Tyr Gly Ala
165 170 175
Ser Lys Val Ala Ala Thr Ala Ser Thr Gly Lys Leu Glu Leu Val Arg
180 185 190
Ser Leu Gly Ala Asp Leu Ala Ile Asp Tyr Thr Lys Glu Asn Ile Glu
195 200 205
Asp Leu Pro Asp Lys Tyr Asp Val Val Phe Asp Ala Ile Gly Met Cys
210 215 220
Asp Lys Ala Val Lys Val Ile Lys Glu Gly Gly Lys Val Val Ala Leu
225 230 235 240
Thr Gly Ala Val Thr Pro Pro Gly Phe Arg Phe Val Val Thr Ser Asn
245 250 255
Gly Asp Val Leu Lys Lys Leu Asn Pro Tyr Ile Glu Ser Gly Lys Val

(2) INFORMATION FOR SEQ ID NO:757:

(A) LENGTH: 1347 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1347
(D) OTHER INFORMATION: / Ceres Seq. ID 1498952

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:757						
acgaataaaga	aagaagaaga	aacatacaac	atctcttggt	tgcttccctc	gtaccgcgtc	60
ttcatacaaga	tatgatcaatc	tgctgtctct	ataatagacat	acatacaaaa	aaaactttga	120
taagattttga	acataaaaata	ttaaatattat	cctctattttt	cgaggcagcg	ctttaattat	180
ggatttgtcat	agaaagtcgt	tctgttgtaa	ttttttgtgc	gtggcaattc	gtttaaacta	240
cagcaagtatt	ggcttttgtat	accgcagcac	aaacattggc	gtgaactacg	cgcctcttgg	300
agacaaacctc	ccgcctccatc	ctgaagtatt	caacctctac	aagctcttaa	gtgttaacca	360
tattcggatc	ttcgacacga	ctacggatgt	cttaacgcgc	tttcgaggga	atcgcgatat	420
tgagatttatg	tgtagcgctga	agacaaaga	cttagaggct	ctttcggcta	cggaagacgc	480
tgttaaacacc	tggttcgtga	caaaacttga	gccttaetta	ctgtagtcta	acatacagtt	540
catctgtctc	gggaacgaga	tcttccaggc	ggaaatcgcg	ttctatgtgc	taccgcgtat	600
gaaattctctc	accaacttgc	tcaagtcgag	gagttctccg	atctttgatca	gcacacaggt	660
ggctatgacc	acaactggcc	actcgctatc	accttcggcg	ggagatttca	tacctcaagc	720
cggtgaacaa	cttaccgccg	tgctgaagtt	tttgtctcaa	acaaaatcgc	ctatcctctg	780
caacatctac	ccctacttcg	catatctgtc	tgatctctac	acatttcagc	ttgattattg	840
catcttcaac	accaacaagt	ttgtgttcca	agttatacaa	acatgttcga	tgtgattatt	900
gatgcttttg	tatgggcaat	ggagaagaag	ggcgtgaagg	atttaccaat	gtgttgtaac	960
tacacggatg	ggccatctgc	tggtaaacga	aacttaacaa	ctccagatat	cgcatctata	1020
tactaatcaa	attttgtttaa	acatgtggaa	agcggtaaat	ggagccgaaa	gagaccaaa	1080
atgagcattc	gtgattttct	attttgcagc	ttcaaatgaga	atcaaaagcc	agcgggaacg	1140
gaacacaaatt	ttgggttata	taattccaaca	gatattgaagc	ccactctaca	gatgttttga	1200
tttttagatt	cttgatttta	tagacatacc	caaatcatac	gtaatttaat	gatgtcttaa	1260
tagttgttaat	agagcgggat	aaatccaaga	tctacaacaa	cattcatttt	atatgttga	1320
tgatcttctt	aaataaaaaa	accttaag				

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..238
(D) OTHER INFORMATION: / Ceres Seq. ID 1498953

(X1)		SEQUENCE DESCRIPTION										SEQUENCE NUMBER									
Met	Asp	Cys	His	Arg	Lys	Ser	Phe	Leu	Lys	Phe	Leu	Cys	Val	Ala							
1				5				10					15								
	Phe	Leu	Asn	Tyr	Ser	Asn	Val	Gly		Phe	Val	Asp	Ala	Ala	Thr	Asn					
			20					25					30								
	Ile	Gly	Leu	Asn	Tyr	Gly	Leu	Leu	Gly	Asp	Asn	Leu	Pro	Pro	Pro	Ser					
			35					40					45								
	Glu	Val	Ile	Asn	Leu	Tyr	Lys	Ser	Leu	Ser	Val	Thr	Asn	Ile	Arg	Ile					

50 55 60
Phe Asp Thr Thr Thr Asp Val Leu Asn Ala Phe Arg Gly Asn Arg Asp
65 70 75 80
Ile Gly Val Met Val Gly Val Lys Asn Gln Asp Leu Glu Ala Leu Ser
85 90 95
Val Ser Glu Asp Ala Val Asn Thr Trp Phe Val Thr Asn Ile Glu Pro
100 105 110
Tyr Leu Ala Asp Val Asn Ile Thr Phe Ile Ala Val Gly Asn Glu Val
115 120 125
Ile Pro Gly Glu Ile Gly Ser Tyr Val Leu Pro Val Met Lys Ser Leu
130 135 140
Thr Asn Ile Val Lys Ser Arg Ser Leu Pro Ile Leu Ile Ser Thr Thr
145 150 155 160
Val Ala Met Thr Asn Leu Gly Gln Ser Tyr Pro Pro Ser Ala Gly Asp
165 170 175
Phe Ile Pro Gln Ala Arg Glu Gln Leu Thr Pro Val Leu Lys Phe Leu
180 185 190
Ser Gln Thr Asn Thr Pro Ile Leu Val Asn Ile Tyr Pro Tyr Phe Ala
195 200 205
Tyr Ala Ala Asp Pro Ile Asn Ile Gln Leu Asp Tyr Ala Ile Phe Asn
210 215 220
Thr Asn Lys Val Val Val Gln Val Ile Gln Thr Cys Ser Met
225 230 235

(2) INFORMATION FOR SEQ ID NO:759:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..155

- (D) OTHER INFORMATION: / Ceres Seq. ID 1498954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:759:

Met Val Gly Val Lys Asn Gln Asp Leu Glu Ala Leu Ser Val Ser Glu
1 5 10 15
Asp Ala Val Asn Thr Trp Phe Val Thr Asn Ile Glu Pro Tyr Leu Ala
20 25 30
Asp Val Asn Ile Thr Phe Ile Ala Val Gly Asn Glu Val Ile Pro Gly
35 40 45
Glu Ile Gly Ser Tyr Val Leu Pro Val Met Lys Ser Leu Thr Asn Ile
50 55 60
Val Lys Ser Arg Ser Leu Pro Ile Leu Ile Ser Thr Thr Val Ala Met
65 70 75 80
Thr Asn Leu Gly Gln Ser Tyr Pro Pro Ser Ala Gly Asp Phe Ile Pro
85 90 95
Gln Ala Arg Glu Gln Leu Thr Pro Val Leu Lys Phe Leu Ser Gln Thr
100 105 110
Asn Thr Pro Ile Leu Val Asn Ile Tyr Pro Tyr Phe Ala Tyr Ala Ala
115 120 125
Asp Pro Ile Asn Ile Gln Leu Asp Tyr Ala Ile Phe Asn Thr Asn Lys
130 135 140
Val Val Val Gln Val Ile Gln Thr Cys Ser Met
145 150 155

(2) INFORMATION FOR SEQ ID NO:760:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1453

(D) OTHER INFORMATION: / Ceres Seq. ID 1498958

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:760:

aaaagaaaaat	tgtaaatgtt	gaaaaatgtt	gagcacaagc	tctgatcttc	atggccgctct	60
tctccgatta	tcagaaccaa	tagcagagat	tcttagacgt	acacagtaga	caccgcgaaga	120
gagcagcaaa	gtatccacca	aaagataact	cttgtccctg	ttaccaaaac	cttcgtcttc	180
tgtctcgcgc	aatgaagaat	cgvtcaaaag	tctcgcgctt	gcttgtgccc	ttctcgcttc	240
ttcactgtta	tccactcagc	aacttctctc	atggatttgc	agaaaaacct	tctgtcatgg	300
gggaatctac	attttgggag	atttcaaggg	attgtttcag	tattttttct	agcaaacagta	360
atgctgagaa	gcttgtggaa	ttggtagagg	atagtggaaa	gatcgaaatg	ttgcccagata	420
ttttgcggga	gttaaaagat	ggaatcgaaa	agagttcact	tggtaaaagg	agtgtatgag	480
aggatgtttc	agctgcaatg	gctagaacac	ctgttggtta	tgctataact	gctgtctacc	540
agctcagggt	gtttgttact	caggttaaaa	aaccgaattt	ggtgaaat	tgtaacttgg	600
tggttctctg	tgctttgaca	gcacttgatc	attggtctcc	tgaagtcaaa	gggcagggta	660
tgataacctt	tggtcatctt	gtcaaaaatg	tgagttccgg	tgatcttggg	ttgtatggag	720
atgtggtttc	tgatgctgtg	tgccagaata	tagcttcoga	tgatgagatt	tggtatcatg	780
tggttagagt	atctgtgctt	cttgttacta	aaatccaccc	aaataatctt	cgaagcccggt	840
ggatgagaaa	gagatgctcg	ggcatttggg	acgccaaacca	agaaaataag	gagaaataag	900
agcgacgtat	cacttggcta	agatttgggt	agccactctt	gaactctcta	gggtttttct	960
tacttgccta	ttttcgacgt	atcttccctc	tttttttcca	gtggatgcat	tcagacgacg	1020
ccgaaacagt	tctgttgggt	cttgagagac	tgagacagat	tgtaggttgg	acgtgggata	1080
gacactcacc	tggtgttcca	agatttgggt	atgagcttgg	ttccttggac	aaagagtcac	1140
cgatgcgtaa	ggatcgcgat	gacattagac	ctcttatctc	ccgtatctgt	atgctactcc	1200
gccagtgcaa	aggtctacgg	tttgagtcag	cgtggagcta	ataccagagg	gattcaaatc	1260
tgagactagt	tagtcaacat	atatgagcta	gttcaagttg	atctcaagag	cgtatgtttg	1320
actaaaacag	ccattttttt	tctaattttt	gatattagtt	tggtctaggg	ctagtgatgc	1380
aagttaattac	tgccgaatcc	tcgaattttt	gtaagcattt	ggctcttgac	tcttcttaag	1440
ctaactctgat	ttg					

(2) INFORMATION FOR SEQ ID NO:761:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 369 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..369

(D) OTHER INFORMATION: / Ceres Seq. ID 1498959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:761:

Met	Lys	Asn	Xaa	Ser	Lys	Val	Ser	Arg	Leu	Leu	Val	Pro	Phe	Ser	Leu	
1		5						10					15			
Leu	His	Val	His	Pro	Leu	Thr	Asn	Phe	Ser	His	Gly	Xaa	Pro	Glu	Asn	
		20						25				30				
Leu	Ser	Val	Met	Gly	Glu	Ser	Thr	Phe	Trp	Glu	Ile	Ser	Arg	Asp	Cys	
		35					40					45				
Phe	Ser	Asp	Phe	Ser	Ser	Asn	Ser	Asn	Ala	Glu	Lys	Leu	Val	Glu	Leu	
		50				55				60						
Val	Glu	Asp	Ser	Glu	Lys	Ile	Glu	Met	Leu	Pro	Ile	Val	Leu	Pro	Glu	
		65				70				75				80		
Leu	Lys	Asp	Gly	Ile	Glu	Lys	Ser	Ser	Leu	Gly	Lys	Gly	Ser	Asp	Ala	
		85						90					95			
Glu	Asp	Val	Ser	Ala	Ala	Met	Ala	Arg	Thr	Pro	Val	Gly	Tyr	Ala	Ile	
		100						105					110			
Leu	Ala	Ala	His	Gln	Leu	Arg	Trp	Phe	Val	Thr	Gln	Val	Lys	Lys	Pro	
		115					120					125				
Asn	Leu	Val	Lys	Phe	Cys	Asn	Leu	Val	Val	Pro	Cys	Ala	Leu	Thr	Ala	
		130					135					140				

```

Leu Asp His Trp Ser Pro Glu Val Lys Gly Gln Gly Met Ile Thr Phe
145                               150           155           160
Val His Leu Ala Lys Asn Val Ser Ser Gly Asp Leu Gly Leu Tyr Gly
                               165           170           175
Asp Val Val Leu Asp Ala Cys Cys Gln Asn Ile Ala Ser Asp Asp Glu
                               180           185           190
Ile Trp Ile His Val Val Glu Leu Ser Val Leu Leu Val Thr Lys Ile
                               195           200           205
His Pro Asn Asn Pro Arg Ser Pro Trp Tyr Glu Lys Ile Met Asn Glu
                               210           215           220
Met Leu Gly His Leu Glu Arg Gln Pro Arg Asn Lys Glu Arg Arg Ile
225                               230           235           240
Thr Trp Leu Arg Phe Val Glu Pro Leu Leu Asn Ser Leu Gly Leu Phe
                               245           250           255
Leu Leu Ala His Phe Arg Arg Ile Phe Pro Leu Phe Phe Gln Trp Met
                               260           265           270
His Ser Asp Asp Ala Glu Thr Val Leu Leu Val Leu Glu Arg Leu Glu
                               275           280           285
Thr Val Val Arg Leu Thr Trp Ile Arg His Ser Pro Val Phe Pro Arg
                               290           295           300
Leu Val Asp Glu Leu Val Ser Leu Tyr Lys Glu Ser Ser Met Arg Lys
305                               310           315           320
Asp Arg Asp Asp Ile Arg Pro Leu Ile Leu Arg Ile Leu Met Leu Leu
                               325           330           335
Arg Gln Cys Lys Gly Leu Arg Phe Glu Ser Ala Trp Ser Gln Tyr Gln
                               340           345           350
Glu Asp Pro Asn Leu Ser Thr Val Ser Gln His Ile Trp Thr Ser Ser
                               355           360           365
Ser

```

(2) INFORMATION FOR SEQ ID NO:762:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..334

(D) OTHER INFORMATION: / Ceres Seq. ID 1498960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:762:

```

Met Gly Glu Ser Thr Phe Trp Glu Ile Ser Arg Asp Cys Phe Ser Asp
1                               5           10           15
Phe Ser Ser Asn Ser Asn Ala Glu Lys Leu Val Glu Leu Val Glu Asp
                               20           25           30
Ser Glu Lys Ile Glu Met Leu Pro Ile Val Leu Pro Glu Leu Lys Asp
                               35           40           45
Gly Ile Glu Lys Ser Ser Leu Gly Lys Gly Ser Asp Ala Glu Asp Val
                               50           55           60
Ser Ala Ala Met Ala Arg Thr Pro Val Gly Tyr Ala Ile Leu Ala Ala
65                               70           75           80
His Gln Leu Arg Trp Phe Val Thr Gln Val Lys Lys Pro Asn Leu Val
                               85           90           95
Lys Phe Cys Asn Leu Val Val Pro Cys Ala Leu Thr Ala Leu Asp His
                               100          105          110
Trp Ser Pro Glu Val Lys Gly Gln Gly Met Ile Thr Phe Val His Leu
                               115          120          125
Ala Lys Asn Val Ser Ser Gly Asp Leu Gly Leu Tyr Gly Asp Val Val
                               130          135          140
Leu Asp Ala Cys Cys Gln Asn Ile Ala Ser Asp Asp Glu Ile Trp Ile

```

145		150		155		160
His Val Val Glu Leu Ser Val Leu Leu Val Thr Lys Ile His Pro Asn						
	165		170			175
Asn Pro Arg Ser Pro Trp Tyr Glu Lys Ile Met Asn Glu Met Leu Gly						
	180		185			190
His Leu Glu Arg Gln Pro Arg Asn Lys Glu Arg Arg Ile Thr Trp Leu						
	195		200			205
Arg Phe Val Glu Pro Leu Leu Asn Ser Leu Gly Leu Phe Leu Leu Ala						
	210		215			220
His Phe Arg Arg Ile Phe Pro Leu Phe Phe Gln Trp Met His Ser Asp						
	225		230			235
Asp Ala Glu Thr Val Leu Leu Val Leu Glu Arg Leu Glu Thr Val Val						
	245		250			255
Arg Leu Thr Trp Ile Arg His Ser Pro Val Phe Pro Arg Leu Val Asp						
	260		265			270
Glu Leu Val Ser Leu Tyr Lys Glu Ser Ser Met Arg Lys Asp Arg Asp						
	275		280			285
Asp Ile Arg Pro Leu Ile Leu Arg Ile Leu Met Leu Leu Arg Gln Cys						
	290		295			300
Lys Gly Leu Arg Phe Glu Ser Ala Trp Ser Gln Tyr Gln Glu Asp Pro						
	305		310			315
Asn Leu Ser Thr Val Ser Gln His Ile Trp Thr Ser Ser Ser						
	325		330			

(2) INFORMATION FOR SEQ ID NO:763:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 297 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..297

(D) OTHER INFORMATION: / Ceres Seq. ID 1498961

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:763:

Met Leu Pro Ile Val Leu Pro Glu Leu Lys Asp Gly Ile Glu Lys Ser						
1	5		10			15
Ser Leu Gly Lys Gly Ser Asp Ala Glu Asp Val Ser Ala Ala Met Ala						
	20		25			30
Arg Thr Pro Val Gly Tyr Ala Ile Leu Ala Ala His Gln Leu Arg Trp						
	35		40			45
Phe Val Thr Gln Val Lys Lys Pro Asn Leu Val Lys Phe Cys Asn Leu						
	50		55			60
Val Val Pro Cys Ala Leu Thr Ala Leu Asp His Trp Ser Pro Glu Val						
	65		70			75
Lys Gly Gln Gly Met Ile Thr Phe Val His Leu Ala Lys Asn Val Ser						
	85		90			95
Ser Gly Asp Leu Gly Leu Tyr Gly Asp Val Val Leu Asp Ala Cys Cys						
	100		105			110
Gln Asn Ile Ala Ser Asp Asp Glu Ile Trp Ile His Val Val Glu Leu						
	115		120			125
Ser Val Leu Leu Val Thr Lys Ile His Pro Asn Asn Pro Arg Ser Pro						
	130		135			140
Trp Tyr Glu Lys Ile Met Asn Glu Met Leu Gly His Leu Glu Arg Gln						
	145		150			155
Pro Arg Asn Lys Glu Arg Arg Ile Thr Trp Leu Arg Phe Val Glu Pro						
	165		170			175
Leu Leu Asn Ser Leu Gly Leu Phe Leu Leu Ala His Phe Arg Arg Ile						
	180		185			190
Phe Pro Leu Phe Phe Gln Trp Met His Ser Asp Asp Ala Glu Thr Val						
	195		200			205

Leu Leu Val Leu Glu Arg Leu Glu Thr Val Val Arg Leu Thr Trp Ile
210 215 220
Arg His Ser Pro Val Phe Pro Arg Leu Val Asp Glu Leu Val Ser Leu
225 230 235 240
Tyr Lys Glu Ser Ser Met Arg Lys Asp Arg Asp Ile Arg Pro Leu
245 250 255
Ile Leu Arg Ile Leu Met Leu Leu Arg Gln Cys Lys Gly Leu Arg Phe
260 265 270
Glu Ser Ala Trp Ser Gln Tyr Gln Glu Asp Pro Asn Leu Ser Thr Val
275 280 285
Ser Gln His Ile Trp Thr Ser Ser Ser
290 295

(2) INFORMATION FOR SEQ ID NO:764:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 637 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..637
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498962

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:764:

rgaatttcac	cgcattgtatc	gtgcattggc	tgaacgttat	gatcaagcta	gtgggtgagct	60
acagaagaac	catacatctg	agatccagtc	acagagctct	cttgagttat	catctcctac	120
caaagagaa	ttgagtcgcc	gtcaatctgg	ccataaagaa	gaggaagatt	catcatcttt	180
gacagattcc	ggttctgatt	ctgatcattc	ctctgccaat	gatgaagacg	gtgacgaggg	240
attgatccgt	agaatggctg	aacttgagct	tgagcttcaa	gagacgaaac	agaagctcct	300
tctccagcag	gaaagtgttg	atggtgacaa	caatgttgat	ctccttcaca	aaattactac	360
atatgagggg	gagcttaaa	aagctaata	gaagatgcga	atgcacgaag	acgagattgc	420
taattcgaag	aatcagcttc	agagctgcac	gtccttgac	gcagagggatc	aacttggtac	480
tgacagaaa	agtcttgatt	tgataaaga	ggacactgaa	gcagatgcag	aagctacaaa	540
agtgcctagc	ctggaggaag	agctgagtat	cgcgaaagag	aagcttcagc	actttgagaa	600
agagacttat	tctctgaaaa	atgagctcga	gattagt			

(2) INFORMATION FOR SEQ ID NO:765:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..212
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498963

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:765:

Glu Xaa His Arg Met Tyr Arg Ala Leu Ala Glu Arg Tyr Asp Gln Ala	
1 5 10 15	
Ser Gly Glu Leu Gln Lys Asn His Thr Ser Glu Ile Gln Ser Gln Ser	
20 25 30	
Ser Leu Glu Leu Ser Ser Pro Thr Lys Glu Lys Leu Ser Arg Arg Gln	
35 40 45	
Ser Gly His Lys Glu Glu Glu Asp Ser Ser Ser Leu Thr Asp Ser Gly	
50 55 60	
Ser Asp Ser Asp His Ser Ser Ala Asn Asp Glu Asp Gly Asp Glu Ala	
65 70 75 80	
Leu Ile Arg Arg Met Ala Glu Leu Glu Glu Leu Gln Thr Lys	
85 90 95	
Gln Lys Leu Leu Leu Gln Gln Glu Ser Val Asp Gly Asp Asn Asn Val	
100 105 110	

Asp Leu Leu His Lys Ile Thr Thr Tyr Glu Gly Glu Leu Lys Glu Ala
115 120 125
Asn Glu Lys Met Arg Met His Glu Asp Glu Ile Ala Asn Leu Lys Asn
130 135 140
Gln Leu Gln Ser Cys Met Ser Phe Asp Ala Glu Asp Gln Leu Gly Thr
145 150 155 160
Ala Glu Lys Ser Leu Asp Leu Asp Lys Glu Asp Thr Glu Ala Asp Ala
165 170 175
Glu Ala Thr Lys Val Leu Ala Leu Glu Glu Glu Leu Ser Ile Ala Lys
180 185 190
Glu Lys Leu Gln His Phe Glu Lys Glu Thr Tyr Ser Leu Lys Asn Glu
195 200 205
Leu Glu Ile Ser
210

(2) INFORMATION FOR SEQ ID NO:766:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..208

(D) OTHER INFORMATION: / Ceres Seq. ID 1498964

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:766:

Met Tyr Arg Ala Leu Ala Glu Arg Tyr Asp Gln Ala Ser Gly Glu Leu
1 5 10 15
Gln Lys Asn His Thr Ser Glu Ile Gln Ser Gln Ser Ser Leu Glu Leu
20 25 30
Ser Ser Pro Thr Lys Glu Lys Leu Ser Arg Arg Gln Ser Gly His Lys
35 40 45
Glu Glu Glu Asp Ser Ser Ser Leu Thr Asp Ser Gly Ser Asp Ser Asp
50 55 60
His Ser Ser Ala Asn Asp Glu Asp Gly Asp Glu Ala Leu Ile Arg Arg
65 70 75 80
Met Ala Glu Leu Glu Leu Glu Leu Gln Glu Thr Lys Gln Lys Leu Leu
85 90 95
Leu Gln Gln Glu Ser Val Asp Gly Asp Asn Asn Val Asp Leu Leu His
100 105 110
Lys Ile Thr Thr Tyr Glu Gly Glu Leu Lys Glu Ala Asn Gln Lys Met
115 120 125
Arg Met His Glu Asp Glu Ile Ala Asn Leu Lys Asn Gln Leu Gln Ser
130 135 140
Cys Met Ser Phe Asp Ala Glu Asp Gln Leu Gly Thr Ala Glu Lys Ser
145 150 155 160
Leu Asp Leu Asp Lys Glu Asp Thr Glu Ala Asp Ala Glu Ala Thr Lys
165 170 175
Val Leu Ala Leu Glu Glu Glu Leu Ser Ile Ala Lys Glu Lys Leu Gln
180 185 190
His Phe Glu Lys Glu Thr Tyr Ser Leu Lys Asn Glu Leu Glu Ile Ser
195 200 205

(2) INFORMATION FOR SEQ ID NO:767:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..128
 (D) OTHER INFORMATION: / Ceres Seq. ID 1498965
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:767:
Met Ala Glu Leu Glu Leu Glu Leu Gln Glu Thr Lys Gln Lys Leu Leu
1 5 10 15
Leu Gln Gln Glu Ser Val Asp Gly Asp Asn Asn Val Asp Leu Leu His
20 25 30
Lys Ile Thr Thr Tyr Glu Gly Glu Leu Lys Glu Ala Asn Glu Lys Met
35 40 45
Arg Met His Glu Asp Glu Ile Ala Asn Leu Lys Asn Gln Leu Gln Ser
50 55 60
Cys Met Ser Phe Asp Ala Glu Asp Gln Leu Gly Thr Ala Glu Lys Ser
65 70 75 80
Leu Asp Leu Asp Lys Glu Asp Thr Glu Ala Asp Ala Glu Ala Thr Lys
85 90 95
Val Leu Ala Leu Glu Glu Glu Leu Ser Ile Ala Lys Glu Lys Leu Gln
100 105 110
His Phe Glu Lys Glu Thr Tyr Ser Leu Lys Asn Glu Leu Glu Ile Ser
115 120 125

(2) INFORMATION FOR SEQ ID NO:768:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1513 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1513
(D) OTHER INFORMATION: / Ceres Seq. ID 1498966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:768:

aaaacaaact ctgccttcct gcctcgttga ttctccaaaa ccagctttca ctctctattg 60
ccgattctcg ttctgcttga tatcttagga atctataaac aaaggcatcg gttcagattt 120
ctgttgattt tctcaatcaa ttctcagctt attttcagtc ttaaggtctt ggtccatggg 180
ttgctcgaga aaatgtggaa aaagtgatgg tctgagtact taatcgtaaa atgcaaatac 240
aaagcttttg tgggtttatt aaagttggta acttttgata gaattttgag gactcttact 300
tgtttgccta catgcctcgc tagtgtttgt ttaaatgcct gtgagaaaata ctttttagtg 360
aaaagctctt tttttttttt ttgttttagt gtctgtttta gtatgatagt aatgtgaaac 420
taatttctga atctctgttt tgagtactgt agagttatga aattggattt ttgctaattc 480
atgtctacat tgtgtccaga ttcttataaa aacagaaact ttgatcttat cttatgggat 540
aattacttta ggttactgat gatgatttgt ataacctaga tgttcgtttc agagaaaaaac 600
ctggaaaata ctgtctactt ccttttctct tctctgtgat ctttcagttt tgattttttc 660
cagagctctt ctcaatatct tcctttgaga agaagtgtgat gatagtaaa tttcttatt 720
ctctggtaca atgatgatag ctatgtgaca ttgctttgat ttggttttga aggttgaaac 780
atgtttctca aagtcacatt accatggaac gtgatgattc cagctgaaaa catggatgcc 840
aaagggctga tgttgaagag agctataact gtatagttac tagaggcggt cgcttccaag 900
aaagcaacca aggagctctg ctactacgtg gcagtcacaa ctttgagacaa gattggagaa 960
ggcaaaaact gggagcacac cgttgaagtt ttgttcccgg taatgttca ggaatgaact 1020
ttcaagatct tcaaaaggaga gataattcac ggtgtggtgc acaaggtgtt gaagcacggt 1080
gtcttcata ggtgtggtcc aatcgagaat gtttacctct cctacacgaa gtagcccggt 1140
tacaagtata tcctctggaga gaacccgatc ttcataaatg agaagacgtc taggattcag 1200
gttgagacta cagtgaaggt tgttggtatt gggataaagt gtaggaaagt agagagggag 1260
tttcaggcgt tggctagctt ggaaggtgac tatcttgag cattatctga agagttagct 1320
gcttgatttc ttcatgtgat ggcgtttttt ggcaatctct tatgtctata taactcggct 1380
ttagttcatg ttgtgtatga actagtaact actctctagc tgtgcaaaaa atgaaaaaat 1440
tgatctttga atgtaaatga atctccacc ttcaagagga aagattggtc taatttaggt 1500
tttttattt ggc

(2) INFORMATION FOR SEQ ID NO:769:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..178
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498967

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:769:

Met Phe Leu Lys Val Gln Leu Pro Trp Asn Val Met Ile Pro Ala Glu
1 5 10 15
Asn Met Asp Ala Lys Gly Leu Met Leu Lys Arg Ala Ile Leu Val Glu
20 25 30
Leu Leu Glu Ala Phe Ala Ser Lys Lys Ala Thr Lys Glu Leu Gly Tyr
35 40 45
Tyr Val Ala Val Thr Thr Leu Asp Lys Ile Gly Glu Gly Lys Ile Arg
50 55 60
Glu His Thr Gly Glu Val Leu Phe Pro Val Met Phe Ser Gly Met Thr
65 70 75 80
Phe Lys Ile Phe Lys Gly Glu Ile Ile His Gly Val Val His Lys Val
85 90 95
Leu Lys His Gly Val Phe Met Arg Cys Gly Pro Ile Glu Asn Val Tyr
100 105 110
Leu Ser Tyr Thr Lys Met Pro Asp Tyr Lys Tyr Ile Pro Gly Glu Asn
115 120 125
Pro Ile Phe Met Asn Glu Lys Thr Ser Arg Ile Gln Val Glu Thr Thr
130 135 140
Val Arg Val Val Val Ile Gly Ile Lys Trp Met Glu Val Glu Arg Glu
145 150 155 160
Phe Gln Ala Leu Ala Ser Leu Glu Gly Asp Tyr Leu Gly Pro Leu Ser
165 170 175
Glu Glu

(2) INFORMATION FOR SEQ ID NO:770:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..167
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498968

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:770:

Met Ile Pro Ala Glu Asn Met Asp Ala Lys Gly Leu Met Leu Lys Arg
1 5 10 15
Ala Ile Leu Val Glu Leu Leu Glu Ala Phe Ala Ser Lys Lys Ala Thr
20 25 30
Lys Glu Leu Gly Tyr Tyr Val Ala Val Thr Thr Leu Asp Lys Ile Gly
35 40 45
Glu Gly Lys Ile Arg Glu His Thr Gly Glu Val Leu Phe Pro Val Met
50 55 60
Phe Ser Gly Met Thr Phe Lys Ile Phe Lys Gly Glu Ile Ile His Gly
65 70 75 80
Val Val His Lys Val Leu Lys His Gly Val Phe Met Arg Cys Gly Pro
85 90 95
Ile Glu Asn Val Tyr Leu Ser Tyr Thr Lys Met Pro Asp Tyr Lys Tyr

	100		105		110
Ile Pro Gly Glu Asn Pro Ile Phe Met Asn Glu Lys Thr Ser Arg Ile					
115		120		125	
Gln Val Glu Thr Thr Val Arg Val Val Val Ile Gly Ile Lys Trp Met					
130		135		140	
Glu Val Glu Arg Glu Phe Gln Ala Leu Ala Ser Leu Glu Gly Asp Tyr					
145		150		155	160
Leu Gly Pro Leu Ser Glu Glu					

(2) INFORMATION FOR SEQ ID NO:771:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..161
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498969

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:771:

Met Asp Ala Lys Gly Leu Met Leu Lys Arg Ala Ile Leu Val Glu Leu	
1 5 10 15	
Leu Glu Ala Phe Ala Ser Lys Lys Ala Thr Lys Glu Leu Gly Tyr Tyr	
20 25 30	
Val Ala Val Thr Thr Leu Asp Lys Ile Gly Glu Gly Lys Ile Arg Glu	
35 40 45	
His Thr Gly Glu Val Leu Phe Pro Val Met Phe Ser Gly Met Thr Phe	
50 55 60	
Lys Ile Phe Lys Gly Glu Ile Ile His Gly Val Val His Lys Val Leu	
65 70 75 80	
Lys His Gly Val Phe Met Arg Cys Gly Pro Ile Glu Asn Val Tyr Leu	
85 90 95	
Ser Tyr Thr Lys Met Pro Asp Tyr Lys Tyr Ile Pro Gly Glu Asn Pro	
100 105 110	
Ile Phe Met Asn Glu Lys Thr Ser Arg Ile Gln Val Glu Thr Thr Val	
115 120 125	
Arg Val Val Val Ile Gly Ile Lys Trp Met Glu Val Glu Arg Glu Phe	
130 135 140	
Gln Ala Leu Ala Ser Leu Glu Gly Asp Tyr Leu Gly Pro Leu Ser Glu	
145 150 155 160	
Glu	

(2) INFORMATION FOR SEQ ID NO:772:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 695 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..695
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:772:

caactsgagt gttatggcat ggaatccgta tttagggcwg acgaaattga ttcaaccaag	60
aaaaaaactc cacagatatg acaagtttgc tcttggatac gacaacaacc gtaaccacaa	120
aattttgaag ttctctttatg aggggagtc aagaaacgctc attattgatg tttaacgattt	180
tagctctgat tcatggaggg ttcttgatat tgatatagat tggcattgaac tgttttagtca	240
cwtagcysy tswwtgmcgg gaaataactta cttttttggt cgawagggac cacktttgcc	300
tatgctgttt aaacctcywt ctgcgtgttt tgaatatattg actctatctt gtgttagaaa	360

tgagaaactc gctgtgttat acagccacct caacagattt ggcacaatag agatttgtat	420
tgcgactaag attgatccca gtgcagatc atggaccact tttttgagaa ttgatattgac	480
actaatcaat ggtttaccgg ataacttttt tgttcaactct tatgctwcga gctttttctt	540
ckaygakgag aaraakgtcg ytgwkctttt cggkacaaac agatatagag gacgtgagac	600
ctgtcagtac taccagagag ctgtcatcgt tggagatagt ggatacttca aagctgtcaa	660
catcgaaacta gttttcaatt cacagctgca atctt	

(2) INFORMATION FOR SEQ ID NO:773:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..231

(D) OTHER INFORMATION: / Ceres Seq. ID 1498971

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:773:

Asn	Xaa	Ser	Val	Met	Ala	Trp	Asn	Pro	Tyr	Leu	Gly	Xaa	Thr	Lys	Leu
1			5						10					15	
Ile	Gln	Pro	Arg	Lys	Lys	Leu	His	Arg	Tyr	Asp	Lys	Phe	Ala	Leu	Gly
			20					25					30		
Tyr	Asp	Asn	Asn	Arg	Asn	His	Lys	Ile	Leu	Arg	Phe	Leu	Tyr	Glu	Gly
		35					40					45			
Ser	Pro	Arg	Asn	Val	Ile	Ile	Asp	Val	Tyr	Asp	Phe	Ser	Ser	Asp	Ser
		50				55					60				
Trp	Arg	Val	Leu	Asp	Ile	Asp	Ile	Asp	Trp	His	Glu	Leu	Phe	Ser	His
65					70					75					80
Xaa	Ser	Xaa	Xaa	Xaa	Xaa	Gly	Asn	Thr	Tyr	Phe	Phe	Gly	Arg	Xaa	Gly
			85						90				95		
Pro	Xaa	Leu	Pro	Met	Leu	Phe	Lys	Pro	Xaa	Ser	Arg	Arg	Phe	Glu	Tyr
			100					105					110		
Leu	Thr	Leu	Ser	Cys	Val	Arg	Asn	Glu	Lys	Leu	Ala	Val	Leu	Tyr	Ser
			115					120				125			
His	Leu	Asn	Arg	Phe	Gly	Thr	Ile	Glu	Ile	Cys	Ile	Ser	Thr	Lys	Ile
			130			135					140				
Asp	Pro	Ser	Ala	Val	Ser	Trp	Thr	Thr	Phe	Leu	Arg	Ile	Asp	Met	Thr
145					150					155				160	
Leu	Ile	Asn	Gly	Leu	Pro	Asp	Asn	Phe	Phe	Val	His	Ser	Tyr	Ala	Xaa
			165					170					175		
Ser	Phe	Phe	Phe	Xaa	Xaa	Glu	Xaa	Xaa	Val	Xaa	Xaa	Leu	Phe	Xaa	Thr
			180					185					190		
Asn	Arg	Tyr	Arg	Gly	Arg	Glu	Thr	Cys	Gln	Tyr	Tyr	Gln	Arg	Ala	Cys
			195				200						205		
Ile	Val	Gly	Asp	Ser	Gly	Tyr	Phe	Lys	Ala	Val	Asn	Ile	Glu	Leu	Val
			210				215					220			
Phe	Asn	Ser	Gln	Leu	Gln	Ser									
225					230										

(2) INFORMATION FOR SEQ ID NO:774:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 227 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..227

(D) OTHER INFORMATION: / Ceres Seq. ID 1498972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:774:

Met Ala Trp Asn Pro Tyr Leu Gly Xaa Thr Lys Leu Ile Gln Pro Arg

```

1           5           10           15
Lys Lys Leu His Arg Tyr Asp Lys Phe Ala Leu Gly Tyr Asp Asn Asn
20           25           30
Arg Asn His Lys Ile Leu Arg Phe Leu Tyr Glu Gly Ser Pro Arg Asn
35           40           45
Val Ile Ile Asp Val Tyr Asp Phe Ser Ser Asp Ser Trp Arg Val Leu
50           55           60
Asp Ile Asp Ile Asp Trp His Glu Leu Phe Ser His Xaa Ser Xaa Xaa
65           70           75           80
Xaa Xaa Gly Asn Thr Tyr Phe Phe Gly Arg Xaa Gly Pro Xaa Leu Pro
85           90           95
Met Leu Phe Lys Pro Xaa Ser Arg Arg Phe Glu Tyr Leu Thr Leu Ser
100          105          110
Cys Val Arg Asn Glu Lys Leu Ala Val Leu Tyr Ser His Leu Asn Arg
115          120          125
Phe Gly Thr Ile Glu Ile Cys Ile Ser Thr Lys Ile Asp Pro Ser Ala
130          135          140
Val Ser Trp Thr Thr Phe Leu Arg Ile Asp Met Thr Leu Ile Asn Gly
145          150          155          160
Leu Pro Asp Asn Phe Phe Val His Ser Tyr Ala Xaa Ser Phe Phe Phe
165          170          175
Xaa Xaa Glu Xaa Xaa Val Xaa Xaa Leu Phe Xaa Thr Asn Arg Tyr Arg
180          185          190
Gly Arg Glu Thr Cys Gln Tyr Tyr Gln Arg Ala Cys Ile Val Gly Asp
195          200          205
Ser Gly Tyr Phe Lys Ala Val Asn Ile Glu Leu Val Phe Asn Ser Gln
210          215          220
Leu Gln Ser
225

```

(2) INFORMATION FOR SEQ ID NO:775:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..131
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:775:

```

Met Leu Phe Lys Pro Xaa Ser Arg Arg Phe Glu Tyr Leu Thr Leu Ser
1           5           10           15
Cys Val Arg Asn Glu Lys Leu Ala Val Leu Tyr Ser His Leu Asn Arg
20           25           30
Phe Gly Thr Ile Glu Ile Cys Ile Ser Thr Lys Ile Asp Pro Ser Ala
35           40           45
Val Ser Trp Thr Thr Phe Leu Arg Ile Asp Met Thr Leu Ile Asn Gly
50           55           60
Leu Pro Asp Asn Phe Phe Val His Ser Tyr Ala Xaa Ser Phe Phe Phe
65           70           75           80
Xaa Xaa Glu Xaa Xaa Val Xaa Xaa Leu Phe Xaa Thr Asn Arg Tyr Arg
85           90           95
Gly Arg Glu Thr Cys Gln Tyr Tyr Gln Arg Ala Cys Ile Val Gly Asp
100          105          110
Ser Gly Tyr Phe Lys Ala Val Asn Ile Glu Leu Val Phe Asn Ser Gln
115          120          125
Leu Gln Ser
130

```

(2) INFORMATION FOR SEQ ID NO:776:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1266 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1266
(D) OTHER INFORMATION: / Ceres Seq. ID 1498974
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:776:
gaaaatggaa taatgcttgt gacgagagag agagagcgag cgaggaggct agagaatcga 60
gaatcgatct tcgcgcgaacc accctgtott ctcttagctc atcgaaatctc tccgtcgccg 120
tcgatttctc ccgcgcgaaga ggaggctcatg gacgtttctg ctagaaagtc acaaaaagct 180
ggcgcgcaaaa agttgaggag ggaaaaactg aatgagcatt ttgttgaact gggaaatgta 240
ctcgatccag agagacccaa gaatgacaaa gccacgatto tgactgatac tgttcagttg 300
ttgaaagagc tcacatctga agtcaacaaa ctgaaatctg agtacaccgc attgacagat 360
gagtcgcccg agttgacaca ggagaaaaac gacctgagag aagaaaaagac atcgctgaaa 420
tcagatatag agaattctcaa tcttcaatac cagcagagat taagggtcaat gtctccatgg 480
ggagctgcga tggatcacac agtcatgatg gctccaccac cctcctttcc ataccctatg 540
cctattgcta tgcctcccg gtcacatccc atgcatccat caatgccatc ttacacatcc 600
tttgggaacc agaaccctag catgatccca gctccatgct ctacatacat gccctacatg 660
cctcctaata cagtcgttga gcaacaatcc gtgcacatcc cacagaaccc cggtaacctg 720
tctcgggaac ctagagcaaaa ggtttcaaga gagagcagat ctgagaaaagc agaggactcc 780
aacgaagtgt caacacaaact cgaattaaaa acccctggat ctactcttga taaggatata 840
ttgcaaaaggc cagagaagac aaagagatgt aagagaaaaa acaacaacaa ctaaatagaa 900
gaaagctctc attctagcaa gtgttcaatc tctccgagcg tacgagacca cagttcttcc 960
agtagcgtag ctggtggcca aaaacctgat gatgcataat gattcgaaa atcttgatgt 1020
tgatcatctc aagtatccaa gtatcgtttc gatgagtact gtatatagtg ccagtagacaaa 1080
atgcacttag ctggtttaaag cagtgttttg atgcacccgt gcatctgtht tctcgggata 1140
gcattttctc agatgatatt catccttaat aggtctgctt tagttctaaa atccgagta 1200
tttgtaattt ccaagtgtcca aatctactaa ttttattaat cctataaatt aaacaaactt 1260
atatcc
(2) INFORMATION FOR SEQ ID NO:777:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 333 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..333
(D) OTHER INFORMATION: / Ceres Seq. ID 1498975
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:777:
Glu Asn Gly Ile Met Leu Val Ser Arg Glu Arg Glu Arg Ala Arg Arg
1 5 10 15
Leu Glu Asn Arg Glu Ser Ile Phe Ala Glu Pro Pro Cys Leu Leu Leu
20 25 30
Ala His Arg Ile Ser Pro Ser Pro Ser Ile Leu Pro Ala Glu Glu Glu
35 40 45
Val Met Asp Val Ser Ala Arg Lys Ser Gln Lys Ala Gly Arg Glu Lys
50 55 60
Leu Arg Arg Glu Lys Leu Asn Glu His Phe Val Glu Leu Gly Asn Val
65 70 75 80
Leu Asp Pro Glu Arg Pro Lys Asn Asp Lys Ala Thr Ile Leu Thr Asp
85 90 95
Thr Val Gln Leu Leu Lys Glu Leu Thr Ser Glu Val Asn Lys Leu Lys
100 105 110
Ser Glu Tyr Thr Ala Leu Thr Asp Glu Ser Arg Glu Leu Thr Gln Glu
115 120 125
Lys Asn Asp Leu Arg Glu Glu Lys Thr Ser Leu Lys Ser Asp Ile Glu

130 135 140
Asn Leu Asn Leu Gln Tyr Gln Gln Arg Leu Arg Ser Met Ser Pro Trp
145 150 155 160
Gly Ala Ala Met Asp His Thr Val Met Met Ala Pro Pro Pro Ser Phe
165 170 175
Pro Tyr Pro Met Pro Ile Ala Met Pro Pro Gly Ser Ile Pro Met His
180 185 190
Pro Ser Met Pro Ser Tyr Thr Tyr Phe Gly Asn Gln Asn Pro Ser Met
195 200 205
Ile Pro Ala Pro Cys Pro Thr Tyr Met Pro Tyr Met Pro Pro Asn Thr
210 215 220
Val Val Glu Gln Gln Ser Val His Ile Pro Gln Asn Pro Gly Asn Arg
225 230 235 240
Ser Arg Glu Pro Arg Ala Lys Val Ser Arg Glu Ser Arg Ser Glu Lys
245 250 255
Ala Glu Asp Ser Asn Glu Val Ala Thr Gln Leu Glu Leu Lys Thr Pro
260 265 270
Gly Ser Thr Ser Asp Lys Asp Thr Leu Gln Arg Pro Glu Lys Thr Lys
275 280 285
Arg Cys Lys Arg Asn Asn Asn Asn Asn Ser Ile Glu Glu Ser Ser His
290 295 300
Ser Ser Lys Cys Ser Ser Pro Ser Val Arg Asp His Ser Ser Ser
305 310 315 320
Ser Ser Val Ala Gly Gly Gln Lys Pro Asp Asp Ala Lys
325 330

(2) INFORMATION FOR SEQ ID NO:778:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 329 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..329

(D) OTHER INFORMATION: / Ceres Seq. ID 1498976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:778:

Met Leu Val Ser Arg Glu Arg Glu Arg Ala Arg Arg Leu Glu Asn Arg
1 5 10 15
Glu Ser Ile Phe Ala Glu Pro Pro Cys Leu Leu Leu Ala His Arg Ile
20 25 30
Ser Pro Ser Pro Ser Ile Leu Pro Ala Glu Glu Glu Val Met Asp Val
35 40 45
Ser Ala Arg Lys Ser Gln Lys Ala Gly Arg Glu Lys Leu Arg Arg Glu
50 55 60
Lys Leu Asn Glu His Phe Val Glu Leu Gly Asn Val Leu Asp Pro Glu
65 70 75 80
Arg Pro Lys Asn Asp Lys Ala Thr Ile Leu Thr Asp Thr Val Gln Leu
85 90 95
Leu Lys Glu Leu Thr Ser Glu Val Asn Lys Leu Lys Ser Glu Tyr Thr
100 105 110
Ala Leu Thr Asp Glu Ser Arg Glu Leu Thr Gln Glu Lys Asn Asp Leu
115 120 125
Arg Glu Glu Lys Thr Ser Leu Lys Ser Asp Ile Glu Asn Leu Asn Leu
130 135 140
Gln Tyr Gln Gln Arg Leu Arg Ser Met Ser Pro Trp Gly Ala Ala Met
145 150 155 160
Asp His Thr Val Met Met Ala Pro Pro Ser Phe Pro Tyr Pro Met
165 170 175
Pro Ile Ala Met Pro Pro Gly Ser Ile Pro Met His Pro Ser Met Pro
180 185 190

Ser Tyr Thr Tyr Phe Gly Asn Gln Asn Pro Ser Met Ile Pro Ala Pro
195 200 205
Cys Pro Thr Tyr Met Pro Tyr Met Pro Pro Asn Thr Val Val Glu Gln
210 215 220
Gln Ser Val His Ile Pro Gln Asn Pro Gly Asn Arg Ser Arg Glu Pro
225 230 235 240
Arg Ala Lys Val Ser Arg Glu Ser Arg Ser Glu Lys Ala Glu Asp Ser
245 250 255
Asn Glu Val Ala Thr Gln Leu Glu Leu Lys Thr Pro Gly Ser Thr Ser
260 265 270
Asp Lys Asp Thr Leu Gln Arg Pro Glu Lys Thr Lys Arg Cys Lys Arg
275 280 285
Asn Asn Asn Asn Asn Ser Ile Glu Glu Ser Ser His Ser Ser Lys Cys
290 295 300
Ser Ser Ser Pro Ser Val Arg Asp His Ser Ser Ser Ser Val Ala
305 310 315 320
Gly Gly Gln Lys Pro Asp Asp Ala Lys
325

(2) INFORMATION FOR SEQ ID NO:779:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 284 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..284

(D) OTHER INFORMATION: / Ceres Seq. ID 1498977

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:779:

Met Asp Val Ser Ala Arg Lys Ser Gln Lys Ala Gly Arg Glu Lys Leu
1 5 10 15
Arg Arg Glu Lys Leu Asn Glu His Phe Val Glu Leu Gly Asn Val Leu
20 25 30
Asp Pro Glu Arg Pro Lys Asn Asp Lys Ala Thr Ile Leu Thr Asp Thr
35 40 45
Val Gln Leu Leu Lys Glu Leu Thr Ser Glu Val Asn Lys Leu Lys Ser
50 55 60
Glu Tyr Thr Ala Leu Thr Asp Glu Ser Arg Glu Leu Thr Gln Glu Lys
65 70 75 80
Asn Asp Leu Arg Glu Glu Lys Thr Ser Leu Lys Ser Asp Ile Glu Asn
85 90 95
Leu Asn Leu Gln Tyr Gln Gln Arg Leu Arg Ser Met Ser Pro Trp Gly
100 105 110
Ala Ala Met Asp His Thr Val Met Met Ala Pro Pro Pro Phe Pro
115 120 125
Tyr Pro Met Pro Ile Ala Met Pro Pro Gly Ser Ile Pro Met His Pro
130 135 140
Ser Met Pro Ser Tyr Thr Tyr Phe Gly Asn Gln Asn Pro Ser Met Ile
145 150 155 160
Pro Ala Pro Cys Pro Thr Tyr Met Pro Tyr Met Pro Pro Asn Thr Val
165 170 175
Val Glu Gln Gln Ser Val His Ile Pro Gln Asn Pro Gly Asn Arg Ser
180 185 190
Arg Glu Pro Arg Ala Lys Val Ser Arg Glu Ser Arg Ser Glu Lys Ala
195 200 205
Glu Asp Ser Asn Glu Val Ala Thr Gln Leu Glu Leu Lys Thr Pro Gly
210 215 220
Ser Thr Ser Asp Lys Asp Thr Leu Gln Arg Pro Glu Lys Thr Lys Arg
225 230 235 240
Cys Lys Arg Asn Asn Asn Asn Ser Ile Glu Ser Ser His Ser

245 250 255
Ser Lys Cys Ser Ser Ser Pro Ser Val Arg Asp His Ser Ser Ser Ser
260 265 270
Ser Val Ala Gly Gly Gln Lys Pro Asp Asp Ala Lys
275 280

(2) INFORMATION FOR SEQ ID NO:780:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1239

(D) OTHER INFORMATION: / Ceres Seq. ID 1498978

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:780:

gtcaaaagcaa ccaaacacat aaaagagaga ttaatacaaa aagaaagaga aaaaagaaag 60
atatggcagg actcatcaac aagatcggag acgcactcca cattggagga ggcaacaagg 120
aaggtgagca caagaaggaa gaggaacaca agaaacacgt tgacgagcac aagartgggt 180
agcacaaaga aggtattgtt gacaagatca aagacaagat ccacgggtgt gaaggtaaaa 240
gccacgacgg agaaggcaaa agccacgacg gtgagaagaa aaagaagaag gacaagaagg 300
agaagaacaa tcattgatgat ggtcaccaca gcacgacgac tgacacgacg agcgagttaa 360
ggtaggaagg tgaggaggat cgcctgaata aaacagatct ggttctggct attattaatt 420
aatgttgctg tatgttctta tcattctaga gagaggttaa agacaggaga accgtgcatac 480
tatctttgat cttgtcaaca ataccttctt tgtgtctacc actcttatga actctttctt 540
ctttaaagtc ggtctcattc tctctgttct tatcagtggt attcaattct gcgccactgc 600
atttgatat tatgtctcaag ccacgcgcgc tcaggagata tttggccaca ctttcgactc 660
ccttcgcggt attaagtaac tctacaagta caatgtgttc cagatcgggt ttgttctctc 720
cgctggattg acccttttat attacattgc ctttggatgg agaagaaaaa agccgagcgg 780
cagattccag ctctctacct aatgtaaatt tcttcttttg attttatcgt ttatgtttcc 840
tcgtctctgg gatcgatcgc gtgccactga ggattgctgt gtccacaatt ataccgatag 900
tggtctcatg atctgtgcaa gtggtcttat atcataagaa caagcacctg ccaaaaaagc 960
ttctctttct tctgttcttc ttgtctgctg aggtttgttt tcatttcaat tgaattgtaa 1020
attattcttc tttttctctt atcttttctc ctgtatctat tgcttttatt ttgtttgatt 1080
aattacaaga aagatctctt tgcgcgcgtc ttctcatggc ctattgaaat atttcaata 1140
ctttcttgta accattactt ggttgagagt ttgactgtc agaacaatt caggttttgg 1200
agttatttgt gtgtatagtg tgatgacaag agacttcat

(2) INFORMATION FOR SEQ ID NO:781:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..119

(D) OTHER INFORMATION: / Ceres Seq. ID 1498979

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:781:

Val Lys Ala Thr Lys His Ile Lys Glu Arg Phe Asn Thr Lys Glu Arg
1 5 10 15
Glu Lys Arg Lys Ile Trp Gln Asp Ser Ser Thr Arg Ser Glu Thr His
20 25 30
Ser Thr Leu Glu Glu Ala Thr Arg Lys Val Ser Thr Arg Arg Lys Arg
35 40 45
Asn Thr Arg Asn Thr Leu Thr Ser Thr Arg Xaa Val Ser Thr Lys Lys
50 55 60
Val Leu Leu Thr Arg Ser Lys Thr Arg Ser Thr Val Val Lys Val Lys
65 70 75 80
Ala Thr Thr Glu Lys Ala Lys Ala Thr Thr Val Arg Arg Lys Arg Arg

85 95
Arg Thr Arg Arg Arg Asn Ile Met Met Met Val Thr Thr Ala Ala
100 105 110
Ala Val Thr Ala Thr Ala Ser
115

(2) INFORMATION FOR SEQ ID NO:782:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..100
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498980

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:782:

Met Ala Gly Leu Ile Asn Lys Ile Gly Asp Ala Leu His Ile Gly Gly
1 5 10 15
Gly Asn Lys Glu Gly Glu His Lys Lys Glu Glu Glu His Lys Lys His
20 25 30
Val Asp Glu His Lys Xaa Gly Glu His Lys Glu Gly Ile Val Asp Lys
35 40 45
Ile Lys Asp Lys Ile His Gly Gly Glu Gly Lys Ser His Asp Gly Glu
50 55 60
Gly Lys Ser His Asp Gly Glu Lys Lys Lys Lys Lys Asp Lys Lys Glu
65 70 75 80
Lys Lys His His Asp Asp Gly His His Ser Ser Ser Asp Ser Asp
85 90 95
Ser Glu Leu Arg
100

(2) INFORMATION FOR SEQ ID NO:783:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498981

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:783:

Met Asn Ser Phe Leu Phe Asn Val Gly Leu Ile Leu Leu Cys Ser Ile
1 5 10 15
Ser Val Ile Gln Phe Cys Ala Thr Ala Phe Gly Tyr Tyr Ala Gln Ala
20 25 30
Thr Ala Ala Gln Glu Ile Phe Gly His Thr Leu Gln Ser Leu Arg Gly
35 40 45
Ile Lys Tyr Leu Tyr Lys Tyr Asn Val Phe Gln Ile Gly Phe Val Val
50 55 60
Leu Ala Gly Leu Thr Phe Leu Tyr Tyr Ile Ala Phe Gly Trp Arg Arg
65 70 75 80
Lys Lys Pro Ser Gly Arg Phe Gln Leu Ser Thr
85 90

(2) INFORMATION FOR SEQ ID NO:784:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1329

(D) OTHER INFORMATION: / Ceres Seq. ID 1498982

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:784:

agagctctag	aatctctcaa	caatggcgga	atcgatttcc	agaaagctca	gagatgggtg	60
cgaagaaggg	gaactcgcac	cagctctcac	tatagaagaa	actgtagctt	ccctcttcgg	120
actcgatgtc	tcocggctatc	ttctcacaaa	tctatcttct	tcaattttag	ctggaaaaatc	180
ctcgctcgag	ggctcttggt	tgatcacatt	ctcgcgaggc	cttgcgttct	tttgcaattg	240
ttgaagcaaa	aaggaaatcgt	tgtctcttca	tcttctaaat	ggattcgat	tttgggaattg	300
tacaactgac	cattgggagat	gattgatcaa	tcttcaacta	gttttagtga	aggttcaagt	360
ttgattaagt	tacataaagt	tgtgagtgac	ttgaaaaagc	ttttttcttc	aatcattgaa	420
gcagggaagag	agttgggttg	aactgggaag	acacgtttct	gogttgocat	tgattcggta	480
aatgagttgc	taagacattc	agcgatgcca	ttagtttctg	gtcttttaac	agatcttcga	540
agccatgcgc	aaatttccag	tgctcttttg	tcaattgaaca	ctgaccttca	ccaagagaag	600
gtcacaaatg	cgcttgaata	tatatccaca	atgaaagcga	acttagaacc	tttgtgtcca	660
tcttcagatg	ggcgaaggaa	tgctttagaa	aacctctttt	cggttcatca	ggatttcggt	720
aaaggacggt	ttcatgtccg	gtttaaagctt	agaaaaaggac	gtgtgagagt	aatgtctgaa	780
gaatatcatg	ttgatcaatc	ggggataaac	ttttcaccca	tttctctgtg	ggatactggt	840
attgcagcgc	ctaaaaagcct	tttgccctaa	gttcaattca	atctccagtt	gtctgagaaa	900
gaacgggtcg	agaaagaaaa	agttgtgctt	ccttttgagc	accaagatga	tggaaaatcg	960
aacgagagct	atgatgggag	gagatctctt	gtggatggca	agattgagac	aacaccattg	1020
tcgtcaatg	agttgcagac	cgatgtggtt	tcgtcgggtg	aggggtggtg	gatttatatat	1080
ttcagagatt	cagacgatga	gcactcctgat	tctgatgaag	atcctgatga	tgatttggac	1140
atttaaggtt	cttaattttc	acttgtaaga	ccagagaata	gctccagatt	tggttttggc	1200
aatagttggg	atcttagtat	ccaactttgt	acactaaata	gaagatttga	ttggtttatta	1260
gatgtgtatt	acagttataa	ttgttacagt	aatgatctca	ttctctatta	ttcttgagtt	1320
gtttgttgt						

(2) INFORMATION FOR SEQ ID NO:785:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 381 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..381

(D) OTHER INFORMATION: / Ceres Seq. ID 1498983

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:785:

Arg	Ala	Leu	Glu	Ser	Leu	Asn	Asn	Gly	Gly	Ile	Asp	Phe	Gln	Lys	Ala
1			5						10					15	
Gln	Arg	Trp	Trp	Arg	Arg	Arg	Arg	Thr	Arg	Thr	Ser	Ser	His	Tyr	Arg
			20					25					30		
Arg	Asn	Cys	Ser	Phe	Pro	Phe	Arg	Thr	Arg	Cys	Leu	Arg	Leu	Ser	Ser
			35				40					45			
His	Lys	Ser	Ile	Phe	Phe	Asn	Phe	Ser	Trp	Lys	Ile	Leu	Val	Ala	Gly
			50			55					60				
Ser	Cys	Val	Asp	His	Ile	Leu	Ala	Glu	Pro	Ser	Phe	Thr	Leu	Gln	Leu
			65			70			75				80		
Leu	Lys	Gln	Lys	Gly	Ile	Val	Val	Ser	Ser	Ser	Ser	Lys	Trp	Ile	Arg
			85					90					95		
Ile	Leu	Asp	Cys	Tyr	Thr	Asp	Pro	Leu	Gly	Trp	Ile	Asp	Gln	Ser	Ser
			100				105						110		
Thr	Ser	Phe	Ser	Glu	Gly	Ser	Ser	Leu	Ile	Lys	Leu	His	Lys	Cys	Val
			115			120						125			
Ser	Asp	Leu	Lys	Lys	Leu	Phe	Ser	Ser	Ile	Ile	Glu	Ala	Gly	Arg	Glu
	130				135						140				
Leu	Val	Gly	Thr	Gly	Lys	Thr	Arg	Phe	Cys	Val	Ala	Ile	Asp	Ser	Val
145				150					155					160	

Asn Glu Leu Leu Arg His Ser Ala Met Pro Leu Val Ser Gly Leu Leu
165 170 175
Thr Asp Leu Arg Ser His Ala Gln Ile Ser Ser Val Phe Trp Ser Leu
180 185 190
Asn Thr Asp Leu His Gln Glu Lys Val Thr Asn Ala Leu Glu Tyr Ile
195 200 205
Ser Thr Met Lys Ala Asn Leu Glu Pro Leu Cys Pro Ser Ser Asp Gly
210 215 220
Gln Arg Asn Ala Leu Glu Asn Leu Phe Ser Val His Gln Asp Phe Gly
225 230 235 240
Lys Gly Arg Phe His Val Arg Phe Lys Leu Arg Lys Gly Arg Val Arg
245 250 255
Val Met Ser Glu Glu Tyr His Val Asp Gln Ser Gly Ile Asn Phe Ser
260 265 270
Pro Ile Ser Ser Val Asp Thr Val Ile Ala Ala Thr Lys Ser Leu Leu
275 280 285
Pro Lys Val Gln Phe Asn Leu Gln Leu Ser Glu Lys Glu Arg Val Glu
290 295 300
Lys Glu Lys Val Val Leu Pro Phe Glu His Gln Asp Asp Gly Lys Ser
305 310 315 320
Asn Glu Ile Tyr Asp Gly Arg Arg Ser Leu Val Asp Gly Lys Ile Glu
325 330 335
Thr Thr Pro Leu Ser Ser Met Glu Leu Gln Thr Asp Val Val Ser Ser
340 345 350
Gly Lys Gly Glu Ile Ile Tyr Phe Arg Asp Ser Asp Asp Glu His
355 360 365
Pro Asp Ser Asp Glu Asp Pro Asp Asp Asp Leu Asp Ile
370 375 380

(2) INFORMATION FOR SEQ ID NO:786:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..213
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:786:

Met Pro Leu Val Ser Gly Leu Leu Thr Asp Leu Arg Ser His Ala Gln
1 5 10 15
Ile Ser Ser Val Phe Trp Ser Leu Asn Thr Asp Leu His Gln Glu Lys
20 25 30
Val Thr Asn Ala Leu Glu Tyr Ile Ser Thr Met Lys Ala Asn Leu Glu
35 40 45
Pro Leu Cys Pro Ser Ser Asp Gly Gln Arg Asn Ala Leu Asn Leu
50 55 60
Phe Ser Val His Gln Asp Phe Gly Lys Gly Arg Phe His Val Arg Phe
65 70 75 80
Lys Leu Arg Lys Gly Arg Val Arg Val Met Ser Glu Glu Tyr His Val
85 90 95
Asp Gln Ser Gly Ile Asn Phe Ser Pro Ile Ser Ser Val Asp Thr Val
100 105 110
Ile Ala Ala Thr Lys Ser Leu Leu Pro Lys Val Gln Phe Asn Leu Gln
115 120 125
Leu Ser Glu Lys Glu Arg Val Glu Lys Glu Lys Val Val Leu Pro Phe
130 135 140
Glu His Gln Asp Asp Gly Lys Ser Asn Glu Ile Tyr Asp Gly Arg Arg
145 150 155 160
Ser Leu Val Asp Gly Lys Ile Glu Thr Thr Pro Leu Ser Ser Met Glu

	165					170						175	
Leu	Gln	Thr	Asp	Val	Val	Ser	Ser	Gly	Lys	Gly	Glu	Ile	Tyr
			180					185				190	
Phe	Arg	Asp	Ser	Asp	Asp	Glu	His	Pro	Asp	Ser	Asp	Glu	Asp
			195				200					205	
Asp	Asp	Leu	Asp	Ile									
			210										

(2) INFORMATION FOR SEQ ID NO:787:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1944 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1944
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498985

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:787:

tttttttccc	cattttcttta	ctctcttgcc	ctttctcttc	tcactctccg	gcgactgtta	60
cgaggttttta	acactctccg	cgctctctca	gttggtgttg	ttgtttatga	caagatcttg	120
ttctatcccat	taaaacacaaa	gaaatggagg	aaggtcataa	agaaccattg	gtgctaagag	180
ttgaaggatc	acattgttct	ttatcaagaga	tggatgattt	tgatctaaat	cgggctttag	240
agaagccgag	gcagctaaag	atcgaacgga	agagatcggt	tgacgaaagg	tcgatgagcg	300
agttatcgac	tggctatgta	agacaagata	gcattttaga	aatggctcat	tctccgaagt	360
aggtcaatgg	tggaacactcc	tctctctggt	aggaactcct	tcgagcctca	tcogatgggt	420
gcgtgaggctt	gggaagcttt	gagaagggtca	atgggtttct	ttcgtgggtca	accogtttgt	480
accattgcag	ctttatgacca	tgctctcgag	gaggtcttga	actatgatca	ggtgttttga	540
cgtagctttg	taccaaagtgc	attggcggtt	ctgatgaatg	gagagcccga	tatagtgaaa	600
aaactcttgc	tcaagacact	tcagcttcaa	gggtgggaga	aacgggttga	ccggtttcaa	660
cttgggggaag	gggttatgcc	agcgagtttc	aaggtgcttc	atgatccagt	tcgtaaaacc	720
gacacaattta	tgcgggattt	tggagaaagc	gctataggaa	gagtagcacc	ggtggattca	780
ggattctcgt	ggatcatact	tctccgtgct	tacacgaaat	ctacgggaga	ttgactttta	840
tctgagacac	cgaggtgttca	gaggggaatg	aggcttatac	tctctctttg	cttatccgaa	900
ggtttttgata	ctttccctac	gcttctttgt	gctgacgggt	gttctatggt	tgataggaga	960
atgggtgtttt	atggatatcc	aatagagatt	caagctctgt	tttctatggc	attgagatgc	1020
gccttctcga	tgcttaaacc	agacgaggaa	ggctcgagatt	tcatagaaag	gattgtgaag	1080
agacttcaag	cgctgagttt	ccatatgcgc	agttactttt	ggcttgactt	tcaacataac	1140
aacgatatct	ataggtacaa	gacagaggag	tactcaacaca	ccgcggtgaa	caagtccaac	1200
gtgatgccgg	actcgataac	agactggggt	ttcgacttta	tgctctctcc	tgaggagatg	1260
tttgtcgcca	atgtaagccc	ggcccgatg	gatttcaggt	ggtttctctt	aggaaattgt	1320
gtctccatcc	tttctctcct	ggcaactccg	gatcagtcac	tggtctattat	ggacctctct	1380
gagcaccggt	gggaggagct	agtaggcgag	atgcgcctca	agatatgtta	cccttgatcc	1440
gaaagccacg	agtggcgagat	tgttaccggt	tgtgatccta	aaaacacgag	gtggagttac	1500
cacaacgggt	gatcttggcc	agttattgtg	tggacgctga	cggaggcagat	ctcaagactc	1560
ggagcgccct	aaatagcgag	acgtgcgatt	gatctaattg	aatcacggct	acaccgagat	1620
tgtctggccg	aatacatgta	tggttaagcaa	ggaaggtacg	ttggaaaaca	agcaaggaaag	1680
taccagactt	gggtcaatgc	gggttacttg	gttcgcaaaa	tgatgcttga	agatctctca	1740
catattgga	tgatctctct	tgaagaagac	aaacagatga	aacctgttta	caagagatct	1800
gcttcatgga	cttctggaat	ttgttttctt	gttttgtatt	ataatgtcat	ttgatgaagc	1860
attcaaaaga	cccttaatac	gcgagagagt	agttctgttt	gtattttctc	ttgatccaac	1920
tatgggttat	tttcaactga	gcct				

(2) INFORMATION FOR SEQ ID NO:788:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..483

(D) OTHER INFORMATION: / Ceres Seq. ID 1498986

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:788:

Met	Val	Asp	Thr	Pro	Leu	Ser	Val	Arg	Asn	Ser	Phe	Glu	Pro	His	Pro
1				5					10				15		
Met	Val	Ala	Glu	Ala	Trp	Glu	Ala	Leu	Arg	Arg	Ser	Met	Val	Phe	Phe
			20					25				30			
Arg	Gly	Gln	Pro	Val	Gly	Thr	Ile	Ala	Tyr	Asp	His	Ala	Ser	Glu	
		35				40					45				
Glu	Val	Leu	Asn	Tyr	Asp	Gln	Val	Phe	Val	Arg	Asp	Phe	Val	Pro	Ser
		50				55					60				
Ala	Leu	Ala	Phe	Leu	Met	Asn	Gly	Glu	Pro	Asp	Ile	Val	Lys	Asn	Phe
65					70					75				80	
Leu	Leu	Lys	Thr	Leu	Gln	Leu	Gln	Gly	Trp	Glu	Lys	Arg	Val	Asp	Arg
			85						90				95		
Phe	Lys	Leu	Gly	Glu	Gly	Val	Met	Pro	Ala	Ser	Phe	Lys	Val	Leu	His
		100						105					110		
Asp	Pro	Val	Arg	Lys	Thr	Asp	Thr	Ile	Ile	Ala	Asp	Phe	Gly	Glu	Ser
		115					120					125			
Ala	Ile	Gly	Arg	Val	Ala	Pro	Val	Asp	Ser	Gly	Phe	Trp	Trp	Ile	Ile
		130				135					140				
Leu	Leu	Arg	Ala	Tyr	Thr	Lys	Ser	Thr	Gly	Asp	Leu	Thr	Leu	Ser	Glu
145				150						155				160	
Thr	Pro	Glu	Cys	Gln	Arg	Gly	Met	Arg	Leu	Ile	Leu	Ser	Leu	Cys	Leu
			165						170					175	
Ser	Glu	Gly	Phe	Asp	Thr	Phe	Pro	Thr	Leu	Leu	Cys	Ala	Asp	Gly	Cys
			180					185					190		
Ser	Met	Val	Asp	Arg	Arg	Met	Gly	Val	Tyr	Gly	Tyr	Pro	Ile	Glu	Ile
		195					200					205			
Gln	Ala	Leu	Phe	Phe	Met	Ala	Leu	Arg	Cys	Ala	Leu	Ser	Met	Leu	Lys
		210				215					220				
Pro	Asp	Glu	Glu	Gly	Arg	Asp	Phe	Ile	Glu	Arg	Ile	Val	Lys	Arg	Leu
225				230						235				240	
His	Ala	Leu	Ser	Phe	His	Met	Arg	Ser	Tyr	Phe	Trp	Leu	Asp	Phe	Gln
			245						250					255	
Gln	Leu	Asn	Asp	Ile	Tyr	Arg	Tyr	Lys	Thr	Glu	Glu	Tyr	Ser	His	Thr
		260						265					270		
Ala	Val	Asn	Lys	Phe	Asn	Val	Met	Pro	Asp	Ser	Ile	Pro	Asp	Trp	Val
		275					280					285			
Phe	Asp	Phe	Met	Pro	Leu	Arg	Gly	Gly	Tyr	Phe	Val	Gly	Asn	Val	Ser
		290					295				300				
Pro	Ala	Arg	Met	Asp	Phe	Arg	Trp	Phe	Ser	Leu	Gly	Asn	Cys	Val	Ser
305				310						315				320	
Ile	Leu	Ser	Ser	Leu	Ala	Thr	Pro	Asp	Gln	Ser	Met	Ala	Ile	Met	Asp
			325						330					335	
Leu	Leu	Glu	His	Arg	Trp	Glu	Glu	Leu	Val	Gly	Glu	Met	Pro	Leu	Lys
			340					345					350		
Ile	Cys	Tyr	Pro	Cys	Ile	Glu	Ser	His	Glu	Trp	Arg	Ile	Val	Thr	Gly
		355					360					365			
Cys	Asp	Pro	Lys	Asn	Thr	Arg	Trp	Ser	Tyr	His	Asn	Gly	Gly	Ser	Trp
	370					375					380				
Pro	Val	Leu	Leu	Trp	Thr	Leu	Thr	Glu	Ala	Cys	Ile	Lys	Thr	Gly	Arg
385					390					395				400	
Pro	Gln	Ile	Ala	Arg	Arg	Ala	Ile	Asp	Leu	Ile	Glu	Ser	Arg	Leu	His
			405					410						415	
Arg	Asp	Cys	Trp	Pro	Glu	Tyr	Tyr	Asp	Gly	Lys	Gln	Gly	Arg	Tyr	Val
		420						425				430			
Gly	Lys	Gln	Ala	Arg	Lys	Tyr	Gln	Thr	Trp	Ser	Ile	Ala	Gly	Tyr	Leu
		435					440					445			
Val	Ala	Lys	Met	Met	Leu	Glu	Asp	Pro	Ser	His	Ile	Gly	Met	Ile	Ser
		450				455						460			

Leu Glu Glu Asp Lys Gln Met Lys Pro Val Ile Lys Arg Ser Ala Ser
465 470 475 480
Trp Thr Cys

(2) INFORMATION FOR SEQ ID NO:789:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 467 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..467

(D) OTHER INFORMATION: / Ceres Seq. ID 1498987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:789:

Met	Val	Ala	Glu	Ala	Trp	Glu	Ala	Leu	Arg	Arg	Ser	Met	Val	Phe	Phe		
1				5					10					15			
Arg	Gly	Gln	Pro	Val	Gly	Thr	Ile	Ala	Ala	Tyr	Asp	His	Ala	Ser	Glu		
			20					25					30				
Glu	Val	Leu	Asn	Tyr	Asp	Gln	Val	Phe	Val	Arg	Asp	Phe	Val	Pro	Ser		
		35				40					45						
Ala	Leu	Ala	Phe	Leu	Met	Asn	Gly	Glu	Pro	Asp	Ile	Val	Lys	Asn	Phe		
		50				55				60							
Leu	Leu	Lys	Thr	Leu	Gln	Leu	Gln	Gly	Trp	Glu	Lys	Arg	Val	Asp	Arg		
			70					75						80			
Phe	Lys	Leu	Gly	Glu	Gly	Val	Met	Pro	Ala	Ser	Phe	Lys	Val	Leu	His		
			85					90						95			
Asp	Pro	Val	Arg	Lys	Thr	Asp	Thr	Ile	Ile	Ala	Asp	Phe	Gly	Glu	Ser		
			100					105					110				
Ala	Ile	Gly	Arg	Val	Ala	Pro	Val	Asp	Ser	Gly	Phe	Trp	Trp	Ile	Ile		
			115					120					125				
Leu	Leu	Arg	Ala	Tyr	Thr	Lys	Ser	Thr	Gly	Asp	Leu	Thr	Leu	Ser	Glu		
			130					135					140				
Thr	Pro	Glu	Cys	Gln	Arg	Gly	Met	Arg	Leu	Ile	Leu	Ser	Leu	Cys	Leu		
			145					150						160			
Ser	Glu	Gly	Phe	Asp	Thr	Phe	Pro	Thr	Leu	Leu	Cys	Ala	Asp	Gly	Cys		
			165					170						175			
Ser	Met	Val	Asp	Arg	Arg	Met	Gly	Val	Tyr	Gly	Tyr	Pro	Ile	Glu	Ile		
			180					185					190				
Gln	Ala	Leu	Phe	Phe	Met	Ala	Leu	Arg	Cys	Ala	Leu	Ser	Met	Leu	Lys		
			195					200					205				
Pro	Asp	Glu	Glu	Gly	Arg	Asp	Phe	Ile	Glu	Arg	Ile	Val	Lys	Arg	Leu		
			210					215					220				
His	Ala	Leu	Ser	Phe	His	Met	Arg	Ser	Tyr	Phe	Trp	Leu	Asp	Phe	Gln		
			225					230					235				
Gln	Leu	Asn	Asp	Ile	Tyr	Arg	Tyr	Lys	Thr	Glu	Glu	Tyr	Ser	His	Thr		
			245					250					255				
Ala	Val	Asn	Lys	Phe	Asn	Val	Met	Pro	Asp	Ser	Ile	Pro	Asp	Trp	Val		
			260					265					270				
Phe	Asp	Phe	Met	Pro	Leu	Arg	Gly	Gly	Tyr	Phe	Val	Gly	Asn	Val	Ser		
			275					280					285				
Pro	Ala	Arg	Met	Asp	Phe	Arg	Trp	Phe	Ser	Leu	Gly	Asn	Cys	Val	Ser		
			290					295					300				
Ile	Leu	Ser	Ser	Leu	Ala	Thr	Pro	Asp	Gln	Ser	Met	Ala	Ile	Met	Asp		
			305					310					315				
Leu	Leu	Glu	His	Arg	Trp	Glu	Glu	Leu	Val	Gly	Glu	Met	Pro	Leu	Lys		
			325					330					335				
Ile	Cys	Tyr	Pro	Cys	Ile	Glu	Ser	His	Glu	Trp	Arg	Ile	Val	Thr	Gly		
			340					345					350				
Cys	Asp	Pro	Lys	Asn	Thr	Arg	Trp	Ser	Tyr	His	Asn	Gly	Gly	Ser	Trp		

355	360	365
Pro Val Leu Leu Trp Thr	Leu Thr Glu Ala Cys Ile	Lys Thr Gly Arg
370	375	380
Pro Gln Ile Ala Arg Arg	Ala Ile Asp Leu Ile	Glu Ser Arg Leu His
385	390	395
Arg Asp Cys Trp Pro Glu Tyr Tyr	Asp Gly Lys Gln Gly Arg Tyr Val	400
405	410	415
Gly Lys Gln Ala Arg Lys Tyr Gln Thr Trp Ser	Ile Ala Gly Tyr Leu	420
420	425	430
Val Ala Lys Met Met Leu Glu Asp Pro Ser His	Ile Gly Met Ile Ser	435
435	440	445
Leu Glu Glu Asp Lys Gln Met Lys Pro Val Ile	Lys Arg Ser Ala Ser	450
450	455	460
Trp Thr Cys		
465		

(2) INFORMATION FOR SEQ ID NO:790:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..455
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498988

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:790:

Met Val Phe Phe Arg Gly Gln Pro Val Gly Thr Ile Ala Ala Tyr Asp	
1	5 10 15
His Ala Ser Glu Glu Val Leu Asn Tyr Asp Gln Val Phe Val Arg Asp	
20	25 30
Phe Val Pro Ser Ala Leu Ala Phe Leu Met Asn Gly Glu Pro Asp Ile	
35	40 45
Val Lys Asn Phe Leu Leu Lys Thr Leu Gln Leu Gln Gly Trp Glu Lys	
50	55 60
Arg Val Asp Arg Phe Lys Leu Gly Glu Gly Val Met Pro Ala Ser Phe	
65	70 75 80
Lys Val Leu His Asp Pro Val Arg Lys Thr Asp Thr Ile Ile Ala Asp	
85	90 95
Phe Gly Glu Ser Ala Ile Gly Arg Val Ala Pro Val Asp Ser Gly Phe	
100	105 110
Trp Trp Ile Ile Leu Leu Arg Ala Tyr Thr Lys Ser Thr Gly Asp Leu	
115	120 125
Thr Leu Ser Glu Thr Pro Glu Cys Gln Arg Gly Met Arg Leu Ile Leu	
130	135 140
Ser Leu Cys Leu Ser Glu Gly Phe Asp Thr Phe Pro Thr Leu Leu Cys	
145	150 155 160
Ala Asp Gly Cys Ser Met Val Asp Arg Arg Met Gly Val Tyr Gly Tyr	
165	170 175
Pro Ile Glu Ile Gln Ala Leu Phe Phe Met Ala Leu Arg Cys Ala Leu	
180	185 190
Ser Met Leu Lys Pro Asp Glu Glu Gly Arg Asp Phe Ile Glu Arg Ile	
195	200 205
Val Lys Arg Leu His Ala Leu Ser Phe His Met Arg Ser Tyr Phe Trp	
210	215 220
Leu Asp Phe Gln Gln Leu Asn Asp Ile Tyr Arg Tyr Lys Thr Glu Glu	
225	230 235 240
Tyr Ser His Thr Ala Val Asn Lys Phe Asn Val Met Pro Asp Ser Ile	
245	250 255
Pro Asp Trp Val Phe Asp Phe Met Pro Leu Arg Gly Gly Tyr Phe Val	
260	265 270

Gly Asn Val Ser Pro Ala Arg Met Asp Phe Arg Trp Phe Ser Leu Gly
275 280 285
Asn Cys Val Ser Ile Leu Ser Ser Leu Ala Thr Pro Asp Gln Ser Met
290 295 300
Ala Ile Met Asp Leu Leu Glu His Arg Trp Glu Glu Leu Val Gly Glu
305 310 315 320
Met Pro Leu Lys Ile Cys Tyr Pro Cys Ile Glu Ser His Glu Trp Arg
325 330 335
Ile Val Thr Gly Cys Asp Pro Lys Asn Thr Arg Trp Ser Tyr His Asn
340 345 350
Gly Gly Ser Trp Pro Val Leu Leu Trp Thr Leu Thr Glu Ala Cys Ile
355 360 365
Lys Thr Gly Arg Pro Gln Ile Ala Arg Arg Ala Ile Asp Leu Ile Glu
370 375 380
Ser Arg Leu His Arg Asp Cys Trp Pro Glu Tyr Tyr Asp Gly Lys Gln
385 390 395 400
Gly Arg Tyr Val Gly Lys Gln Ala Arg Lys Tyr Gln Thr Trp Ser Ile
405 410 415
Ala Gly Tyr Leu Val Ala Lys Met Met Leu Glu Asp Pro Ser His Ile
420 425 430
Gly Met Ile Ser Leu Glu Glu Asp Lys Gln Met Lys Pro Val Ile Lys
435 440 445
Arg Ser Ala Ser Trp Thr Cys
450 455

(2) INFORMATION FOR SEQ ID NO:791:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1454
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:791:

ctgggtgaaa	catagaaaag	ttctcttgc	tcaagttaat	gataaaagg	tgagagcaat	60
aaacgctgat	aagccttg	tggtccttg	aattttgaat	ttctcttttc	tatcttaact	120
atagtattgg	tagttgaggg	tgctgctgat	aagttgttgt	aggatttgtt	gctotggctc	180
tggttgtagg	tctatgaaat	caaccatcat	cgtgaatgga	ctgcaacatg	gtatcttcgt	240
cccagtgagg	ttgggagcat	ttgatcatgt	ccaatccgtc	aaggactgaa	gatgacagca	300
aacagctacc	tactgagtgg	gaaattgaaa	aaggtgaagg	aattgaatct	atagttccac	360
atttctcagg	ccttgagaga	gtcagtagtg	gctctgccac	cagctttctgg	cacactgtgt	420
tatcgaaaag	ctcacagctg	acctctatca	actcatcatc	tcccgaagcc	aaacgatgca	480
agcttgcata	agaaagttcc	cctggagatt	cttgcagcaa	catagacttt	gtccaggtga	540
aggctcccac	agctctcgag	gtatccgttg	cctcagctga	atcagatctt	tgtttaaaac	600
taggaaagcg	gacatactct	gaagaatact	ggggtagaaa	atttcagcgg	gttcagcgg	660
tttctatgaa	gtgtgtaact	ccatctgttg	tcgtggggaa	atccaaaatt	ttgtggtcaga	720
gcattgcagt	cccgctgtgc	caaatgtgat	gctgtgaact	ggatctctca	tctgctaagg	780
gttatcatcg	taagcacaaa	gtctgcgaaa	agcattcaaa	gtgcccgaaa	gttagcgtga	840
gtggcctgga	acgtcggttc	gtcccaacagt	gtagcagggt	ccatgctgtg	tctgaattgg	900
atgagaagaa	acgaagctgc	cgaaaacgtc	tttctcatca	taatgcgagg	cgctgtaagg	960
cacaaggaggt	attttcaatg	aatcccgaga	gggtgtatga	togaagacag	catacaataa	1020
tggtgtggaa	tggggtgttc	cttaacgcga	gatctgaaa	aaatgtatga	atggggtaat	1080
aacacttatg	atacaaaagc	tagacaaaag	gaaaaaagct	ttactcttgc	cttccagaga	1140
ggtaattggc	ctgagaccac	gtcggttgct	agtgcagcgc	gtatgtttct	tacatctcaa	1200
acctcaggtg	ggttcccgag	aggaaaagtc	aagtttcaac	ttcatgctga	agatgtggga	1260
gaatactcag	gagttctcca	tgaattctca	gatataccac	gtgctctctc	gttctctgca	1320
acctcttcgg	atcccttcgg	gtgcagccat	tttctctact	ctgttctaat	ctgttctaat	1380
gatgttgatc	caaaatagat	gagtaagtaa	tggtgaattt	gtaaaacctg	tactcagttg	1440
gtggatactt	ttcc					

(2) INFORMATION FOR SEQ ID NO:792:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..284
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498994

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:792:

Met Asp Cys Asn Met Val Ser Ser Ser Gln Trp Asp Trp Glu His Leu
1 5 10 15
Ile Met Ser Asn Pro Ser Arg Thr Glu Asp Asp Ser Lys Gln Leu Pro
20 25 30
Thr Glu Trp Glu Ile Glu Lys Gly Glu Gly Ile Glu Ser Ile Val Pro
35 40 45
His Phe Ser Gly Leu Glu Arg Val Ser Ser Gly Ser Ala Thr Ser Phe
50 55 60
Trp His Thr Ala Val Ser Lys Ser Ser Gln Ser Thr Ser Ile Asn Ser
65 70 75 80
Ser Ser Pro Glu Ala Lys Arg Cys Lys Leu Ala Ser Glu Ser Ser Pro
85 90 95
Gly Asp Ser Cys Ser Asn Ile Asp Phe Val Gln Val Lys Ala Pro Thr
100 105 110
Ala Leu Glu Val Ser Val Ala Ser Ala Glu Ser Asp Leu Cys Leu Lys
115 120 125
Leu Gly Lys Arg Thr Tyr Ser Glu Glu Tyr Trp Gly Arg Asn Asn Asn
130 135 140
Glu Ile Ser Ala Val Ser Met Lys Leu Leu Thr Pro Ser Val Val Ala
145 150 155 160
Gly Lys Ser Lys Leu Cys Gly Gln Ser Met Pro Val Pro Arg Cys Gln
165 170 175
Ile Asp Gly Cys Glu Leu Asp Leu Ser Ser Ala Lys Gly Tyr His Arg
180 185 190
Lys His Lys Val Cys Glu Lys His Ser Lys Cys Pro Lys Val Ser Val
195 200 205
Ser Gly Leu Glu Arg Arg Phe Cys Gln Gln Cys Ser Arg Phe His Ala
210 215 220
Val Ser Glu Phe Asp Glu Lys Lys Arg Ser Cys Arg Lys Arg Leu Ser
225 230 235 240
His His Asn Ala Arg Arg Arg Lys Pro Gln Gly Val Phe Ser Met Asn
245 250 255
Pro Glu Arg Val Tyr Asp Arg Arg Gln His Thr Asn Met Leu Trp Asn
260 265 270
Gly Val Ser Leu Asn Ala Arg Ser Glu Arg Asn Val
275 280

(2) INFORMATION FOR SEQ ID NO:793:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..280
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498995

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:793:

Met Val Ser Ser Ser Ser Trp Asp Trp Glu His Leu Ile Met Ser Asn

1	5	10	15
Pro Ser Arg Thr Glu Asp Asp Ser Lys Gln Leu Pro Thr Glu Trp Glu			
	20	25	30
Ile Glu Lys Gly Glu Gly Ile Glu Ser Ile Val Pro His Phe Ser Gly			
	35	40	45
Leu Glu Arg Val Ser Ser Gly Ser Ala Thr Ser Phe Trp His Thr Ala			
	50	55	60
Val Ser Lys Ser Ser Gln Ser Thr Ser Ile Asn Ser Ser Ser Pro Glu			
	65	70	75
Ala Lys Arg Cys Lys Leu Ala Ser Glu Ser Ser Pro Gly Asp Ser Cys			
	85	90	95
Ser Asn Ile Asp Phe Val Gln Val Lys Ala Pro Thr Ala Leu Glu Val			
	100	105	110
Ser Val Ala Ser Ala Glu Ser Asp Leu Cys Leu Lys Leu Gly Lys Arg			
	115	120	125
Thr Tyr Ser Glu Glu Tyr Trp Gly Arg Asn Asn Asn Glu Ile Ser Ala			
	130	135	140
Val Ser Met Lys Leu Leu Thr Pro Ser Val Val Ala Gly Lys Ser Lys			
	145	150	155
Leu Cys Gly Gln Ser Met Pro Val Pro Arg Cys Gln Ile Asp Gly Cys			
	165	170	175
Glu Leu Asp Leu Ser Ser Ala Lys Gly Tyr His Arg Lys His Lys Val			
	180	185	190
Cys Glu Lys His Ser Lys Cys Pro Lys Val Ser Val Ser Gly Leu Glu			
	195	200	205
Arg Arg Phe Cys Gln Gln Cys Ser Arg Phe His Ala Val Ser Glu Phe			
	210	215	220
Asp Glu Lys Lys Arg Ser Cys Arg Lys Arg Leu Ser His His Asn Ala			
	225	230	235
Arg Arg Arg Lys Pro Gln Gly Val Phe Ser Met Asn Pro Glu Arg Val			
	245	250	255
Tyr Asp Arg Arg Gln His Thr Asn Met Leu Trp Asn Gly Val Ser Leu			
	260	265	270
Asn Ala Arg Ser Glu Arg Asn Val			
	275	280	

(2) INFORMATION FOR SEQ ID NO:794:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..267
- (D) OTHER INFORMATION: / Ceres Seq. ID 1498996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:794:

Met Ser Asn Pro Ser Arg Thr Glu Asp Asp Ser Lys Gln Leu Pro Thr	
1	5
Glu Trp Glu Ile Glu Lys Gly Glu Gly Ile Glu Ser Ile Val Pro His	
	20
Phe Ser Gly Leu Glu Arg Val Ser Ser Gly Ser Ala Thr Ser Phe Trp	
	35
His Thr Ala Val Ser Lys Ser Ser Gln Ser Thr Ser Ile Asn Ser Ser	
	50
Ser Pro Glu Ala Lys Arg Cys Lys Leu Ala Ser Glu Ser Ser Pro Gly	
	65
Asp Ser Cys Ser Asn Ile Asp Phe Val Gln Val Lys Ala Pro Thr Ala	
	85
Leu Glu Val Ser Val Ala Ser Ala Glu Ser Asp Leu Cys Leu Lys Leu	
	100
	105
	110

Gly	Lys	Arg	Thr	Tyr	Ser	Glu	Glu	Tyr	Trp	Gly	Arg	Asn	Asn	Asn	Glu	
		115					120					125				
Ile	Ser	Ala	Val	Ser	Met	Lys	Leu	Leu	Thr	Pro	Ser	Val	Val	Ala	Gly	
		130				135					140					
Lys	Ser	Lys	Leu	Cys	Gly	Gln	Ser	Met	Pro	Val	Pro	Arg	Cys	Gln	Ile	
		145			150					155					160	
Asp	Gly	Cys	Glu	Leu	Asp	Leu	Ser	Ser	Ala	Lys	Gly	Tyr	His	Arg	Lys	
			165						170					175		
His	Lys	Val	Cys	Glu	Lys	His	Ser	Lys	Cys	Pro	Lys	Val	Ser	Val	Ser	
			180					185					190			
Gly	Leu	Glu	Arg	Arg	Phe	Cys	Gln	Gln	Cys	Ser	Arg	Phe	His	Ala	Val	
		195						200								
Ser	Glu	Phe	Asp	Glu	Lys	Lys	Arg	Ser	Cys	Arg	Lys	Arg	Leu	Ser	His	
		210				215					220					
His	Asn	Ala	Arg	Arg	Arg	Lys	Pro	Gln	Gly	Val	Phe	Ser	Met	Asn	Pro	
		225			230					235					240	
Glu	Arg	Val	Tyr	Asp	Arg	Arg	Gln	His	Thr	Asn	Met	Leu	Trp	Asn	Gly	
			245						250						255	
Val	Ser	Leu	Asn	Ala	Arg	Ser	Glu	Arg	Asn	Val						
			260					265								

(2) INFORMATION FOR SEQ ID NO:795:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1631 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1631
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:795:

aagcgcagcag	tgactcttct	tctctctctct	cctccacctc	tgttttaggt	tcttagcact	60
gaattttgat	cagaaggtgt	tgacggtgta	gagcttcacg	aaacataaac	tttcatttct	120
tctagcttct	tgatttgctc	ttaaagggtgc	atgttgaagt	gattgaaagc	gatttacctg	180
tgactttcag	ctcggtcaga	cattatacat	tacactcaac	acgagattgg	aaaggatcgt	240
tgagaattca	aagttcgatt	tgccagctgt	tggaatcacc	aacaacgcaca	acaattacta	300
tgcttctacc	caagactttt	atcaaaaagct	cggggaagaa	ggtacaaaaca	gtcttgttga	360
cagtatgcag	acaagtaagt	ctggagggtc	tgtgtcaatg	tctgtcgata	acagtagcgt	420
tggttcgagt	gatgctctta	ttggccatcc	tggtttgaag	cctatgcgcc	atccctactc	480
tctctcggat	ggccaaaagc	tatttcggcc	aggaataagt	actatgcac	ttaacgatga	540
tgctctagca	caagcgttga	tggtagtagta	gtatccaacc	gagggactgg	tgaactatga	600
agagtggaca	atagatctga	ggaaactaca	tatgggtcct	gcttttgctc	agaggggcttt	660
tgaaaagtta	tacagaggga	cttacaacgg	agaagatgta	gccattaagc	tactcgcagag	720
gtcagatgac	aaacctgaaa	aggcacacaag	cctcgaacag	cagtttcacg	aggaagtctc	780
tatgcttga	tttttgaagc	atcctaactc	cgtaggttt	attggtgcgt	gcattaaaac	840
gatggtgtgg	tgcatcgtga	ctgaatatgc	aaaaggaggg	tctgtcagac	agttcttgac	900
taagagacaa	aaccgagctg	tgcttttgaa	gttagctgtt	atgcaggcgt	tggtgtgtgc	960
cagggttatg	gcttacgtcc	atgagcgcaa	ctttatacac	cgggatctaa	agtcgagataa	1020
cctctctata	tcagctgatac	ggtcocatcaa	gattgtcgat	tttgggtgtg	caagaattga	1080
agttcaaac	gaagggatga	caccagagac	tggaacttac	agatggatgg	caccagagat	1140
gatccagcac	agaccctaca	ctcaaaaagt	ggacgtgtat	agtttggaa	tcgtgctgtg	1200
ggagtgtgatt	acaggctctg	taccgtttcca	gaacatgacg	cggtgttcagg	ctgcattttgc	1260
agatggtgac	agaggagctc	gtccaaacagt	ccagcagat	tgcttctcgt	tgcttggaaga	1320
gatcatgaca	cggttgcgtgg	atgcgggaccc	tgaagtccgt	cctgttttg	cagagattgt	1380
caatcttctg	gaggcggtgg	aaactgagat	aatgacgaat	gtgagaaaag	ccgctttcag	1440
atgtttcgtg	acgcaaccac	tgacagtcga	ctaactctgt	gtgaagaaag	agagaggaga	1500
agaagaggaa	tgaacaaaga	agagaacata	aaagaaaaaa	acagagagag	agagagagaa	1560
agcaagaagg	gctttagata	tatgtaagtt	tgtgtgtgta	tctatctatc	tatatatata	1620
tatccgattg	c					

(2) INFORMATION FOR SEQ ID NO:796:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 412 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..412
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499002
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:796:
Met Leu Glu Asn Pro Lys Phe Asp Leu His Ala Val Gly Asn His Asn
1 5 10 15
Asn Asp Asn Asn Tyr Tyr Ala Phe Thr Gln Asp Phe Tyr Gln Lys Leu
 20 25 30
Gly Glu Glu Gly Thr Asn Met Ser Val Asp Ser Met Gln Thr Ser Asn
 35 40 45
Ala Gly Gly Ser Val Ser Met Ser Val Asp Asn Ser Ser Val Gly Ser
50 55 60
Ser Asp Ala Leu Ile Gly His Pro Gly Leu Lys Pro Met Arg His Pro
65 70 75
Tyr Ser Leu Ser Asp Gly Gln Ser Val Phe Arg Pro Gly Lys Val Thr
 85 90 95
His Ala Leu Asn Asp Asp Ala Leu Ala Gln Ala Leu Met Asp Ser Lys
 100 105 110
Tyr Pro Thr Glu Gly Leu Val Asn Tyr Glu Glu Trp Thr Ile Asp Leu
 115 120 125
Arg Lys Leu His Met Gly Pro Ala Phe Ala Gln Gly Ala Phe Gly Lys
130 135 140
Leu Tyr Arg Gly Thr Tyr Asn Gly Glu Asp Val Ala Ile Lys Leu Leu
145 150 155 160
Glu Arg Ser Asp Ser Asn Pro Glu Lys Ala Gln Ala Leu Glu Gln Gln
 165 170 175
Phe Gln Gln Glu Val Ser Met Leu Ala Phe Leu Lys His Pro Asn Ile
 180 185 190
Val Arg Phe Ile Gly Ala Cys Ile Lys Pro Met Val Trp Cys Ile Val
195 200 205
Thr Glu Tyr Ala Lys Gly Gly Ser Val Arg Gln Phe Leu Thr Lys Arg
210 215 220
Gln Asn Arg Ala Val Pro Leu Lys Leu Ala Val Met Gln Ala Leu Asp
225 230 235
Val Ala Arg Gly Met Ala Tyr Val His Glu Arg Asn Phe Ile His Arg
 245 250 255
Asp Leu Lys Ser Asp Asn Leu Leu Ile Ser Ala Asp Arg Ser Ile Lys
260 265 270
Ile Ala Asp Phe Gly Val Ala Arg Ile Glu Val Gln Thr Glu Gly Met
275 280 285
Thr Pro Glu Thr Gly Thr Tyr Arg Trp Met Ala Pro Glu Met Ile Gln
290 295 300
His Arg Pro Tyr Thr Gln Lys Val Asp Val Tyr Ser Phe Gly Ile Val
305 310 315
Leu Trp Glu Leu Ile Thr Gly Leu Leu Pro Phe Gln Asn Met Thr Ala
 325 330 335
Val Gln Ala Ala Phe Ala Val Val Asn Arg Gly Val Arg Pro Thr Val
 340 345 350
Pro Ala Asp Cys Leu Pro Val Leu Gly Glu Ile Met Thr Arg Cys Trp
355 360 365
Asp Ala Asp Pro Glu Val Arg Pro Cys Phe Ala Glu Ile Val Asn Leu
370 375 380
Leu Glu Ala Ala Glu Thr Glu Ile Met Thr Asn Val Arg Lys Ala Arg
385 390 395 400

```
(2) INFORMATION FOR SEQ ID NO:797:
  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 374 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS:
      (D) TOPOLOGY: linear
  (ii) MOLECULE TYPE: peptide
  (ix) FEATURE:
      (A) NAME/KEY: peptide
      (B) LOCATION: 1..374
      (D) OTHER INFORMATION: / Ceres Seq. ID 1499003
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:797:
```

1	Met	Ser	Val	Asp	Ser	Met	Gln	Thr	Ser	Asn	Ala	Gly	Gly	Ser	Val	Ser
Met	Ser	Val	Asp	Asn	Ser	Ser	Val	Gly	Ser	Ser	Asp	Ala	Leu	Ile	Gly	
			20					25						30		
His	Pro	Gly	Leu	Lys	Pro	Met	Arg	His	Pro	Tyr	Ser	Leu	Ser	Asp	Gly	
		35					40					45				
Gln	Ser	Val	Phe	Arg	Pro	Gly	Lys	Val	Thr	His	Ala	Leu	Asn	Asp	Asp	
		50				55					60					
Ala	Leu	Ala	Gln	Ala	Leu	Met	Asp	Ser	Lys	Tyr	Pro	Thr	Glu	Gly	Leu	
65					70					75				80		
Val	Asn	Tyr	Glu	Glu	Trp	Thr	Ile	Asp	Leu	Arg	Lys	Leu	His	Met	Gly	
			85					90					95			
Pro	Ala	Phe	Ala	Gln	Gly	Ala	Phe	Gly	Lys	Leu	Tyr	Arg	Gly	Thr	Tyr	
			100					105					110			
Asn	Gly	Glu	Asp	Val	Ala	Ile	Lys	Leu	Leu	Glu	Arg	Ser	Asp	Ser	Asn	
			115				120					125				
Pro	Glu	Lys	Ala	Gln	Ala	Leu	Glu	Gln	Gln	Phe	Gln	Gln	Val	Ser		
			130				135				140					
Met	Leu	Ala	Phe	Leu	Lys	His	Pro	Asn	Ile	Val	Arg	Phe	Ile	Gly	Ala	
145					150					155				160		
Cys	Ile	Lys	Pro	Met	Val	Trp	Cys	Ile	Val	Thr	Glu	Tyr	Ala	Lys	Gly	
			165					170					175			
Gly	Ser	Val	Arg	Gln	Phe	Leu	Thr	Lys	Arg	Gln	Asn	Arg	Ala	Val	Pro	
			180					185					190			
Leu	Lys	Leu	Ala	Val	Met	Gln	Ala	Leu	Asp	Val	Ala	Arg	Gly	Met	Ala	
		195					200					205				
Tyr	Val	His	Glu	Arg	Asn	Phe	Ile	His	Arg	Asp	Leu	Lys	Ser	Asp	Asn	
		210				215					220					
Leu	Leu	Ile	Ser	Ala	Asp	Arg	Ser	Ile	Lys	Ile	Ala	Asp	Phe	Gly	Val	
225					230					235				240		
Ala	Arg	Ile	Glu	Val	Gln	Thr	Glu	Gly	Met	Thr	Pro	Glu	Thr	Gly	Thr	
			245					250					255			
Tyr	Arg	Trp	Met	Ala	Pro	Glu	Met	Ile	Gln	His	Arg	Pro	Tyr	Thr	Gln	
			260					265					270			
Lys	Val	Asp	Val	Tyr	Ser	Phe	Gly	Ile	Val	Leu	Trp	Glu	Leu	Ile	Thr	
		275					280					285				
Gly	Leu	Leu	Pro	Phe	Gln	Asn	Met	Thr	Ala	Val	Gln	Ala	Ala	Phe	Ala	
			290			295					300					
Val	Val	Asn	Arg	Gly	Val	Arg	Pro	Thr	Val	Pro	Ala	Asp	Cys	Leu	Pro	
305					310					315				320		
Val	Leu	Gly	Glu	Ile	Met	Thr	Arg	Cys	Trp	Asp	Ala	Asp	Pro	Glu	Val	
			325					330								

- 370
(2) INFORMATION FOR SEQ ID NO:798:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 369 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..369
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499004
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:798:

Met	Gln	Thr	Ser	Asn	Ala	Gly	Gly	Ser	Val	Ser	Met	Ser	Val	Asp	Asn	
1				5				10						15		
Ser	Ser	Val	Gly	Ser	Ser	Asp	Ala	Leu	Ile	Gly	His	Pro	Gly	Leu	Lys	
				20				25						30		
Pro	Met	Arg	His	Pro	Tyr	Ser	Leu	Ser	Asp	Gly	Gln	Ser	Val	Phe	Arg	
				35				40						45		
Pro	Gly	Lys	Val	Thr	His	Ala	Leu	Asn	Asp	Asp	Ala	Leu	Ala	Gln	Ala	
				50				55						60		
Leu	Met	Asp	Ser	Lys	Tyr	Pro	Thr	Glu	Gly	Leu	Val	Asn	Tyr	Glu	Glu	
65				70				75						80		
Trp	Thr	Ile	Asp	Leu	Arg	Lys	Leu	His	Met	Gly	Pro	Ala	Phe	Ala	Gln	
				85				90						95		
Gly	Ala	Phe	Gly	Lys	Leu	Tyr	Arg	Gly	Thr	Tyr	Asn	Gly	Glu	Asp	Val	
				100				105						110		
Ala	Ile	Lys	Leu	Leu	Glu	Arg	Ser	Asp	Ser	Asn	Pro	Glu	Lys	Ala	Gln	
				115				120						125		
Ala	Leu	Glu	Gln	Gln	Phe	Gln	Gln	Glu	Val	Ser	Met	Leu	Ala	Phe	Leu	
				130				135						140		
Lys	His	Pro	Asn	Ile	Val	Arg	Phe	Ile	Gly	Ala	Cys	Ile	Lys	Pro	Met	
145				150				155						160		
Val	Trp	Cys	Ile	Val	Thr	Glu	Tyr	Ala	Lys	Gly	Gly	Ser	Val	Arg	Gln	
				165				170						175		
Phe	Leu	Thr	Lys	Arg	Gln	Asn	Arg	Ala	Val	Pro	Leu	Lys	Leu	Ala	Val	
				180				185						190		
Met	Gln	Ala	Leu	Asp	Val	Ala	Arg	Gly	Met	Ala	Tyr	Val	His	Glu	Arg	
				195				200						205		
Asn	Phe	Ile	His	Arg	Asp	Leu	Lys	Ser	Asp	Asn	Leu	Leu	Ile	Ser	Ala	
210				215				220						225		
Asp	Arg	Ser	Ile	Lys	Ile	Ala	Asp	Phe	Gly	Val	Ala	Arg	Ile	Glu	Val	
225				230				235						240		
Gln	Thr	Glu	Gly	Met	Thr	Pro	Glu	Thr	Gly	Thr	Tyr	Arg	Trp	Met	Ala	
				245				250						255		
Pro	Glu	Met	Ile	Gln	His	Arg	Pro	Tyr	Thr	Gln	Lys	Val	Asp	Val	Tyr	
				260				265						270		
Ser	Phe	Gly	Ile	Val	Leu	Trp	Glu	Leu	Ile	Thr	Gly	Leu	Leu	Pro	Phe	
				275				280						285		
Gln	Asn	Met	Thr	Ala	Val	Gln	Ala	Ala	Phe	Ala	Val	Val	Asn	Arg	Gly	
290				295				300						305		
Val	Arg	Pro	Thr	Val	Pro	Ala	Asp	Cys	Leu	Pro	Val	Leu	Gly	Glu	Ile	
				310				315						320		
Met	Thr	Arg	Cys	Trp	Asp	Ala	Asp	Pro	Glu	Val	Arg	Pro	Cys	Phe	Ala	
				325				330						335		
Glu	Ile	Val	Asn	Leu	Leu	Glu	Ala	Ala	Glu	Thr	Glu	Ile	Met	Thr	Asn	
				340				345						350		
Val	Arg	Lys	Ala	Arg	Phe	Arg	Cys	Cys	Met	Thr	Gln	Pro	Met	Thr	Val	
				355				360						365		

Asp

(2) INFORMATION FOR SEQ ID NO:799:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1182
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499009

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:799:

agattaagtc	tctctcgta	tcttcgagtg	tgagtgagtc	cagagagaga	attagatatt	60
tccgacacga	ggcaaatcc	tagtggtcca	tgccgtcctc	atctgatcac	acggcgaaaga	120
taatcgcagc	caaggcgatt	gtctacacca	tcagatcaga	gatgcgccag	gaagtctgcg	180
gtctatctga	gaacacacgc	aaggtccacc	gactagctgt	agttatttgt	gggagccgaa	240
aggattcaca	gacctatgtg	aatacgaaga	ggaaagcgtg	cgctgaggtt	gggattaagt	300
catttgacgt	gggcctacca	gaggaagttt	ctgaagctga	tcttatttag	aaagtctcat	360
aactaaatcc	aaatccggat	gtccatggca	tattagtcca	actcccatgt	ccgaaccata	420
ttaatgagga	gaatatattg	gggtcaatca	gcattgataa	agatgtcgat	ggcttccatc	480
ctttgaatat	tggttaagcta	gccatgaaag	gcagagaacc	cctctctctt	ccttgacacc	540
caaaagggat	tttggaactc	ctagctagaa	ggcgcgtaaa	gataaagggg	caacgacgag	600
ttgttgtagg	tcggagtaac	attgttggtt	tgcccgcttc	acttcttttg	ctcaaggctg	660
atgtctactgt	cacaactgta	cattctcaca	ccaaggatcc	tgaggctatc	atacgggag	720
ctgacattgt	tattgctgta	tcgggacaag	ccacatgat	taagggcaac	tggtataaag	780
caggggctgc	agtaattgat	gttggaacta	atgcagtcag	cgacccgagc	aagaatcag	840
gataccgggt	gggttgagat	gttgatttcg	cagaagcttc	aaaagtgcga	ggtttcataa	900
ctccggctcc	tggttggtga	ggcccaatga	cagtgccaat	gctctcagg	aacaccgtag	960
acggtgccaa	gcgtgtcttt	ggcgagtaaa	acaatctact	gtatgtaata	aagaacccaa	1020
gagtttctcc	attctgtaat	tgtgtactgt	gcttgacgat	attttccac	tcaataaat	1080
tgaaattggc	gtcccttttg	gattacctta	cattgtctcg	caactagcta	gaacgattat	1140
ttccgcaatt	cagttaaata	caagggtgtc	atcatgtgac	cc		

(2) INFORMATION FOR SEQ ID NO:800:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..299
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:800:

Met	Ala	Ser	Ser	Ser	Asp	His	Thr	Ala	Lys	Ile	Ile	Asp	Gly	Lys	Ala
1				5				10					15		
Ile	Ala	His	Thr	Ile	Arg	Ser	Glu	Ile	Ala	Glu	Glu	Val	Arg	Gly	Leu
			20				25					30			
Ser	Glu	Lys	His	Gly	Lys	Val	Pro	Gly	Leu	Ala	Val	Val	Ile	Val	Gly
		35					40					45			
Ser	Arg	Lys	Asp	Ser	Gln	Thr	Tyr	Val	Asn	Thr	Lys	Arg	Lys	Ala	Cys
		50				55					60				
Ala	Glu	Val	Gly	Ile	Lys	Ser	Phe	Asp	Val	Gly	Leu	Pro	Glu	Glu	Val
65				70						75				80	
Ser	Glu	Ala	Asp	Leu	Ile	Ser	Lys	Val	His	Glu	Leu	Asn	Ser	Asn	Pro
			85					90					95		
Asp	Val	His	Gly	Ile	Leu	Val	Gln	Leu	Pro	Leu	Pro	Lys	His	Ile	Asn
			100				105						110		
Glu	Glu	Asn	Ile	Leu	Gly	Ala	Ile	Ser	Ile	Asp	Lys	Asp	Val	Asp	Gly
		115					120					125			
Phe	His	Pro	Leu	Asn	Ile	Gly	Lys	Leu	Ala	Met	Lys	Gly	Arg	Glu	Pro

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..1542
(D) OTHER INFORMATION: / Ceres Seq. ID 1499012

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:802:

```
cttgcgtttt cgtccacaaa tctttgtcgt ggttttctgc tgtcttcttc tccgtcgaac 60
ttctccgacc acttcgtata gagagagaga gtgacgaaga gtttacggaa tcgaatccaa 120
taatgagtac tgcgtcggtc tttagttcaa tccaaggatg ctggttcaag ggcgaagaag 180
aaattcgtgt agcggaataa cgagccaaga ggccttacttt gggatcccat gtggcttcgc 240
catcttcaat gagcttcaga gtttcageta gtatgtctgt taaacctgaa aaggatatta 300
ggattgttgt tcttgggtca agtggtatca ctgggtctga gatcgttagc ctcttgcgaa 360
atcatccgca ttccaggctc actttgatga ctgctgatag aaaagctggc cagtcgaatg 420
aaaagcgttt cccacactcg agagctcaaa aactacctac tttggtctcs gtaaaaggatg 480
cagatttttc tactgtggat gctgtattct gctgtttacc tcacggaaca actcaggaaa 540
tcacaaagga actgcctact gaattgaaaa tctgttgcct ttcacgggac ttccgggttc 600
gtaatatgac agaatatgaa gaattggtatg gtcagcctca caaggcagta gagttacaga 660
aagaagtgtg gtatgtgtcta acagagatag taaggaggga cataaaaaag gcacgacttg 720
tggtcaaccc aggcgtttac ccgactacga tccaacttcc tcttgttctt ttactaaaag 780
caaatctcat caaacatgaa aacatcatta tcgatgcaaa atctggtggt agtgaggcag 840
gacgtgggtg taaggaggca aatctttact ctgagatagc tgaaggcatt tcttcttatg 900
gtgtccaccg tcactgccat gttcctgaaa ttgaacaggg attatctgat gtgcacagt 960
caaaagtaac agtcagtttt acgccacatc tcactgccaa gatccgtgga atgcaatgca 1020
ctatatatgt ggaaatggct cccgggggta gaaccgaaga ttacaccacg caattgaaga 1080
cgtcttatga gtagtaagaa ttgtcctaaa gtttggaata aggaagtgtt cctcggacac 1140
acaacgttag aggatccaac tattgtcata tgagtgtctt tcttgatgca attcctggaa 1200
gagctatcat aatctcagtg attgataatc ttgtgaaagg agcttcggga caagcgttgc 1260
agaatcttaa catacgtgtg ggaatcccg aaacaaacgg gctcctacac cagccgtttt 1320
tcccttaaaa atcccacttt taaatcgatg accaatctga agctgttagg acgcgaatgt 1380
taagcataaa gatgtgttgt tatatgattc atatttatag acaataaagg ctctctcttt 1440
accattacaa ataaatgggt ttgtgtgttg ttattaaagg ttttgatgaa cctttattct 1500
tgttatctct attttctgaa ttgcaatttt cgtttgagtc gc
```

(2) INFORMATION FOR SEQ ID NO:803:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 441 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..441
(D) OTHER INFORMATION: / Ceres Seq. ID 1499013

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:803:

```
Cys Val Phe Val Pro Gln Ser Leu Ser Trp Phe Ser Ala Val Phe Phe
1 5 10 15
Ser Val Glu Leu Leu Arg Pro Leu Arg Ile Glu Arg Glu Ser Asp Glu
20 25 30
Glu Phe Thr Glu Ser Asn Pro Ile Met Ser Thr Ala Ser Ala Phe Ser
35 40 45
Ser Ile Gln Gly Cys Trp Phe Lys Gly Glu Arg Lys Ile Arg Val Ala
50 55 60
Asp Lys Arg Ala Lys Arg Leu Thr Leu Gly Ser His Val Ala Ser Pro
65 70 75 80
Ser Ser Met Ser Phe Arg Val Ser Ala Ser Ser Ser Val Lys Pro Glu
85 90 95
Lys Asp Ile Arg Ile Gly Leu Leu Gly Ala Ser Gly Tyr Thr Gly Ala
100 105 110
Glu Ile Val Arg Leu Leu Ala Asn His Pro His Phe Gln Val Thr Leu
115 120 125
Met Thr Ala Asp Arg Lys Ala Gly Gln Ser Met Glu Ser Val Phe Pro
```

130	135	140
His Leu Arg Ala Gln Lys Leu Pro Thr Leu Val Xaa Val Lys Asp Ala		
145	150	155
Asp Phe Ser Thr Val Asp Ala Val Phe Cys Cys Leu Pro His Gly Thr		
	165	170
Thr Gln Glu Ile Ile Lys Glu Leu Pro Thr Ala Leu Lys Ile Val Asp		
	180	185
Leu Ser Ala Asp Phe Arg Leu Arg Asn Ile Ala Glu Tyr Glu Glu Trp		
	195	200
Tyr Gly Gln Pro His Lys Ala Val Glu Leu Gln Lys Glu Val Val Tyr		
	210	215
Gly Leu Thr Glu Ile Leu Arg Glu Asp Ile Lys Lys Ala Arg Leu Val		
	225	230
Ala Asn Pro Gly Cys Tyr Pro Thr Thr Ile Gln Leu Pro Leu Val Pro		
	245	250
Leu Leu Lys Ala Asn Leu Ile Lys His Glu Asn Ile Ile Asp Ala		
	260	265
Lys Ser Gly Val Ser Gly Ala Gly Arg Gly Ala Lys Glu Ala Asn Leu		
	275	280
Tyr Ser Glu Ile Ala Glu Gly Ile Ser Ser Tyr Gly Val Thr Arg His		
	290	295
Arg His Val Pro Glu Ile Glu Gln Gly Leu Ser Asp Val Ala Gln Ser		
	305	310
Lys Val Thr Val Ser Phe Thr Pro His Leu Met Pro Met Ile Arg Gly		
	325	330
Met Gln Ser Thr Ile Tyr Val Glu Met Ala Pro Gly Val Arg Thr Glu		
	340	345
Asp Leu His Gln Gln Leu Lys Thr Ser Tyr Glu Asp Glu Glu Phe Val		
	355	360
Lys Val Leu Asp Glu Gly Val Val Pro Arg Thr His Asn Val Arg Gly		
	370	375
Ser Asn Tyr Cys His Met Ser Val Phe Pro Asp Arg Ile Pro Gly Arg		
	385	390
Ala Ile Ile Ile Ser Val Ile Asp Asn Leu Val Lys Gly Ala Ser Gly		
	405	410
Gln Ala Leu Gln Asn Leu Asn Ile Met Leu Gly Tyr Pro Glu Thr Thr		
	420	425
Gly Leu Leu His Gln Pro Leu Phe Pro		
	435	440

(2) INFORMATION FOR SEQ ID NO:804:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..401

(D) OTHER INFORMATION: / Ceres Seq. ID 1499014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:804:

Met Ser Thr Ala Ser Ala Phe Ser Ser Ile Gln Gly Cys Trp Phe Lys	
1	5
Gly Glu Arg Lys Ile Arg Val Ala Asp Lys Arg Ala Lys Arg Leu Thr	10
	20
Leu Gly Ser His Val Ala Ser Pro Ser Ser Met Ser Phe Arg Val Ser	25
	30
Ala Ser Ser Ser Val Lys Pro Glu Lys Asp Ile Arg Ile Gly Leu Leu	35
	40
Gly Ala Ser Gly Tyr Thr Gly Ala Glu Ile Val Arg Leu Leu Ala Asn	45
	50
	55
	60
65	70
	75
	80

His Pro His Phe Gln Val Thr Leu Met Thr Ala Asp Arg Lys Ala Gly
85 90 95
Gln Ser Met Glu Ser Val Phe Pro His Leu Arg Ala Gln Lys Leu Pro
100 105 110
Thr Leu Val Xaa Val Lys Asp Ala Asp Phe Ser Thr Val Asp Ala Val
115 120 125
Phe Cys Cys Leu Pro His Gly Thr Thr Gln Glu Ile Ile Lys Glu Leu
130 135 140
Pro Thr Ala Leu Lys Ile Val Asp Leu Ser Ala Asp Phe Arg Leu Arg
145 150 155 160
Asn Ile Ala Glu Tyr Glu Glu Trp Tyr Gly Gln Pro His Lys Ala Val
165 170 175
Glu Leu Gln Lys Glu Val Val Tyr Gly Leu Thr Glu Ile Leu Arg Glu
180 185 190
Asp Ile Lys Lys Ala Arg Leu Val Ala Asn Pro Gly Cys Tyr Pro Thr
195 200 205
Thr Ile Gln Leu Pro Leu Val Pro Leu Leu Lys Ala Asn Leu Ile Lys
210 215 220
His Glu Asn Ile Ile Ile Asp Ala Lys Ser Gly Val Ser Gly Ala Gly
225 230 235 240
Arg Gly Ala Lys Glu Ala Asn Leu Tyr Ser Glu Ile Ala Glu Gly Ile
245 250 255
Ser Ser Tyr Gly Val Thr Arg His Arg His Val Pro Glu Ile Glu Gln
260 265 270
Gly Leu Ser Asp Val Ala Gln Ser Lys Val Thr Val Ser Phe Thr Pro
275 280 285
His Leu Met Pro Met Ile Arg Gly Met Gln Ser Thr Ile Tyr Val Glu
290 295 300
Met Ala Pro Gly Val Arg Thr Glu Asp Leu His Gln Gln Leu Lys Thr
305 310 315 320
Ser Tyr Glu Asp Glu Glu Phe Val Lys Val Leu Asp Glu Gly Val Val
325 330 335
Pro Arg Thr His Asn Val Arg Gly Ser Asn Tyr Cys His Met Ser Val
340 345 350
Phe Pro Asp Arg Ile Pro Gly Arg Ala Ile Ile Ile Ser Val Ile Asp
355 360 365
Asn Leu Val Lys Gly Ala Ser Gly Gln Ala Leu Gln Asn Leu Asn Ile
370 375 380
Met Leu Gly Tyr Pro Glu Thr Thr Gly Leu Leu His Gln Pro Leu Phe
385 390 395 400
Pro

(2) INFORMATION FOR SEQ ID NO:805:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 359 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..359

(D) OTHER INFORMATION: / Ceres Seq. ID 1499015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:805:

Met Ser Phe Arg Val Ser Ala Ser Ser Ser Val Lys Pro Glu Lys Asp
1 5 10 15
Ile Arg Ile Gly Leu Leu Gly Ala Ser Gly Tyr Thr Gly Ala Glu Ile
20 25 30
Val Arg Leu Leu Ala Asn His Pro His Phe Gln Val Thr Leu Met Thr
35 40 45
Ala Asp Arg Lys Ala Gly Gln Ser Met Glu Ser Val Phe Pro His Leu

50	55	60
Arg Ala Gln Lys Leu Pro Thr Leu Val Xaa Val Lys Asp Ala Asp Phe		
65	70	75
Ser Thr Val Asp Ala Val Phe Cys Cys Leu Pro His Gly Thr Thr Gln		
85	90	95
Glu Ile Ile Lys Glu Leu Pro Thr Ala Leu Lys Ile Val Asp Leu Ser		
100	105	110
Ala Asp Phe Arg Leu Arg Asn Ile Ala Glu Tyr Glu Glu Trp Tyr Gly		
115	120	125
Gln Pro His Lys Ala Val Glu Leu Gln Lys Glu Val Val Tyr Gly Leu		
130	135	140
Thr Glu Ile Leu Arg Glu Asp Ile Lys Lys Ala Arg Leu Val Ala Asn		
145	150	155
Pro Gly Cys Tyr Pro Thr Thr Ile Gln Leu Pro Leu Val Pro Leu Leu		
165	170	175
Lys Ala Asn Leu Ile Lys His Glu Asn Ile Ile Ile Asp Ala Lys Ser		
180	185	190
Gly Val Ser Gly Ala Gly Arg Gly Ala Lys Glu Ala Asn Leu Tyr Ser		
195	200	205
Glu Ile Ala Glu Gly Ile Ser Ser Tyr Gly Val Thr Arg His Arg His		
210	215	220
Val Pro Glu Ile Glu Gln Gly Leu Ser Asp Val Ala Gln Ser Lys Val		
225	230	235
Thr Val Ser Phe Thr Pro His Leu Met Pro Met Ile Arg Gly Met Gln		
245	250	255
Ser Thr Ile Tyr Val Glu Met Ala Pro Gly Val Arg Thr Glu Asp Leu		
260	265	270
His Gln Gln Leu Lys Thr Ser Tyr Glu Asp Glu Glu Phe Val Lys Val		
275	280	285
Leu Asp Glu Gly Val Val Pro Arg Thr His Asn Val Arg Gly Ser Asn		
290	295	300
Tyr Cys His Met Ser Val Phe Pro Asp Arg Ile Pro Gly Arg Ala Ile		
305	310	315
Ile Ile Ser Val Ile Asp Asn Leu Val Lys Gly Ala Ser Gly Gln Ala		
325	330	335
Leu Gln Asn Leu Asn Ile Met Leu Gly Tyr Pro Glu Thr Thr Gly Leu		
340	345	350
Leu His Gln Pro Leu Phe Pro		
355		

(2) INFORMATION FOR SEQ ID NO:806:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1481
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:806:

gcgttacact	acaaactctct	atctctctct	cttcttttct	gctcattttt	gggtaattct	60
tctggtttta	tgttcttctt	cttattactg	actcaacatc	agccaaacgca	aattctttct	120
tgaccatttt	taatagattc	tcttagtcac	tggttggtat	tcaaatgcac	agttgacctc	180
atcttctctt	tcttcgaggt	ttatatacaag	ttactccata	aaccttcgag	cttcaccgaa	240
ctttggcttc	tctgttggtga	attattgtct	attatatctc	caacacgaaa	tcaaaatgcc	300
aagacaacga	gtttcagagt	tgctctcagag	gcaagctcca	aggctgaggt	catcgctcat	360
tactcttgat	tccaatcatt	ccaaccgtct	gatcactacg	gatcaaaagt	ttaagcccgg	420
tggtgacctg	aaatctcttc	gaagcgggtg	acctaacagt	gatccgcttg	gtcagaagaa	480
acttggggga	cgaatatcgg	atctagatgc	gcagtttaga	caacgcgcaa	aggaactgag	540
attgctcaag	gagcagttgg	ctaagtgtga	agctgtggaag	aaacaagctc	aagatgagct	600

tcataagaag	tccaagaanaac	caaaccgcgt	ggctcgagtg	gaggaatctg	caactgaggc	660
tgagagagatt	gatagagacg	aaatccctgg	tgatgtgcag	aaagagactg	atgtgtttga	720
gggtcccggt	gaaaagattg	cagtagaaga	agaagaactg	agaagcgcca	atgacgaaag	780
tgagaaattg	gttgcaaaag	aagatgagat	aaagatgctg	aaagctagac	tctatgacat	840
ggagaaagag	catgaatcac	taggcaaaaga	aaacgagagc	ttgaagaatc	agttgagcga	900
ttcagcttca	gagattttcta	atgtgaaaagc	taatgaagat	gagatggttt	caaaggtgag	960
taggattggg	gaagagtttag	aagaagaacg	agcaaaagacg	gctcacctga	aggagaagct	1020
tgagtccatg	gaagaagcaa	aagatgcttt	agaggctgag	atgaagaagc	tcagggttca	1080
aaccgagcag	tgaggagaag	cagcggtatg	tcgacgacga	gttctttctg	gagagtttga	1140
gatgaattgt	cgggctcgat	ctgggtcaac	tgagaagtat	tatgcaggtg	ggttctttga	1200
cccgctcagct	gggttccatg	atccaccggg	aatggctgat	gattatgatg	atggactggg	1260
aagtggcaag	aggaagagtt	ctgggatgaa	gatgttttgt	gagttgtgga	ggaagaaagg	1320
gcataaagtga	gttacagatt	gtgtggagtg	tcattccaaga	atgggtgtgc	tcaccgtttc	1380
ttctttttat	ttgtctgtat	ttacctgsaa	gtttttgtaa	gtgggtccgc	ttcatcagaa	1440
gctaactatc	aattccaaatc	aattgcaaaa	acaatttcat	g		

(2) INFORMATION FOR SEQ ID NO:807:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 344 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..344

(D) OTHER INFORMATION: / Ceres Seq. ID 1499017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:807:

Met	Pro	Arg	Pro	Arg	Val	Ser	Glu	Leu	Ser	Gln	Arg	Gln	Ala	Pro	Arg
1				5						10				15	
Leu	Arg	Ser	Ser	Ser	Ser	Thr	Ser	Asp	Ser	Asn	His	Ser	Asn	Arg	Leu
			20					25					30		
Ile	Thr	Thr	Asp	Gln	Ser	Phe	Lys	Pro	Gly	Val	Asp	Arg	Lys	Ser	Pro
		35				40					45				
Arg	Ser	Gly	Gly	Pro	Asn	Ser	Asp	Pro	Leu	Gly	Gln	Lys	Lys	Leu	Gly
	50				55					60					
Gly	Arg	Ile	Ser	Asp	Leu	Glu	Ser	Gln	Leu	Gly	Gln	Ala	Gln	Glu	Glu
	65			70				75					80		
Leu	Arg	Leu	Leu	Lys	Glu	Gln	Leu	Ala	Asn	Ala	Glu	Ala	Val	Lys	Lys
			85					90					95		
Gln	Ala	Gln	Asp	Glu	Leu	His	Lys	Lys	Ser	Lys	Lys	Pro	Asn	Pro	Leu
		100						105					110		
Ala	Arg	Val	Glu	Glu	Ser	Ala	Thr	Glu	Ala	Glu	Arg	Ile	Asp	Arg	Asp
		115					120					125			
Glu	Ile	Pro	Gly	Asp	Val	Gln	Lys	Glu	Thr	Asp	Val	Phe	Glu	Val	Pro
	130					135					140				
Val	Glu	Lys	Ile	Ala	Val	Glu	Glu	Glu	Glu	Leu	Arg	Ser	Gly	Asn	Asp
	145				150					155				160	
Glu	Ala	Glu	Lys	Leu	Val	Ala	Lys	Glu	Asp	Glu	Ile	Lys	Met	Leu	Lys
			165					170					175		
Ala	Arg	Leu	Tyr	Asp	Met	Glu	Lys	Glu	His	Glu	Ser	Leu	Gly	Lys	Glu
		180						185					190		
Asn	Glu	Ser	Leu	Lys	Asn	Gln	Leu	Ser	Asp	Ser	Ala	Ser	Glu	Ile	Ser
		195					200					205			
Asn	Val	Lys	Ala	Asn	Glu	Asp	Glu	Met	Val	Ser	Lys	Val	Ser	Arg	Ile
		210				215					220				
Gly	Glu	Glu	Leu	Glu	Glu	Ser	Arg	Ala	Lys	Thr	Ala	His	Leu	Lys	Glu
	225				230					235				240	
Lys	Leu	Glu	Ser	Met	Glu	Glu	Ala	Lys	Asp	Ala	Leu	Glu	Ala	Glu	Met
			245					250					255		
Lys	Lys	Leu	Arg	Val	Gln	Thr	Glu	Gln	Trp	Arg	Lys	Ala	Ala	Asp	Ala
		260					265						270		

Ala Ala Ala Val Leu Ser Gly Glu Phe Glu Met Asn Gly Arg Asp Arg
275 280 285
Ser Gly Ser Thr Glu Lys Tyr Tyr Ala Gly Gly Phe Phe Asp Pro Ser
290 295 300
Ala Gly Phe Met Asp Pro Pro Gly Met Ala Asp Asp Tyr Asp Asp Gly
305 310 315 320
Leu Gly Ser Gly Lys Arg Lys Ser Ser Gly Met Lys Met Phe Gly Glu
325 330 335
Leu Trp Arg Lys Lys Gly Gln Lys
340

(2) INFORMATION FOR SEQ ID NO:808:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 559 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..559
(D) OTHER INFORMATION: / Ceres Seq. ID 1499021

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:808:

ggcttttttc aaccactctt ggctctcttc tccactcacc gaaactccca cttctctttt 60
tcctccatct ccacacccaa aatccttgaa actctcactt ttccgaactc ggagcaactc 120
gtctcaccg gaccgctcgt cagagggttg gctcgatgtg gatccggtga agctcgcatt 180
gaagaagacc gaagcttata agaaatcgaa atcagagcaa aaagaaccag agaaaaacgc 240
cgggcagcag gaattgcgcg tctctgttaa ggctgctatg caaaaagcca atgcttataa 300
gaaaaggaaa ggacttgaaa ctgatgcagt cgcaaaagct aaaccagta atacagagca 360
aagttttggt agattaacaa ataaggttgt tgaagataat gatgttaaga agaaagaatt 420
gaaagctcc agcattgatt tcatggggct tggctttgct gataagaaga gcacaagggg 480
gcttcacgc ggacttgttc ctgttggtga ctatcttcct gaaggagact tacctgaggt 540
ggagtttatt gttggtgat

(2) INFORMATION FOR SEQ ID NO:809:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 186 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..186
(D) OTHER INFORMATION: / Ceres Seq. ID 1499022

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:809:

Ala Ser Phe Asn His Ser Trp Leu Ser Ser Pro Leu Thr Glu Thr Pro
1 5 10 15
Thr Phe Phe Phe Pro Pro Ser Pro His Pro Lys Ser Leu Lys Leu Ser
20 25 30
Leu Phe Arg Thr Arg Ser Asn Ser Ser Pro Asp Arg Ser Ser Glu
35 40 45
Val Glu Leu Asp Val Asp Pro Val Lys Leu Ala Leu Lys Lys Ala Glu
50 55 60
Ala Tyr Lys Lys Ser Lys Ser Glu Gln Lys Glu Pro Glu Lys Asn Ala
65 70 75 80
Gly Asp Glu Glu Leu Pro Leu Ser Val Lys Ala Ala Met Gln Lys Ala
85 90 95
Asn Ala Tyr Lys Lys Arg Lys Gly Leu Gly Thr Asp Ala Val Ala Lys
100 105 110
Ala Lys Pro Ser Asn Thr Glu Gln Ser Phe Val Arg Leu Thr Asn Lys
115 120 125
Val Val Glu Asp Asn Asp Val Lys Lys Lys Glu Leu Lys Val Ser Ser

130 135 140
Ile Asp Phe Met Gly Leu Gly Phe Ala Asp Lys Lys Ser Thr Arg Gly
145 150 155 160
Leu Pro Ala Gly Leu Val Pro Val Val Asp Tyr Leu Pro Glu Gly Asp
165 170 175
Leu Pro Glu Val Glu Phe Ile Val Gly Asp
180 185

(2) INFORMATION FOR SEQ ID NO:810:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499023

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:810:

Met Gln Lys Ala Asn Ala Tyr Lys Lys Arg Lys Gly Leu Gly Thr Asp
1 5 10 15
Ala Val Ala Lys Ala Lys Pro Ser Asn Thr Glu Gln Ser Phe Val Arg
20 25 30
Leu Thr Asn Lys Val Val Glu Asp Asn Asp Val Lys Lys Lys Glu Leu
35 40 45
Lys Val Ser Ser Ile Asp Phe Met Gly Leu Gly Phe Ala Asp Lys Lys
50 55 60
Ser Thr Arg Gly Leu Pro Ala Gly Leu Val Pro Val Val Asp Tyr Leu
65 70 75 80
Pro Glu Gly Asp Leu Pro Glu Val Glu Phe Ile Val Gly Asp
85 90

(2) INFORMATION FOR SEQ ID NO:811:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1527 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1527
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499024

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:811:

aacgcattat tgacacgtgt cttttcattt ctctctctcc ggcgttttct ctccgccggt 60
tcgccacggt acgtgacaat gtctgtttct ctctccgccg cctctcaatt actctgttcc 120
tcaccacagat tctctcttcc ccccgccgct acctctctgt cctcgctccc tctctgttct 180
cttctctctc ctacatcgcc acattctctt ggaagcgctg catctctctc tctgttctct 240
cactctctcc tcgtgtctca gaaaaaacat ccatgaatg ggacgagcac gaggatgatt 300
tcacaaaaat gtcccgcttc tgatgcagct caattgataa gcgctaaga agatatcaaa 360
gttctctccc ggactaagtt ttgccatccc atcttggtta gattgggggt gcacagtgtct 420
ggtaattata acaagaatat tgaggagtgg ccactgagag gtggagctaa ttgaactctt 480
aggtttgagg ctgagcttaa gcactgtgc aatgctgttc tgcttaatgc tttaaagctc 540
attcagcttc tcaaaagacaa gtatcctaac atctcttatg cggacttatt ccagttagct 600
agtgccacag caatagagga ggctggtggt cctgatattc ccatgaaata tgggagagtt 660
gatgttgtag cactgaaca gtgtccagaa gaaggaagac tccctgatgc tggacctctc 720
tcaccagctg atcatttgag agatgttttc tacagaatgg gacttgatga caaggaataa 780
gttgcttgtt ctggtgcaca tacccttagg agagccagac cagaccgtag tggttgggga 840
aaacctgaga caaagtacac gaaaactgga cctggagaag caggaggaca gtcattggaca 900
gtgaaattgc tcaagttcga caactcttat tcaagagata tcaaaagaaa gagggacgac 960
gatcttctgc tgttaccac tgatgcggcg ctatttgaag atccttcatt caagaactat 1020
gcagagaagt atgctgaaga tgtgctgc tttttcaagg actacgctga agcccatgcc 1080

(2) INFORMATION FOR SEQ ID NO:812:

(A) LENGTH: 452 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptide

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..452

(D) OTHER INFORMATION: / Ceres Seq. ID 1499025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:812:

Asn	Ala	Leu	Leu	Thr	Arg	Val	Phe	Ser	Phe	Leu	Phe	Phe	Arg	Arg	Phe
1			5					10					15		
Leu	Ser	Ala	Val	Ser	Pro	Pro	Tyr	Val	Thr	Met	Ser	Val	Ser	Leu	Ser
			20					25					30		
Ala	Ala	Ser	His	Leu	Leu	Cys	Ser	Ser	Thr	Arg	Val	Ser	Leu	Ser	Pro
			35				40					45			
Ala	Val	Thr	Ser	Ser	Ser	Ser	Ser	Pro	Val	Val	Ala	Leu	Ser	Ser	Ser
			50				55				60				
Thr	Ser	Pro	His	Ser	Leu	Gly	Ser	Val	Ala	Ser	Ser	Ser	Leu	Phe	Pro
65					70					75				80	
His	Ser	Ser	Xaa	Val	Leu	Gln	Lys	Lys	His	Pro	Ile	Asn	Gly	Thr	Ser
			85						90				95		
Thr	Arg	Met	Ile	Ser	Pro	Lys	Cys	Ala	Ala	Ser	Asp	Ala	Ala	Gln	Leu
			100					105				110			
Ile	Ser	Ala	Lys	Glu	Asp	Ile	Lys	Val	Leu	Leu	Arg	Thr	Lys	Phe	Cys
			115				120				125				
His	Pro	Ile	Leu	Val	Arg	Leu	Gly	Trp	His	Asp	Ala	Gly	Thr	Tyr	Asn
			130				135				140				
Lys	Asn	Ile	Glu	Glu	Trp	Pro	Leu	Arg	Gly	Gly	Ala	Asn	Gly	Ser	Leu
145					150					155					160
Arg	Phe	Glu	Ala	Glu	Leu	Lys	His	Ala	Ala	Asn	Ala	Gly	Leu	Leu	Asn
			165						170				175		
Ala	Leu	Lys	Leu	Ile	Gln	Pro	Leu	Lys	Asp	Lys	Tyr	Pro	Asn	Ile	Ser
			180					185					190		
Tyr	Ala	Asp	Leu	Phe	Gln	Leu	Ala	Ser	Ala	Thr	Ala	Ile	Glu	Glu	Ala
			195				200				205				
Gly	Gly	Pro	Asp	Ile	Pro	Met	Lys	Tyr	Gly	Arg	Val	Asp	Val	Val	Ala
			210			215					220				
Pro	Glu	Gln	Cys	Pro	Glu	Glu	Gly	Arg	Leu	Pro	Asp	Ala	Gly	Pro	Pro
225					230				235					240	
Ser	Pro	Ala	Asp	His	Leu	Arg	Asp	Val	Phe	Tyr	Arg	Met	Gly	Leu	Asp
			245						250				255		
Asp	Lys	Glu	Ile	Val	Ala	Leu	Ser	Gly	Ala	His	Thr	Leu	Gly	Arg	Ala
			260					265					270		
Arg	Pro	Asp	Arg	Ser	Gly	Trp	Gly	Lys	Pro	Glu	Thr	Lys	Tyr	Thr	Lys
			275				280					285			
Thr	Gly	Pro	Gly	Glu	Ala	Gly	Gly	Gln	Ser	Trp	Thr	Val	Lys	Trp	Leu
			290				295					300			
Lys	Phe	Asp	Asn	Ser	Tyr	Phe	Lys	Asp	Ile	Lys	Glu	Lys	Arg	Asp	Asp
305					310					315				320	
Asp	Leu	Leu	Val	Leu	Pro	Thr	Asp	Ala	Ala	Leu	Phe	Glu	Asp	Pro	Ser

	325		330		335
Phe Lys Asn Tyr	Ala Glu Lys Tyr	Ala Glu Asp Val	Ala Ala Phe Phe		
	340		345		350
Lys Asp Tyr Ala	Glu Ala His Ala Lys Leu Ser	Asn Leu Gly Ala Lys			
	355		360		365
Phe Asp Pro Pro	Glu Gly Ile Val Ile Glu Asn Val	Pro Glu Lys Phe			
	370		375		380
Val Ala Ala Lys	Tyr Ser Thr Gly Lys Lys Glu Leu Ser	Asp Ser Met			
	385		390		395
Lys Lys Lys Ile	Arg Ala Glu Tyr Glu Ala Ile Gly Gly Ser	Pro Asp			
	405		410		415
Lys Pro Leu Pro	Thr Asn Tyr Phe Leu Asn Ile Ile Ile Ala Ile Gly				
	420		425		430
Val Leu Val Leu	Leu Ser Thr Leu Phe Gly Gly Asn Asn Asn Ser Asp				
	435		440		445
Phe Ser Gly Phe					
	450				

(2) INFORMATION FOR SEQ ID NO:813:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..426

(D) OTHER INFORMATION: / Ceres Seq. ID 1499026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:813:

Met Ser Val Ser	Leu Ser Ala Ala Ser	His Leu Leu Cys Ser Ser Thr
1	5	10 15
Arg Val Ser Leu Ser	Pro Ala Val Thr Ser Ser Ser Ser Ser Pro Val	
	20	25 30
Val Ala Leu Ser Ser Ser	Thr Ser Pro His Ser Leu Gly Ser Val Ala	
	35	40 45
Ser Ser Ser Leu Phe Pro	His Ser Ser Xaa Val Leu Gln Lys Lys His	
	50	55 60
Pro Ile Asn Gly Thr Ser	Thr Arg Met Ile Ser Pro Lys Cys Ala Ala	
	65	70 75
Ser Asp Ala Ala Gln Leu	Ile Ser Ala Lys Glu Asp Ile Lys Val Leu	
	85	90 95
Leu Arg Thr Lys Phe Cys	His Pro Ile Leu Val Arg Leu Gly Trp His	
	100	105 110
Asp Ala Gly Thr Tyr Asn	Lys Asn Ile Glu Glu Trp Pro Leu Arg Gly	
	115	120 125
Gly Ala Asn Gly Ser Leu	Arg Phe Glu Ala Glu Leu Lys His Ala Ala	
	130	135 140
Asn Ala Gly Leu Leu Asn	Ala Leu Lys Leu Ile Gln Pro Leu Lys Asp	
	145	150 155
Lys Tyr Pro Asn Ile Ser	Tyr Ala Asp Leu Phe Gln Leu Ala Ser Ala	
	165	170 175
Thr Ala Ile Glu Glu Ala	Gly Gly Pro Asp Ile Pro Met Lys Tyr Gly	
	180	185 190
Arg Val Asp Val Val Ala	Pro Glu Gln Cys Pro Glu Glu Gly Arg Leu	
	195	200 205
Pro Asp Ala Gly Pro Pro	Ser Pro Ala Asp His Leu Arg Asp Val Phe	
	210	215 220
Tyr Arg Met Gly Leu Asp	Asp Lys Glu Ile Val Ala Leu Ser Gly Ala	
	225	230 235
His Thr Leu Gly Arg Ala	Arg Pro Asp Arg Ser Gly Trp Gly Lys Pro	
	245	250 255

Glu Thr Lys Tyr Thr Lys Thr Gly Pro Gly Glu Ala Gly Gly Gln Ser
260 265 270
Trp Thr Val Lys Trp Leu Lys Phe Asp Asn Ser Tyr Phe Lys Asp Ile
275 280 285
Lys Glu Lys Arg Asp Asp Asp Leu Leu Val Leu Pro Thr Asp Ala Ala
290 295 300
Leu Phe Glu Asp Pro Ser Phe Lys Asn Tyr Ala Glu Lys Tyr Ala Glu
305 310 315 320
Asp Val Ala Ala Phe Phe Lys Asp Tyr Ala Glu Ala His Ala Lys Leu
325 330 335
Ser Asn Leu Gly Ala Lys Phe Asp Pro Pro Glu Gly Ile Val Ile Glu
340 345 350
Asn Val Pro Glu Lys Phe Val Ala Ala Lys Tyr Ser Thr Gly Lys Lys
355 360 365
Glu Leu Ser Asp Ser Met Lys Lys Lys Ile Arg Ala Glu Tyr Glu Ala
370 375 380
Ile Gly Gly Ser Pro Asp Lys Pro Leu Pro Thr Asn Tyr Phe Leu Asn
385 390 395 400
Ile Ile Ile Ala Ile Gly Val Leu Val Leu Ser Thr Leu Phe Gly
405 410 415
Gly Asn Asn Asn Ser Asp Phe Ser Gly Phe
420 425

(2) INFORMATION FOR SEQ ID NO:814:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..354
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:814:

Met Ile Ser Pro Lys Cys Ala Ala Ser Asp Ala Ala Gln Leu Ile Ser
1 5 10 15
Ala Lys Glu Asp Ile Lys Val Leu Leu Arg Thr Lys Phe Cys His Pro
20 25 30
Ile Leu Val Arg Leu Gly Trp His Asp Ala Gly Thr Tyr Asn Lys Asn
35 40 45
Ile Glu Glu Trp Pro Leu Arg Gly Gly Ala Asn Gly Ser Leu Arg Phe
50 55 60
Glu Ala Glu Leu Lys His Ala Ala Asn Ala Gly Leu Leu Asn Ala Leu
65 70 75 80
Lys Leu Ile Gln Pro Leu Lys Asp Lys Tyr Pro Asn Ile Ser Tyr Ala
85 90 95
Asp Leu Phe Gln Leu Ala Ser Ala Thr Ala Ile Glu Glu Ala Gly Gly
100 105 110
Pro Asp Ile Pro Met Lys Tyr Gly Arg Val Asp Val Val Ala Pro Glu
115 120 125
Gln Cys Pro Glu Glu Gly Arg Leu Pro Asp Ala Gly Pro Pro Ser Pro
130 135 140
Ala Asp His Leu Arg Asp Val Phe Tyr Arg Met Gly Leu Asp Asp Lys
145 150 155 160
Glu Ile Val Ala Leu Ser Gly Ala His Thr Leu Gly Arg Ala Arg Pro
165 170 175
Asp Arg Ser Gly Trp Gly Lys Pro Glu Thr Lys Tyr Thr Lys Thr Gly
180 185 190
Pro Gly Glu Ala Gly Gly Gln Ser Trp Thr Val Lys Trp Leu Lys Phe
195 200 205
Asp Asn Ser Tyr Phe Lys Asp Ile Lys Glu Lys Arg Asp Asp Asp Leu

(2) INFORMATION FOR SEQ ID NO:815:

(A) LENGTH: 631 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..631

(D) OTHER INFORMATION: / Ceres Seq. ID 1499028

aantctgcggg	gatagaactg	tcaagggag	ggatcatcg	aatttcgtaa	tttataatca	60
tctagctact	ggtttctgtg	tcaatgaaga	aactacacaga	tgcacattat	tctataatcg	120
ccaattggaac	aatagcatt	aggtagatg	gggagaatca	acgatgatg	aagcagaaag	180
atgtgtgctt	gcactctgct	tataggatca	ctccaaatca	agattttgtc	tctctctgt	240
catagctggt	coattatagt	actttggcta	tatatataca	tattcttatc	cttcacccag	300
gagttttgtg	gatagttttc	ctcataacta	agagacacgg	tacagtgtga	aaatgtctcc	360
tgtcatcaat	gaagagaaat	ggccaaaagg	atccccagtg	atagctttga	tcaagaagta	420
tgcagagatg	atgttataat	atggtagctg	atccccagtg	tttaaggaat	tctgcaagag	480
atgtcccaact	taggtatcca	atgagggctg	gtgtttctct	aaacagaagc	gagcagactg	540
catccccgat	gaacactatg	tgcacaaact	gcttcagatg	caaggactag	agagtgaaat	600
ggaacgaaga	acagtgacat	acaactgttg	g			

(2) INFORMATION FOR SEQ ID NO:816:

(A) LENGTH: 67 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

FEATURE:

(A) NAME/KEY: pepti

(B) LOCATION: 1..67

(D) OTHER INFORMATION: / Ceres Seq.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:816:																
Xaa	Ser	Arg	Asp	Arg	Leu	Xaa	Lys	Gly	Val	Asp	His	Ala	Asn	Phe	Ser	
1				5				10						15		
Ile	Tyr	Ile		His	Ser	Val	Pro	Gly	Phe	Val	Phe	Asn	Glu	Glu	Thr	Thr
			20					25						30		
Ile	Ser	Gln	Tyr	Phe	Tyr	Asn	Arg	Gln	Leu	Asn	Asn	Ser	Ile	Lys	Val	
			35				40					45				
Val	Trp	Gly	Gly	Ser	Ser	Met	Ile	Glu	Ala	Glu	Arg	Leu	Leu	Leu	Ala	

50
Ser Ala Leu
65

55

60

(2) INFORMATION FOR SEQ ID NO:817:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..93
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:817:

Met	Ser	Pro	Val	Ile	Pro	Glu	Glu	Lys	Trp	Arg	Lys	Gly	Ser	Gln	Trp
1			5					10					15		
Ile	Ala	Leu	Ile	Arg	Ser	His	Ala	Glu	Val	Ile	Val	Asn	Asp	Gly	Ile
			20				25					30			
Val	Phe	Pro	Val	Phe	Lys	Glu	Phe	Cys	Lys	Arg	Cys	Pro	Pro	Leu	Gly
			35				40					45			
Thr	Asn	Glu	Ala	Trp	Leu	Phe	Leu	Lys	Gln	Lys	Arg	Arg	Asn	Cys	Ile
			50				55				60				
Pro	Asp	Glu	His	Tyr	Val	Gln	Thr	Leu	Leu	Thr	Met	Gln	Gly	Leu	Glu
			65			70				75				80	
Ser	Glu	Met	Glu	Arg	Arg	Thr	Val	Thr	Tyr	Thr	Val	Trp			
			85				90								

(2) INFORMATION FOR SEQ ID NO:818:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 674 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..674
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499031

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:818:

mccccctgctc	grgcgcaggg	attgttgcat	tatgtgccac	cagtactact	tatgatgaca	60
ctgaaatagc	tactaggatt	cttccaaata	tgtgtgtgct	aaccattgac	caagacagtg	120
atgttctggct	aaaggcattt	caggccgtag	aacagtttct	tcagatatgt	aaacagaaact	180
atgagaagac	aaatgctgga	gaaataggag	ccagcggagg	agcctcagct	atacctgaaa	240
ctgctggtct	gatcggatgg	gctatgagtt	ctttgacctc	caagggttaag	ccatttagaac	300
aagcgctctt	tgctttctct	tcttcagcac	catccctagc	agctgctgcg	tcaaatgcta	360
caagcacagc	aacggaggca	ccgagtgcta	aagccagtc	tcatacacgt	tccaaactcg	420
atttcacaga	tcaacctgca	ccaccatccc	caacatcaac	agatgggttg	ggagatgctg	480
agaatggcat	tagcgaaagt	catgagagtg	acaagacg	tggggaatct	gaaccgctgtg	540
atgaacacaa	accttttcca	gctcttgcta	acattcaagc	agctcaaaaa	cgacctgtgt	600
ctcagtcctc	tagaccttca	gctgcgacaa	gctcaagacc	aaagattagc	acagtgaag	660
caagctgcgaa	aacg					

(2) INFORMATION FOR SEQ ID NO:819:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..224

(D) OTHER INFORMATION: / Ceres Seq. ID 1499032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:819:

Pro Cys Ser Xaa Ala Gly Ile Val Ala Leu Cys Ala Thr Ser Thr Thr
1 5 10 15
Tyr Asp Asp Thr Glu Ile Ala Thr Arg Ile Leu Pro Asn Ile Val Val
20 25 30
Leu Thr Ile Asp Gln Asp Ser Asp Val Arg Ser Lys Ala Phe Gln Ala
35 40 45
Val Glu Gln Phe Leu Gln Ile Leu Lys Gln Asn Tyr Glu Lys Thr Asn
50 55 60
Ala Gly Glu Ile Gly Ala Ser Gly Gly Ala Ser Ala Ile Pro Glu Thr
65 70 75 80
Ala Gly Leu Ile Gly Trp Ala Met Ser Ser Leu Thr Leu Lys Gly Lys
85 90 95
Pro Leu Glu Gln Ala Pro Leu Ala Ser Ser Ser Ala Pro Ser Leu
100 105 110
Ala Ala Ala Ala Ser Asn Ala Thr Ser Thr Ala Thr Glu Ala Pro Ser
115 120 125
Val Lys Ala Ser His His Thr Arg Ser Asn Ser Asp Phe Thr Asp Gln
130 135 140
Pro Ala Pro Pro Ser Pro Thr Ser Thr Asp Gly Trp Gly Asp Ala Glu
145 150 155 160
Asn Gly Ile Ser Glu Gly His Glu Ser Asp Lys Asp Gly Trp Asp Leu
165 170 175
Glu Pro Leu Asp Glu Pro Lys Pro Ser Pro Ala Leu Ala Asn Ile Gln
180 185 190
Ala Ala Gln Lys Arg Pro Val Ser Gln Ser Ser Arg Pro Ser Ala Ala
195 200 205
Thr Ser Ser Arg Pro Lys Ile Ser Thr Val Lys Ala Ala Lys Thr
210 215 220

(2) INFORMATION FOR SEQ ID NO:820:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..137

(D) OTHER INFORMATION: / Ceres Seq. ID 1499033

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:820:

Met Ser Ser Leu Thr Leu Lys Gly Lys Pro Leu Glu Gln Ala Pro Leu
1 5 10 15
Ala Ser Ser Ser Ser Ala Pro Ser Leu Ala Ala Ala Ser Asn Ala
20 25 30
Thr Ser Thr Ala Thr Glu Ala Pro Ser Val Lys Ala Ser His His Thr
35 40 45
Arg Ser Asn Ser Asp Phe Thr Asp Gln Pro Ala Pro Pro Ser Pro Thr
50 55 60
Ser Thr Asp Gly Trp Gly Asp Ala Glu Asn Gly Ile Ser Glu Gly His
65 70 75 80
Glu Ser Asp Lys Asp Gly Trp Asp Leu Glu Pro Leu Asp Glu Pro Lys
85 90 95
Pro Ser Pro Ala Leu Ala Asn Ile Gln Ala Ala Gln Lys Arg Pro Val
100 105 110
Ser Gln Ser Ser Arg Pro Ser Ala Ala Thr Ser Ser Arg Pro Lys Ile
115 120 125
Ser Thr Val Lys Ala Ala Ala Lys Thr

- 130 135
(2) INFORMATION FOR SEQ ID NO:821:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1639 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1639

(D) OTHER INFORMATION: / Ceres Seq. ID 1499042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:821:

```
accgtgtttg atctgtgtgt ttgtgtgtcga tatggcgagg atctcgtgtg acctgagatt 60
tcttctcttc ccggcgacgtt tcatgttcat ctacatccag atgaggcttt tccagacgca 120
atcacagtat gcagatcgcc tcagttccgc tatcgaatct gagaaccatt gcactagtca 180
aatcgagagc ctcatagatg aagttagcat caaacagtcg cggattgttg cctcgaaga 240
tatgaagaac cgccaggacg aagaacttgt gcagcttaag gatctaattc agacgtttga 300
aaaaaaagga atagcaaaac tcaactcaagg tggacagatg cctgtggctg ctgtagtgg 360
tatggcctgc agtcgtgcag actatcttga aaggacttgt aaatcagttt taacatatca 420
aactcccgct gcttcaaaat atcctctatt tatatctcag gatgattctg atcaagctgt 480
caagagcaag tcattagact ataataaatt aacacatatg cagcacttgg attttgaacc 540
agtgttcact gaaggcctg gtgaactgac tgcgtactac aagattgcac gtcactaaca 600
gtgggcaact gaccagtgtt ttacaaaca caaatttagt cgagtgttta tactagaaga 660
tgatatggaa attgttccag acttctttga ttacttttag gctgcagcta gtctcatgga 720
tagggataaa accattatgg ctgttctcat atggaatgat aatggacaga agcagtttgt 780
cgatcatccc tctgtcgtat accgatcaga ttttttctt ggctctgggt ggatgtctaa 840
gagatcgact ttgggtgagt tatcaccaaa gtggccaaag gcttactgtg atgtattgg 900
gagactaaag gaaaaccata aaggccgccca attcattcga ccggaagtct gtgaacata 960
caatttttgt gaacatgggt ctagttttgg acagtttttc agtcagtatc tggaacctat 1020
aaagctaaac gatgtgacgg ttgacttgaa agcaaaaggc ctgggatacc tgacagaggg 1080
aaactatacc aagtactttt ctggcttagt gagacaagca cgaccaattc aggtgtctga 1140
cctgtcttta aaggctcaaa acataaagga tgatgttctg atccgggata aagaccaagt 1200
agagtttgaa cgattgcag ggaatttgg tatatttgaa gaatgggaag atggtgtg 1260
tcgaacagca tataaaggag tagtggtgtt tcgaatccag acaacaagac gtgtattcct 1320
ggttgggcca gattctgtaa tgcagcttgg aattcgaaat tctgtatgca aaacatatga 1380
aaggaaaaga agattttgga ccgcatcgag cctccttcta gcagctgtta agttgtattg 1440
ttatttatgg atgagtttgt agagcgttgg ggtaacctt aacagcaagg aagctctgtg 1500
gacctggctg attggcttag aagttatggg aacccttga aagggtcagg gttaaatata 1560
tttcagttgt ttattatgtg attatcttgt gggtaactta taagaaatgca aatcattcta 1620
tgcagttttt cctgtccc
```

(2) INFORMATION FOR SEQ ID NO:822:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 454 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..454

(D) OTHER INFORMATION: / Ceres Seq. ID 1499043

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:822:

```
Pro Val Leu Ile Trp Leu Phe Val Val Asp Met Ala Arg Ile Ser Cys
1 5 10 15
Asp Leu Arg Phe Leu Leu Ile Pro Ala Ala Phe Met Phe Ile Tyr Ile
20 25 30
Gln Met Arg Leu Phe Gln Thr Gln Ser Gln Tyr Ala Asp Arg Leu Ser
35 40 45
Ser Ala Ile Glu Ser Gln Asn His Cys Thr Ser Gln Met Arg Gly Leu
50 55 60
```

Ile	Asp	Glu	Val	Ser	Ile	Lys	Gln	Ser	Arg	Ile	Val	Ala	Leu	Glu	Asp	65	70	75	80
Met	Lys	Asn	Arg	Gln	Asp	Glu	Glu	Leu	Val	Gln	Leu	Lys	Asp	Leu	Ile		85	90	95
Gln	Thr	Phe	Glu	Lys	Lys	Gly	Ile	Ala	Lys	Leu	Thr	Gln	Gly	Gly	Gln		100	105	110
Met	Pro	Val	Ala	Ala	Val	Val	Val	Met	Ala	Cys	Ser	Arg	Ala	Asp	Tyr		115	120	125
Leu	Glu	Arg	Thr	Val	Lys	Ser	Val	Leu	Thr	Tyr	Gln	Thr	Pro	Val	Ala		130	135	140
Ser	Lys	Tyr	Pro	Leu	Phe	Ile	Ser	Gln	Asp	Gly	Ser	Asp	Gln	Ala	Val		145	150	155
Lys	Ser	Lys	Ser	Leu	Ser	Tyr	Asn	Gln	Leu	Thr	His	Met	Gln	His	Leu		165	170	175
Asp	Phe	Glu	Pro	Val	Val	Thr	Glu	Arg	Pro	Gly	Glu	Leu	Thr	Ala	Tyr		180	185	190
Tyr	Lys	Ile	Ala	Arg	His	Tyr	Lys	Trp	Ala	Leu	Asp	Gln	Leu	Phe	Tyr		195	200	205
Lys	His	Lys	Phe	Ser	Arg	Val	Ile	Ile	Leu	Glu	Asp	Asp	Met	Glu	Ile		210	215	220
Ala	Pro	Asp	Phe	Phe	Asp	Tyr	Phe	Glu	Ala	Ala	Ala	Ser	Leu	Met	Asp		225	230	235
Arg	Asp	Lys	Thr	Ile	Met	Ala	Ala	Ser	Ser	Trp	Asn	Asp	Asn	Gly	Gln		245	250	255
Lys	Gln	Phe	Val	His	Asp	Pro	Tyr	Ala	Leu	Tyr	Arg	Ser	Asp	Phe	Phe		260	265	270
Pro	Gly	Leu	Gly	Trp	Met	Leu	Lys	Arg	Ser	Thr	Trp	Asp	Glu	Leu	Ser		275	280	285
Pro	Lys	Trp	Pro	Lys	Ala	Tyr	Trp	Asp	Asp	Trp	Leu	Arg	Leu	Lys	Glu		290	295	300
Asn	His	Lys	Gly	Arg	Gln	Phe	Ile	Arg	Pro	Glu	Val	Cys	Arg	Thr	Tyr		305	310	315
Asn	Phe	Gly	Glu	His	Gly	Ser	Ser	Leu	Gly	Gln	Phe	Phe	Ser	Gln	Tyr		325	330	335
Leu	Glu	Pro	Ile	Lys	Leu	Asn	Asp	Val	Thr	Val	Asp	Trp	Lys	Ala	Lys		340	345	350
Asp	Leu	Gly	Tyr	Leu	Thr	Glu	Gly	Asn	Tyr	Thr	Lys	Tyr	Phe	Ser	Gly		355	360	365
Leu	Val	Arg	Gln	Ala	Arg	Pro	Ile	Gln	Gly	Ser	Asp	Leu	Val	Leu	Lys		370	375	380
Ala	Gln	Asn	Ile	Lys	Asp	Asp	Val	Arg	Ile	Arg	Tyr	Lys	Asp	Gln	Val		385	390	395
Glu	Phe	Glu	Arg	Ile	Ala	Gly	Glu	Phe	Gly	Ile	Phe	Glu	Glu	Trp	Lys		405	410	415
Asp	Gly	Val	Pro	Arg	Thr	Ala	Tyr	Lys	Gly	Val	Val	Val	Phe	Arg	Ile		420	425	430
Gln	Thr	Thr	Arg	Val	Phe	Leu	Val	Gly	Pro	Asp	Ser	Val	Met	Gln			435	440	445
Leu	Gly	Ile	Arg	Asn	Ser												450		

(2) INFORMATION FOR SEQ ID NO:823:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..444
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499044

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:823:

Met Ala Arg Ile Ser Cys Asp Leu Arg Phe Leu Leu Ile Pro Ala Ala
1 5 10 15
Phe Met Phe Ile Tyr Ile Gln Met Arg Leu Phe Gln Thr Gln Ser Gln
20 25
Tyr Ala Asp Arg Leu Ser Ser Ala Ile Glu Ser Glu Asn His Cys Thr
35 40 45
Ser Gln Met Arg Gly Leu Ile Asp Glu Val Ser Ile Lys Gln Ser Arg
50 55 60
Ile Val Ala Leu Glu Asp Met Lys Asn Arg Gln Asp Glu Glu Leu Val
65 70 75 80
Gln Leu Lys Asp Leu Ile Gln Thr Phe Glu Lys Lys Gly Ile Ala Lys
85 90 95
Leu Thr Gln Gly Gly Gln Met Pro Val Ala Ala Val Val Val Met Ala
100 105 110
Cys Ser Arg Ala Asp Tyr Leu Glu Arg Thr Val Lys Ser Val Leu Thr
115 120 125
Tyr Gln Thr Pro Val Ala Ser Lys Tyr Pro Leu Phe Ile Ser Gln Asp
130 135 140
Gly Ser Asp Gln Ala Val Lys Ser Lys Ser Leu Ser Tyr Asn Gln Leu
145 150 155 160
Thr His Met Gln His Leu Asp Phe Glu Pro Val Val Thr Glu Arg Pro
165 170 175
Gly Glu Leu Thr Ala Tyr Tyr Lys Ile Ala Arg His Tyr Lys Trp Ala
180 185 190
Leu Asp Gln Leu Phe Tyr Lys His Lys Phe Ser Arg Val Ile Ile Leu
195 200 205
Glu Asp Asp Met Glu Ile Ala Pro Asp Phe Phe Asp Tyr Phe Glu Ala
210 215 220
Ala Ala Ser Leu Met Asp Arg Asp Lys Thr Ile Met Ala Ala Ser Ser
225 230 235 240
Trp Asn Asp Asn Gly Gln Lys Gln Phe Val His Asp Pro Tyr Ala Leu
245 250 255
Tyr Arg Ser Asp Phe Phe Pro Gly Leu Gly Trp Met Leu Lys Arg Ser
260 265 270
Thr Trp Asp Glu Leu Ser Pro Lys Trp Pro Lys Ala Tyr Trp Asp Asp
275 280 285
Trp Leu Arg Leu Lys Glu Asn His Lys Gly Arg Gln Phe Ile Arg Pro
290 295 300
Glu Val Cys Arg Thr Tyr Asn Phe Gly Glu His Gly Ser Ser Leu Gly
305 310 315 320
Gln Phe Phe Ser Gln Tyr Leu Glu Pro Ile Lys Leu Asn Asp Val Thr
325 330 335
Val Asp Trp Lys Ala Lys Asp Leu Gly Tyr Leu Thr Glu Gly Asn Tyr
340 345 350
Thr Lys Tyr Phe Ser Gly Leu Val Arg Gln Ala Arg Pro Ile Gln Gly
355 360 365
Ser Asp Leu Val Leu Lys Ala Gln Asn Ile Lys Asp Asp Val Arg Ile
370 375 380
Arg Tyr Lys Asp Gln Val Glu Phe Glu Arg Ile Ala Gly Glu Phe Gly
385 390 395 400
Ile Phe Glu Glu Trp Lys Asp Gly Val Pro Arg Thr Ala Tyr Lys Gly
405 410 415
Val Val Val Phe Arg Ile Gln Thr Thr Arg Arg Val Phe Leu Val Gly
420 425 430
Pro Asp Ser Val Met Gln Leu Gly Ile Arg Asn Ser
435 440

(2) INFORMATION FOR SEQ ID NO:824:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..427
(D) OTHER INFORMATION: / Ceres Seq. ID 1499045
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:824:

Met	Phe	Ile	Tyr	Ile	Gln	Met	Arg	Leu	Phe	Gln	Thr	Gln	Ser	Gln	Tyr
1			5						10					15	
Ala	Asp	Arg	Leu	Ser	Ser	Ala	Ile	Glu	Ser	Glu	Asn	His	Cys	Thr	Ser
			20					25					30		
Gln	Met	Arg	Gly	Leu	Ile	Asp	Glu	Val	Ser	Ile	Lys	Gln	Ser	Arg	Ile
			35					40				45			
Val	Ala	Leu	Glu	Asp	Met	Lys	Asn	Arg	Gln	Asp	Glu	Glu	Leu	Val	Gln
			50					55			60				
Leu	Lys	Asp	Leu	Ile	Gln	Thr	Phe	Glu	Lys	Lys	Gly	Ile	Ala	Lys	Leu
			65					70			75			80	
Thr	Gln	Gly	Gly	Gln	Met	Pro	Val	Ala	Ala	Val	Val	Val	Met	Ala	Cys
				85					90					95	
Ser	Arg	Ala	Asp	Tyr	Leu	Glu	Arg	Thr	Val	Lys	Ser	Val	Leu	Thr	Tyr
			100					105					110		
Gln	Thr	Pro	Val	Ala	Ser	Lys	Tyr	Pro	Leu	Phe	Ile	Ser	Gln	Asp	Gly
			115					120					125		
Ser	Asp	Gln	Ala	Val	Lys	Ser	Lys	Ser	Leu	Ser	Tyr	Asn	Gln	Leu	Thr
			130					135				140			
His	Met	Gln	His	Leu	Asp	Phe	Glu	Pro	Val	Val	Thr	Glu	Arg	Pro	Gly
			145					150			155			160	
Glu	Leu	Thr	Ala	Tyr	Tyr	Lys	Ile	Ala	Arg	His	Tyr	Lys	Trp	Ala	Leu
			165					170					175		
Asp	Gln	Leu	Phe	Tyr	Lys	His	Lys	Phe	Ser	Arg	Val	Ile	Ile	Leu	Glu
			180					185				190			
Asp	Asp	Met	Glu	Ile	Ala	Pro	Asp	Phe	Phe	Asp	Tyr	Phe	Glu	Ala	Ala
			195					200				205			
Ala	Ser	Leu	Met	Asp	Arg	Asp	Lys	Thr	Ile	Met	Ala	Ala	Ser	Ser	Trp
			210					215			220				
Asn	Asp	Asn	Gly	Gln	Lys	Gln	Phe	Val	His	Asp	Pro	Tyr	Ala	Leu	Tyr
			225					230			235			240	
Arg	Ser	Asp	Phe	Phe	Pro	Gly	Leu	Gly	Trp	Met	Leu	Lys	Arg	Ser	Thr
			245						250				255		
Trp	Asp	Glu	Leu	Ser	Pro	Lys	Trp	Pro	Lys	Ala	Tyr	Trp	Asp	Asp	Trp
			260					265				270			
Leu	Arg	Leu	Lys	Glu	Asn	His	Lys	Gly	Arg	Gln	Phe	Ile	Arg	Pro	Glu
			275					280				285			
Val	Cys	Arg	Thr	Tyr	Asn	Phe	Gly	Glu	His	Gly	Ser	Ser	Leu	Gly	Gln
			290					295			300				
Phe	Phe	Ser	Gln	Tyr	Leu	Glu	Pro	Ile	Lys	Leu	Asn	Asp	Val	Thr	Val
			305					310			315			320	
Asp	Trp	Lys	Ala	Lys	Asp	Leu	Gly	Tyr	Leu	Thr	Glu	Gly	Asn	Tyr	Thr
			325					330					335		
Lys	Tyr	Phe	Ser	Gly	Leu	Val	Arg	Gln	Ala	Arg	Pro	Ile	Gln	Gly	Ser
			340					345				350			
Asp	Leu	Val	Leu	Lys	Ala	Gln	Asn	Ile	Lys	Asp	Asp	Val	Arg	Ile	Arg
			355					360				365			
Tyr	Lys	Asp	Gln	Val	Glu	Phe	Glu	Arg	Ile	Ala	Gly	Glu	Phe	Gly	Ile
			370					375			380				
Phe	Glu	Glu	Trp	Lys	Asp	Gly	Val	Pro	Arg	Thr	Ala	Tyr	Lys	Gly	Val
			385					390			395			400	
Val	Val	Phe	Arg	Ile	Gln	Thr	Thr	Arg	Arg	Val	Phe	Leu	Val	Gly	Pro
			405					410						415	
Asp	Ser	Val	Met	Gln	Leu	Gly	Ile	Arg	Asn	Ser					

420 425

(2) INFORMATION FOR SEQ ID NO:825:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1220 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1220

(D) OTHER INFORMATION: / Ceres Seq. ID 1499046

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:825:

agcgattgtc	cttttttgac	tcacttggtc	ttcttctaaa	gaaagcgaag	tttcttctct	60
ccagaataat	gttgattctc	tgtgtttgtg	tcctccatag	gataaatccc	tagacaaatcc	120
ttctgatcgc	gcttttcgtt	tcgaaaaaatt	taaaactttt	aactccgttg	atcgagatgg	180
tacagtacgc	gggtggaagt	ctattaccgt	cgcggtggga	gattgaggtc	gcggtgtctg	240
ctctctgtgt	tttaatcgct	tcctattggc	tattcgctta	cagaggaggc	ggagatgacg	300
atgtcgtcgg	gtttggattt	gatcgggtct	gtctcatgca	gaatctcgat	tcoggtgacg	360
cttttgacaa	agacaagata	ggacacttga	gaggagacac	tcaaaactaat	gctgcttata	420
tagtcaaggt	ggaactcttg	gctgctaaga	atctaaattg	tgctaactta	aatgggaacat	480
cagatcctta	tgctatttgt	aattgtggat	cagaaaagcg	atcagttctt	atggtccctg	540
gctcgagaaa	tccaatgtgg	gggtgaagagt	tcaattttcc	cacagatgaa	cttctcgcta	600
agattaatgt	aaacaattcat	gattgggata	tcaatttgaa	aagtactgtt	cttggtctag	660
tacattataa	tgttgaaagt	gaaggccaaa	cggttcacgt	gtggcactca	ttagacagcc	720
cgctgtggca	gggtttgcct	aacattaatg	caatcaaaat	acccgtgaat	gctcctaggg	780
ctgtaactgg	atatgctgta	gcggttagaa	gaagggtcac	atgggatcag	caaggcccaa	840
caattgtaca	tcaaaagcca	gggcctctgc	agacgatatt	tgatctctct	ccggatgagg	900
tgtgcagaca	cagttatctc	tgtgcccctg	agaggtcatt	ccctgatcat	ggccgaatgt	960
atgtttccgc	gtggcacata	tgtttccact	ccaatgtttt	ctctaagcaa	atgaaggttg	1020
tgttccctct	cagagatata	gatgagattc	gtagaagtca	acacgattg	ataaacccag	1080
ctataacaat	catactacgg	atgggtgctg	gtggacatgg	tgttccccct	cttgggactc	1140
ctgatgtag	agtgagggtat	aaatttgcat	cgttttgtaa	caggaaacct	acactaaaaa	1200
catgtcaacg	tcggcgtgaa					

(2) INFORMATION FOR SEQ ID NO:826:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 348 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..348

(D) OTHER INFORMATION: / Ceres Seq. ID 1499047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:826:

Met	Val	Gln	Ser	Ala	Val	Glu	Val	Leu	Leu	Pro	Ser	Ser	Ala	Trp	Glu	Ile	
1		5						10						15			
Glu	Val	Ala	Val	Val	Ala	Ser	Val	Phe	Leu	Ile	Ala	Ser	Tyr	Trp	Leu		
		20						25					30				
Phe	Ala	Tyr	Arg	Gly	Gly	Gly	Asp	Asp	Val	Val	Gly	Val	Gly	Phe			
		35						40					45				
Asp	Arg	Ser	Arg	Leu	Met	Gln	Asn	Leu	Asp	Ser	Gly	Asp	Ala	Phe	Asp		
		50					55						60				
Lys	Asp	Lys	Ile	Gly	His	Leu	Arg	Gly	Asp	Thr	Gln	Thr	Asn	Ala	Ala		
		65				70				75				80			
Tyr	Ile	Val	Lys	Val	Glu	Leu	Leu	Ala	Ala	Lys	Asn	Leu	Ile	Gly	Ala		
			85					90					95				
Asn	Leu	Asn	Gly	Thr	Ser	Asp	Pro	Tyr	Ala	Ile	Val	Asn	Cys	Gly	Ser		
			100					105					110				
Glu	Lys	Arg	Phe	Ser	Ser	Met	Val	Pro	Gly	Ser	Arg	Asn	Pro	Met	Trp		

115	120	125
Gly Glu Glu Phe Asn Phe Pro Thr Asp Glu Leu Pro Ala Lys Ile Asn		
130	135	140
Val Thr Ile His Asp Trp Asp Ile Ile Trp Lys Ser Thr Val Leu Gly		
145	150	155
Ser Val Thr Ile Asn Val Glu Arg Glu Gly Gln Thr Gly Pro Val Trp		
165	170	175
His Ser Leu Asp Ser Pro Ser Gly Gln Val Cys Leu Asn Ile Asn Ala		
180	185	190
Ile Lys Leu Pro Val Asn Ala Pro Arg Ala Val Thr Gly Tyr Ala Gly		
195	200	205
Ala Gly Arg Arg Arg Val Thr Leu Asp Gln Gln Gly Pro Thr Ile Val		
210	215	220
His Gln Lys Pro Gly Pro Leu Gln Thr Ile Phe Asp Leu Leu Pro Asp		
225	230	235
Glu Val Val Glu His Ser Tyr Ser Cys Ala Leu Glu Arg Ser Phe Leu		
245	250	255
Tyr His Gly Arg Met Tyr Val Ser Ala Trp His Ile Cys Phe His Ser		
260	265	270
Asn Val Phe Ser Lys Gln Met Lys Val Val Val Pro Leu Gly Asp Ile		
275	280	285
Asp Glu Ile Arg Arg Ser Gln His Ala Leu Ile Asn Pro Ala Ile Thr		
290	295	300
Ile Ile Leu Arg Met Gly Ala Gly Gly His Gly Val Pro Pro Leu Gly		
305	310	315
Thr Pro Asp Gly Arg Val Arg Tyr Lys Phe Ala Ser Phe Trp Asn Arg		
325	330	335
Asn His Thr Leu Lys Ala Leu Gln Arg Ala Val Asn		
340	345	

(2) INFORMATION FOR SEQ ID NO:827:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 295 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..295

(D) OTHER INFORMATION: / Ceres Seq. ID 1499048

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:827:

Met	Gln	Asn	Leu	Asp	Ser	Gly	Asp	Ala	Phe	Asp	Lys	Asp	Lys	Ile	Gly
1			5				10						15		
His	Leu	Arg	Gly	Asp	Thr	Gln	Thr	Asn	Ala	Ala	Tyr	Ile	Val	Lys	Val
			20					25					30		
Glu	Leu	Leu	Ala	Ala	Lys	Asn	Leu	Ile	Gly	Ala	Asn	Leu	Asn	Gly	Thr
			35				40					45			
Ser	Asp	Pro	Tyr	Ala	Ile	Val	Asn	Cys	Gly	Ser	Glu	Lys	Arg	Phe	Ser
50						55					60				
Ser	Met	Val	Pro	Gly	Ser	Arg	Asn	Pro	Met	Trp	Gly	Glu	Glu	Phe	Asn
65				70					75					80	
Phe	Pro	Thr	Asp	Glu	Leu	Pro	Ala	Lys	Ile	Asn	Val	Thr	Ile	His	Asp
				85					90				95		
Trp	Asp	Ile	Ile	Trp	Lys	Ser	Thr	Val	Leu	Gly	Ser	Val	Thr	Ile	Asn
				100				105					110		
Val	Glu	Arg	Glu	Gly	Gln	Thr	Gly	Pro	Val	Trp	His	Ser	Leu	Asp	Ser
				115			120					125			
Pro	Ser	Gly	Gln	Val	Cys	Leu	Asn	Ile	Asn	Ala	Ile	Lys	Leu	Pro	Val
130						135					140				
Asn	Ala	Pro	Arg	Ala	Val	Thr	Gly	Tyr	Ala	Gly	Ala	Gly	Arg	Arg	Arg
145					150					155					160

Val Thr Leu Asp Gln Gln Gly Pro Thr Ile Val His Gln Lys Pro Gly
165 170 175
Pro Leu Gln Thr Ile Phe Asp Leu Leu Pro Asp Glu Val Val Glu His
180 185 190
Ser Tyr Ser Cys Ala Leu Glu Arg Ser Phe Leu Tyr His Gly Arg Met
195 200 205
Tyr Val Ser Ala Trp His Ile Cys Phe His Ser Asn Val Phe Ser Lys
210 215 220
Gln Met Lys Val Val Val Pro Leu Gly Asp Ile Asp Glu Ile Arg Arg
225 230 235 240
Ser Gln His Ala Leu Ile Asn Pro Ala Ile Thr Ile Ile Leu Arg Met
245 250 255
Gly Ala Gly Gly His Gly Val Pro Pro Leu Gly Thr Pro Asp Gly Arg
260 265 270
Val Arg Tyr Lys Phe Ala Ser Phe Trp Asn Arg Asn His Thr Leu Lys
275 280 285
Ala Leu Gln Arg Ala Val Asn
290 295

(2) INFORMATION FOR SEQ ID NO:828:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 230 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..230

(D) OTHER INFORMATION: / Ceres Seq. ID 1499049

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:828:

Met Val Pro Gly Ser Arg Asn Pro Met Trp Gly Glu Glu Phe Asn Phe
1 5 10 15
Pro Thr Asp Glu Leu Pro Ala Lys Ile Asn Val Thr Ile His Asp Trp
20 25 30
Asp Ile Ile Trp Lys Ser Thr Val Leu Gly Ser Val Thr Ile Asn Val
35 40 45
Glu Arg Glu Gly Gln Thr Gly Pro Val Trp His Ser Leu Asp Ser Pro
50 55 60
Ser Gly Gln Val Cys Leu Asn Ile Asn Ala Ile Lys Leu Pro Val Asn
65 70 75 80
Ala Pro Arg Ala Val Thr Gly Tyr Ala Gly Ala Gly Arg Arg Arg Val
85 90 95
Thr Leu Asp Gln Gln Gly Pro Thr Ile Val His Gln Lys Pro Gly Pro
100 105 110
Leu Gln Thr Ile Phe Asp Leu Leu Pro Asp Glu Val Val Glu His Ser
115 120 125
Tyr Ser Cys Ala Leu Glu Arg Ser Phe Leu Tyr His Gly Arg Met Tyr
130 135 140
Val Ser Ala Trp His Ile Cys Phe His Ser Asn Val Phe Ser Lys Gln
145 150 155 160
Met Lys Val Val Val Pro Leu Gly Asp Ile Asp Glu Ile Arg Arg Ser
165 170 175
Gln His Ala Leu Ile Asn Pro Ala Ile Thr Ile Ile Leu Arg Met Gly
180 185 190
Ala Gly Gly His Gly Val Pro Pro Leu Gly Thr Pro Asp Gly Arg Val
195 200 205
Arg Tyr Lys Phe Ala Ser Phe Trp Asn Arg Asn His Thr Leu Lys Ala
210 215 220
Leu Gln Arg Ala Val Asn
225 230

(2) INFORMATION FOR SEQ ID NO:829:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1226 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1226
(D) OTHER INFORMATION: / Ceres Seq. ID 1499050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:829:

gacgagacaa	aagatagaga	agcaaaagta	agctgataag	gtttgatata	gtagaaaata	60
cactctcttta	acttctctctt	cttctctcttc	ttcttctcct	atcttttgaaa	atggcgatga	120
ctccggtcgcg	gtoatcatct	ccagtttcaa	cctgcagact	ctttcgtctg	aatctctctc	180
ctgatctctt	acctaaagcct	ctgtttctct	ccctccccaa	acgaaacaga	attgctctgt	240
gcgcgttcac	tgtaagctgc	tcgcggaatg	ctacgcgtga	atcccttaac	gggtgctcctg	300
ctctcacatc	agatacggat	acggagacgg	ataccacctc	ctatggccga	cagtttttcc	360
ctttggccgc	agttgtgtgc	caggaagcca	taaaaactgc	tcttttactt	ggcgcggttg	420
atcgtgaat	cggagggtat	gccatttcag	gtcgtagagg	cactgcacaa	acagtcattg	480
cgcgagggtc	tcatgaatc	ctccctccta	ttgaagttgt	tgtaggctca	atatcaaatg	540
ctgacccagc	ttgtccagat	gagtggaag	atgacttaga	tgagcgcata	gagtagaatg	600
ctgacaatac	cattaagact	gagattgtca	aatctccttt	cattcagatt	ccactaggag	660
ttacagaaga	cagactcatt	gggtctgttg	atgttgagga	gtctgtgaaa	agggggacaa	720
ctgtttttcca	acctggtctt	ttggctgaag	cccatagagg	agtggtgtat	gttgatgaaa	780
taaatctctt	agatgagga	attagtaatt	tgcttctcaa	tgattgaacg	gatggtgtta	840
atatagtgtg	aagagaagga	atcagcttta	ggcaccctgt	caaacacctt	ttaattgcaa	900
ccataaccc	tgaagaaggt	gctgttcgag	agcacttgct	agaccgtgtt	gcggtgtgct	960
ctgtacatc	tgagagtgga	ggaggtggtg	gtgctctctg	tgctgagtc	aagaaagaa	1020
agaagaagga	agaaaagaa	gaatccgatg	atgacatggg	tttcagtcga	ttcagtagaa	1080
ctggtagtag	catgaaaagt	ccggttttgt	tgctcctctt	taatatgtkg	accttttgaa	1140
atctatatgt	tggttggtgt	tagtttgtat	tcgatcatct	tttttagaca	ttgctgaaat	1200
ttccaagagt	ttttgaccgc	aatgcc				

(2) INFORMATION FOR SEQ ID NO:830:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..322
(D) OTHER INFORMATION: / Ceres Seq. ID 1499051

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:830:

Met	Ala	Met	Thr	Pro	Val	Ala	Ser	Ser	Pro	Val	Ser	Thr	Cys	Arg
1				5					10				15	
Leu	Phe	Arg	Cys	Asn	Leu	Leu	Pro	Asp	Leu	Leu	Pro	Lys	Pro	Leu
			20					25				30		
Leu	Ser	Leu	Pro	Lys	Arg	Asn	Arg	Ile	Ala	Ser	Cys	Arg	Phe	Thr
			35				40				45			Val
Arg	Ala	Ser	Ala	Asn	Ala	Thr	Val	Glu	Ser	Pro	Asn	Gly	Val	Pro
			50				55				60			Ala
Ser	Thr	Ser	Asp	Thr	Asp	Thr	Glu	Thr	Asp	Thr	Ser	Tyr	Gly	Arg
			65				70				75			80
Gln	Phe	Phe	Pro	Leu	Ala	Ala	Val	Val	Gly	Gln	Glu	Gly	Ile	Leu
			85						90				95	
Ala	Leu	Leu	Leu	Gly	Ala	Val	Asp	Arg	Glu	Ile	Gly	Gly	Ile	Ala
			100					105					110	
Ser	Gly	Arg	Arg	Gly	Thr	Ala	Lys	Thr	Val	Met	Ala	Arg	Gly	Leu
			115				120				125			His
Glu	Ile	Leu	Pro	Pro	Ile	Glu	Val	Val	Val	Gly	Ser	Ile	Ser	Asn

130	135	140
Asp Pro Ala Cys Pro Asp Glu Trp Glu Asp Asp Leu Asp Glu Arg Ile		
145	150	155
Glu Tyr Asn Ala Asp Asn Thr Ile Lys Thr Glu Ile Val Lys Ser Pro		
	165	170
Phe Ile Gln Ile Pro Leu Gly Val Thr Glu Asp Arg Leu Ile Gly Ser		
	180	185
Val Asp Val Glu Glu Ser Val Lys Arg Gly Thr Thr Val Phe Gln Pro		
	195	200
Gly Leu Leu Ala Glu Ala His Arg Gly Val Leu Tyr Val Asp Glu Ile		
	210	215
Asn Leu Leu Asp Glu Gly Ile Ser Asn Leu Leu Asn Val Leu Thr		
225	230	235
Asp Gly Val Asn Ile Val Glu Arg Glu Gly Ile Ser Phe Arg His Pro		
	245	250
Cys Lys Pro Leu Leu Ile Ala Thr Tyr Asn Pro Glu Glu Gly Ala Val		
	260	265
Arg Glu His Leu Leu Asp Arg Val Ala Val Ala Ser Ala Thr Ser Gly		
	275	280
Gly Gly Gly Gly Gly Gly Ala Pro Ala Ala Glu Ser Lys Lys Glu Glu		
	290	295
Lys Lys Glu Glu Lys Glu Glu Ser Asp Asp Asp Met Gly Phe Ser Leu		
305	310	315
Phe Glu		320

(2) INFORMATION FOR SEQ ID NO:831:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..320
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499052

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:831:

Met Thr Pro Val Ala Ser Ser Ser Pro Val Ser Thr Cys Arg Leu Phe	
1	5
Arg Cys Asn Leu Leu Pro Asp Leu Leu Pro Lys Pro Leu Phe Leu Ser	
	20
Leu Pro Lys Arg Asn Arg Ile Ala Ser Cys Arg Phe Thr Val Arg Ala	
	35
Ser Ala Asn Ala Thr Val Glu Ser Pro Asn Gly Val Pro Ala Ser Thr	
	50
Ser Asp Thr Asp Thr Glu Thr Asp Thr Thr Ser Tyr Gly Arg Gln Phe	
65	70
Phe Pro Leu Ala Ala Val Val Gly Gln Gly Ile Lys Thr Ala Leu	
	85
Leu Leu Gly Ala Val Asp Arg Glu Ile Gly Gly Ile Ala Ile Ser Gly	
	100
Arg Arg Gly Thr Ala Lys Thr Val Met Ala Arg Gly Leu His Glu Ile	
	115
Leu Pro Pro Ile Glu Val Val Val Gly Ser Ile Ser Asn Ala Asp Pro	
	130
Ala Cys Pro Asp Glu Trp Glu Asp Asp Leu Asp Glu Arg Ile Glu Tyr	
145	150
Asn Ala Asp Asn Thr Ile Lys Thr Glu Ile Val Lys Ser Pro Phe Ile	
	165
Gln Ile Pro Leu Gly Val Thr Glu Asp Arg Leu Ile Gly Ser Val Asp	
	180
	185
	190

Val	Glu	Glu	Ser	Val	Lys	Arg	Gly	Thr	Thr	Val	Phe	Gln	Pro	Gly	Leu
	195						200					205			
Leu	Ala	Glu	Ala	His	Arg	Gly	Val	Leu	Tyr	Val	Asp	Glu	Ile	Asn	Leu
	210					215					220				
Leu	Asp	Glu	Gly	Ile	Ser	Asn	Leu	Leu	Leu	Asn	Val	Leu	Thr	Asp	Gly
	225					230					235				240
Val	Asn	Ile	Val	Glu	Arg	Glu	Gly	Ile	Ser	Phe	Arg	His	Pro	Cys	Lys
			245						250					255	
Pro	Leu	Leu	Ile	Ala	Thr	Tyr	Asn	Pro	Glu	Glu	Gly	Ala	Val	Arg	Glu
			260						265					270	
His	Leu	Leu	Asp	Arg	Val	Ala	Val	Ala	Ser	Ala	Thr	Ser	Gly	Gly	Gly
			275						280					285	
Gly	Gly	Gly	Gly	Ala	Pro	Ala	Ala	Glu	Ser	Lys	Lys	Glu	Glu	Lys	Lys
			290						295			300			
Glu	Glu	Lys	Glu	Glu	Ser	Asp	Asp	Asp	Met	Gly	Phe	Ser	Leu	Phe	Glu
	305				310					315					320

(2) INFORMATION FOR SEQ ID NO:832:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..200

(D) OTHER INFORMATION: / Ceres Seq. ID 1499053

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:832:

Met	Ala	Arg	Gly	Leu	His	Glu	Ile	Leu	Pro	Pro	Ile	Glu	Val	Val	Val
1			5					10					15		
Gly	Ser	Ile	Ser	Asn	Ala	Asp	Pro	Ala	Cys	Pro	Asp	Glu	Trp	Glu	Asp
			20				25						30		
Asp	Leu	Asp	Glu	Arg	Ile	Glu	Tyr	Asn	Ala	Asp	Asn	Thr	Ile	Lys	Thr
			35				40					45			
Glu	Ile	Val	Lys	Ser	Pro	Phe	Ile	Gln	Ile	Pro	Leu	Gly	Val	Thr	Glu
			50				55				60				
Asp	Arg	Leu	Ile	Gly	Ser	Val	Asp	Val	Glu	Glu	Ser	Val	Lys	Arg	Gly
			65				70				75				80
Thr	Thr	Val	Phe	Gln	Pro	Gly	Leu	Leu	Ala	Glu	Ala	His	Arg	Gly	Val
			85						90					95	
Leu	Tyr	Val	Asp	Glu	Ile	Asn	Leu	Leu	Asp	Glu	Gly	Ile	Ser	Asn	Leu
			100						105				110		
Leu	Leu	Asn	Val	Leu	Thr	Asp	Gly	Val	Asn	Ile	Val	Glu	Arg	Glu	Gly
			115				120					125			
Ile	Ser	Phe	Arg	His	Pro	Cys	Lys	Pro	Leu	Leu	Ile	Ala	Thr	Tyr	Asn
			130				135				140				
Pro	Glu	Glu	Gly	Ala	Val	Arg	Glu	His	Leu	Leu	Asp	Arg	Val	Ala	Val
					150						155				160
Ala	Ser	Ala	Thr	Ser	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Ala	Pro	Ala	Ala
					165					170				175	
Glu	Ser	Lys	Lys	Glu	Glu	Lys	Lys	Glu	Glu	Lys	Glu	Glu	Ser	Asp	Asp
			180					185					190		
Asp	Met	Gly	Phe	Ser	Leu	Phe	Glu								
			195				200								

(2) INFORMATION FOR SEQ ID NO:833:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 540 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..540
(D) OTHER INFORMATION: / Ceres Seq. ID 1499054

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:833:

acatctgtcg	ccgcccgtga	gaccgccact	taaggccgtc	tctccgctc	tatccatatac	60
caaaacagct	ataaagataa	acttccagag	cttggtgaag	gagcagcaac	cctagttttc	120
aatccctaaa	gatattagtt	ctccagcgag	tgacacaaa	accgattac	gtttcatccg	180
gcgactcgct	ttgatattcc	atggattctc	agtgaaatcc	ttccaagaga	cgcaagataa	240
gtgtcaaggca	cagatgcggtt	gcgtgctata	agatgttcaa	tagacgagaa	cacotcgttg	300
agcacatgaa	gatttctac	cactcacttc	accagcctcg	ctgtgggggtt	tgcoctcaagc	360
actgtaaatc	cttcgaatcc	gtgaggggaac	acotaaacgt	tccagaccat	ctttccaaag	420
gaaactgcaa	agccattttc	actaaacgag	gctgtactct	ctgtcttcaa	atctttgagg	480
aggcctttgc	tctccgcgag	cataaaaaca	agtgtcacct	ctccccamct	cgctcctctt	540

(2) INFORMATION FOR SEQ ID NO:834:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..113
(D) OTHER INFORMATION: / Ceres Seq. ID 1499055

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:

Met	Asp	Ser	Gln	Leu	Asn	Pro	Ser	Lys	Arg	Arg	Lys	Ile	Ser	Val	Arg
1			5					10						15	
His	Arg	Cys	Val	Ala	Cys	Tyr	Lys	Met	Phe	Asn	Arg	Arg	Glu	His	Leu
			20					25					30		
Val	Glu	His	Met	Lys	Ile	Ser	Tyr	His	Ser	Leu	His	Gln	Pro	Arg	Cys
			35				40				45				
Gly	Val	Cys	Leu	Lys	His	Cys	Lys	Ser	Phe	Glu	Ser	Val	Arg	Glu	His
			50				55				60				
Leu	Asn	Val	Pro	Asp	His	Leu	Ser	Lys	Gly	Asn	Cys	Lys	Ala	Ile	Phe
			70						75					80	
Thr	Lys	Arg	Gly	Cys	Thr	Leu	Cys	Leu	Gln	Ile	Phe	Glu	Glu	Ala	Phe
			85					90					95		
Ala	Leu	Ala	Glu	His	Lys	Asn	Lys	Cys	His	Leu	Ser	Pro	Xaa	Arg	Pro
			100				105						110		
Leu															

(2) INFORMATION FOR SEQ ID NO:835:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..89
(D) OTHER INFORMATION: / Ceres Seq. ID 1499056

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:835:

Met	Phe	Asn	Arg	Arg	Glu	His	Leu	Val	Glu	His	Met	Lys	Ile	Ser	Tyr
1			5						10					15	
His	Ser	Leu	His	Gln	Pro	Arg	Cys	Gly	Val	Cys	Leu	Lys	His	Cys	Lys
			20					25					30		

Ser Phe Glu Ser Val Arg Glu His Leu Asn Val Pro Asp His Leu Ser
35 40 45
Lys Gly Asn Cys Lys Ala Ile Phe Thr Lys Arg Gly Cys Thr Leu Cys
50 55 60
Leu Gln Ile Phe Glu Glu Ala Phe Ala Leu Ala Glu His Lys Asn Lys
65 70 75 80
Cys His Leu Ser Pro Xaa Arg Pro Leu

85

(2) INFORMATION FOR SEQ ID NO:836:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1499057

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:836:

Met Lys Ile Ser Tyr His Ser Leu His Gln Pro Arg Cys Gly Val Cys
1 5 10 15
Leu Lys His Cys Lys Ser Phe Glu Ser Val Arg Glu His Leu Asn Val
20 25 30
Pro Asp His Leu Ser Lys Gly Asn Cys Lys Ala Ile Phe Thr Lys Arg
35 40 45
Gly Cys Thr Leu Cys Leu Gln Ile Phe Glu Glu Ala Phe Ala Leu Ala
50 55 60
Glu His Lys Asn Lys Cys His Leu Ser Pro Xaa Arg Pro Leu
65 70 75

(2) INFORMATION FOR SEQ ID NO:837:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1347 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1347

(D) OTHER INFORMATION: / Ceres Seq. ID 1499066

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:837:

acaaacccta	agaagcttct	catcttcctc	agaagcttct	catcttctct	60
ttctctcgaa	gattccgatt	tgctcttttg	aaacttcgga	actcgatcca	120
ccaacggcac	cttcaagcga	cgaagatgac	gtcgagactt	ccgaagatga	180
ttctaagaag	acgaaccaat	caaatccctt	cccgccacaa	ccgcgcgtgc	240
ttcacccgcg	ttctccgcgc	tactccagct	aaatccaccg	ccgtctccgc	300
tctaatacca	ccgcgcgtct	cgccgcgtct	gattcagatt	ctgggtccga	360
gattcggatt	ctgaatcgac	ggatccctcg	aaatctggat	ccggtaaaaa	420
aagaagaaag	aggaatccgt	gtcgtcgtct	gctactttag	ctttaccgcg	480
ggagcaaaag	ggcgacgcga	tgaagctcgc	acgacttcaa	cgaaacagat	540
gaagagagtg	taaaagagcc	agcacttttt	caaagactat	ggagtgcaga	600
ttctatgttac	aaggaatgat	agattatcat	gctgatcacg	ggaagctccc	660
actaatcgct	tttacgagtt	ccagaagaaa	tctatcagct	ttgaggttag	720
ttctcggata	aggttaggag	tttaagggaag	aagtaccgtg	ctaaagaagg	780
cctaggtttg	tgaagctcca	tgataagaaa	gcttttgtat	tgctcaagtt	840
cttaaaaggaa	tagctcttga	ttctaatgct	aagtccaacg	gtgtgtcgaa	900
agtaagacga	aggaagaagct	tgattctgta	aagcaagact	tggcgtttgt	960
tcaactaatg	gagatgattg	gtttgagaag	tcgtctcttg	ctagatgatg	1020
ggatattgat	agttattatg	gaggcagaaa	tggagttcgt	ttactcttga	1080
attgttgaag	agaagtttca	gttgatgcga	gctaaagagc	ttgaggtcaa	1140

aatgtgcgctt tgactgacct tacgtctctac ttcgttgatg cttogaagaa cttagagctat 1200
tagttactta gatttgcgg ttttttctat cggaatgcta tgcataatgc tttcttttgt 1260
ttttcggatt taggatttga ttctttctgg ttgtttttt tgggggtgaa agattctcta 1320
cattataata tttattttt tattcgt

(2) INFORMATION FOR SEQ ID NO:838:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..397
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:838:

Thr Asn Pro Lys Lys Leu Leu Ile Phe Leu Thr Asn Pro Lys Lys Leu
1 5 10 15
Leu Ile Phe Ser Phe Ser Arg Arg Phe Arg Phe Ala Leu Leu Lys Leu
20 25 30
Pro Met Thr Lys Lys Leu Asp Pro Pro Thr Ala Pro Ser Ser Asp Glu
35 40 45
Asp Asp Val Glu Thr Ser Glu Asp Asp Ser Ser Ser Glu Glu Asp
50 55 60
Glu Pro Ile Lys Ser Leu Pro Ala Thr Thr Ala Ala Pro Ala Lys
65 70 75 80
Ser Thr Ala Val Ser Ala Ala Thr Pro Ala Lys Ser Thr Ala Val Ser
85 90 95
Ala Ala Ala Pro Ser Lys Ser Thr Ala Val Ser Ala Ala Asp Ser
100 105 110
Asp Ser Gly Ser Glu Ser Glu Thr Asp Ser Asp Ser Glu Ser Thr Asp
115 120 125
Pro Pro Lys Ser Gly Ser Gly Lys Thr Ile Ala Ser Lys Lys Lys Glu
130 135 140
Asp Pro Ser Ser Ser Ser Ala Thr Leu Ala Leu Pro Ala Val Lys Ser
145 150 155 160
Gly Ala Lys Arg Ala Ala Ser Glu Ala Ala Thr Thr Ser Thr Lys Arg
165 170 175
Val Lys Lys Asp Glu Glu Ser Val Lys Lys Pro Ala Leu Phe Gln Arg
180 185 190
Leu Trp Ser Asp Asp Asp Glu Ile Ser Met Leu Gln Gly Met Ile Asp
195 200 205
Tyr His Ala Asp Thr Gly Lys Ser Pro Ser Ala Asp Thr Asn Ala Phe
210 215 220
Tyr Glu Phe Gln Lys Lys Ser Ile Ser Phe Glu Val Ser Lys Ser Gln
225 230 235 240
Phe Ser Asp Lys Val Arg Ser Leu Arg Lys Lys Tyr Arg Ala Lys Glu
245 250 255
Gly Lys Asp Glu Pro Arg Phe Val Lys Ala His Asp Lys Lys Ala Phe
260 265 270
Val Leu Ser Lys Phe Ile Trp Gly Pro Lys Gly Ile Ala Leu Asp Ser
275 280 285
Asn Ala Lys Ser Asn Gly Val Ser Lys Lys Asn Ala Ser Lys Thr Lys
290 295 300
Glu Lys Leu Asp Ser Val Lys Gln Asp Leu Ala Phe Val Gly Val Ser
305 310 315 320
Ser Thr Asn Gly Asp Asp Trp Phe Glu Lys Ser Ser Leu Ala Arg Met
325 330 335
Ile Ala Gly Ser Gly Ile Asp Glu Tyr Tyr Val Arg Gln Lys Trp Ser
340 345 350
Ser Phe Thr Leu Glu Thr Lys Lys Ile Val Glu Glu Lys Phe Gln Leu

355 360 365
Met Gln Ala Lys Glu Leu Glu Ala Lys Leu Glu Lys Asn Val Arg Leu
370 375 380
Thr Asp Leu Thr Ser Tyr Phe Val Asp Ala Ser Lys Asn
385 390 395

(2) INFORMATION FOR SEQ ID NO:839:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..364
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499068

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:839:

Met Thr Lys Lys Leu Asp Pro Pro Thr Ala Pro Ser Ser Asp Glu Asp
1 5 10 15
Asp Val Glu Thr Ser Glu Asp Asp Ser Ser Ser Ser Glu Glu Asp Glu
20 25 30
Pro Ile Lys Ser Leu Pro Ala Thr Thr Ala Ala Pro Ala Lys Ser
35 40 45
Thr Ala Val Ser Ala Ala Thr Pro Ala Lys Ser Thr Ala Val Ser Ala
50 55 60
Ala Ala Pro Ser Lys Ser Thr Ala Val Ser Ala Ala Asp Ser Asp
65 70 75 80
Ser Gly Ser Glu Ser Glu Thr Asp Ser Asp Ser Glu Ser Thr Asp Pro
85 90 95
Pro Lys Ser Gly Ser Gly Lys Thr Ile Ala Ser Lys Lys Lys Glu Asp
100 105 110
Pro Ser Ser Ser Ser Ala Thr Leu Ala Leu Pro Ala Val Lys Ser Gly
115 120 125
Ala Lys Arg Ala Ala Ser Glu Ala Ala Thr Thr Ser Thr Lys Arg Val
130 135 140
Lys Lys Asp Glu Glu Ser Val Lys Lys Pro Ala Leu Phe Gln Arg Leu
145 150 155 160
Trp Ser Asp Asp Asp Glu Ile Ser Met Leu Gln Gly Met Ile Asp Tyr
165 170 175
His Ala Asp Thr Gly Lys Ser Pro Ser Ala Asp Thr Asn Ala Phe Tyr
180 185 190
Glu Phe Gln Lys Lys Ser Ile Ser Phe Glu Val Ser Lys Ser Gln Phe
195 200 205
Ser Asp Lys Val Arg Ser Leu Arg Lys Lys Tyr Arg Ala Lys Glu Gly
210 215 220
Lys Asp Glu Pro Arg Phe Val Lys Ala His Asp Lys Lys Ala Phe Val
225 230 235 240
Leu Ser Lys Phe Ile Trp Gly Pro Lys Gly Ile Ala Leu Asp Ser Asn
245 250 255
Ala Lys Ser Asn Gly Val Ser Lys Lys Asn Ala Ser Lys Thr Lys Glu
260 265 270
Lys Leu Asp Ser Val Lys Gln Asp Leu Ala Phe Val Gly Val Ser Ser
275 280 285
Thr Asn Gly Asp Asp Trp Phe Glu Lys Ser Ser Leu Ala Arg Met Ile
290 295 300
Ala Gly Ser Gly Ile Asp Glu Tyr Tyr Val Arg Gln Lys Trp Ser Ser
305 310 315 320
Phe Thr Leu Glu Thr Lys Lys Ile Val Glu Glu Lys Phe Gln Leu Met
325 330 335
Gln Ala Lys Glu Leu Glu Ala Lys Leu Glu Lys Asn Val Arg Leu Thr
340 345 350

(2) INFORMATION FOR SEO ID NO:840:

(A) LENGTH: 1565 base pairs

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1565
(D) OTHER INFORMATION: / Ceres Seq. ID 1499073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:840:

atgggtccag	tgtgtctttt	tcctttattg	atagataaat	caaaaatccg	agtcggagac	60
gacgaagacc	cgaggtccag	cttttaacta	tgcgacatcc	atcgaagacg	catagtttca	120
ctctatttct	cttcataatc	gtttttgtaa	tgtgtgtctg	ctgtgtacgt	gcacctgatt	180
ctaatgtcta	cgctctcgac	aattcaagtc	gtcttgtctg	tattgaccgc	tggatcgctc	240
atccattttt	atatgatggc	aggaaattat	atttgggtgt	ttagatttgc	aggatgtgtg	300
aaacaagag	cgaggcgggg	tatgttgtat	tgtgacgatt	tgaccctgtc	agctcaattt	360
ttcttgattc	tgaaaaattc	gatctgtctg	aagggtttta	cgactggcac	ctgtcaaaat	420
gtgacacag	tttatgacaa	ctgtggacga	cagcacaggt	taattattat	tgtgggaact	480
gtagtgtgtg	acgggtgtaa	ggtgtgactg	gctgcataat	tgtgtcaacc	caagatctaa	540
cttgtagagt	tactgtcgac	ttgctctatt	catgtgagaa	acctggtctc	cggtgtgtta	600
agggattttc	agtcggtttg	catctctcgt	catgggaaat	tatctataat	gggatgacac	660
agcttggatt	tgataagccg	cgctgtgagt	ttagcttcaa	gacgcagcag	actcatctca	720
ctctctatat	gactgcaatt	gtctctcttt	caaacattgt	agggaagact	atcatacaag	780
tttcccacga	gaatggtctt	gatgttaaga	tactgtgttc	ttctctgact	gggaactcat	840
caacaacttt	atcaaccgtc	acttttagat	tggattggaa	tgtgtgaaa	cttcggcgaa	900
ctccatattc	agtcacatgc	accatccocg	tggaatgtta	tgatcttgtt	cagtttttcc	960
ttacaaaact	ctgcgaatac	aatacaagta	acggaaggag	atacgcgaaa	ggttgggctc	1020
tatttggagt	ttttctctgc	gtattctctg	ttgcactctg	acttttctgc	tgtgggggct	1080
ttattattaa	aaacaagata	gagcgtgtgc	gtggaactga	tgcatttcgc	gggatgtcac	1140
ctctatcggg	cttactagaa	actgtgagtg	gaagtggaca	aagctactca	agaactgaag	1200
acatacaaca	tgtcttttgc	ataagaagtc	catggggacg	ctcttcgca	ttctctactc	1260
aagcgacaaa	caacacagaa	ccaagtgtat	gaacataatg	tgcgtactaa	ttttgtcaag	1320
tgcctcaaca	gaggtacttt	ttcaagcaga	gtatgtggac	ctgtgtgctc	tgcgatttct	1380
ggatttttgt	tattgtatgt	attttctacc	ttctagaaga	aggtctaaaa	gttaaatagc	1440
tccacgtgag	aatgtttgtt	tccaccagat	catgtgtctat	gtgacaaaaa	gacaaagcaa	1500
acaagagttc	tttcttttgt	tagttataca	gaacaagagt	atcgttataa	agtcaacaaa	1560
gattg						

(2) INFORMATION FOR SEQ ID NO:841:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..435
(D) OTHER INFORMATION: / Ceres Seq. ID 1499074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:841:

Gly	Ser	Ser	Arg	Leu	Cys	Ser	Leu	Ile	Asp	Arg	Ile	Ile	Lys	Asn	Pro
1				5					10					15	
Ser	Arg	Arg	Arg	Arg	Arg	Pro	Glu	Phe	Gln	Leu	Leu	Thr	Met	Gln	Ile
			20					25					30		
Pro	Ser	Arg	Glu	His	Ser	Phe	Ile	Leu	Phe	Leu	Phe	Ile	Ser	Ala	Phe
			35				40					45			
Val	Ile	Gly	Ala	Ala	Ser	Val	Pro	Val	Pro	Asp	Ser	Asn	Cys	Tyr	Ala
50						55					60				

Leu Asp Asn Ser Ser Arg Leu Val Asp Phe Ser Ser Trp Ile Gly His
65 70 75 80
Pro Phe Glu Tyr Asp Gly Lys Glu Phe Asp Leu Val Val Arg Phe Cys
85 90 95
Lys Asp Val Glu Thr Arg Gly Gln Ala Gly Tyr Val Asp Phe Gly Arg
100 105 110
Phe Asp Pro Leu Ser Tyr Phe Val Ser Ser Ser Glu Asn Phe Asp Phe
115 120 125
Val Gln Gly Phe Tyr His Gly Asp Leu Ser Asn Cys Glu Gln Ser Tyr
130 135 140
Asp Lys Leu Gly Arg Thr Ala Gln Val Asn Ile Ile Cys Gly Asn Cys
145 150 155 160
Ser Asp Gly Arg Cys Lys Gly Gly Leu Gly Cys Ile Cys Ser Val Thr
165 170 175
Gln Asp Ser Thr Cys Arg Val Thr Val Asp Leu Ala Ile Pro Cys Glu
180 185 190
Lys Pro Gly Pro Arg Val Phe Lys Gly Phe Thr Val Gly Leu His Pro
195 200 205
Arg Ser Trp Glu Ile Ile Tyr Asn Gly Met Thr Gln Phe Gly Phe Asp
210 215 220
Lys Pro Arg Arg Glu Phe Ser Phe Lys Thr Glu Gln Thr His Leu Thr
225 230 235 240
Leu Tyr Met Thr Ala Ile Ala Ser Leu Ser Thr Leu Val Gly Lys Pro
245 250 255
Ile Ile Lys Val Ser Pro Glu Asn Gly Leu Asp Val Lys Ile Ala Gly
260 265 270
Ser Ser Leu Thr Gly Asn His Pro Thr Thr Leu Ser Pro Ser Thr Leu
275 280 285
Val Leu Asp Trp Asn Cys Glu Lys Ser Arg Arg Thr Pro Tyr Glu Val
290 295 300
Asn Val Thr Ile Pro Val Asp Gly Tyr Asp Pro Val Gln Phe Phe Leu
305 310 315 320
Thr Lys Leu Cys Glu Tyr Asn Gln Gly Asn Glu Gly Gly Ser Ala Lys
325 330 335
Gly Trp Ala Ile Phe Gly Val Phe Ser Cys Val Phe Leu Val Ala Ser
340 345 350
Ala Leu Phe Cys Cys Gly Gly Phe Ile Tyr Lys Thr Arg Val Glu Arg
355 360 365
Val Arg Gly Thr Asp Ala Leu Pro Gly Met Ser Leu Leu Ser Gly Leu
370 375 380
Leu Glu Thr Val Ser Gly Ser Gly Gln Ser Tyr Ser Arg Thr Glu Asp
385 390 395 400
Ile Asn Asn Ala Phe Ala Asn Glu Val Ser Trp Asp Arg Ser Ser Ala
405 410 415
Ser Ser Thr Gln Ala Thr Thr Thr Gln Arg Pro Ser Glu Arg Thr Tyr
420 425 430
Gly Ala Ile
435

(2) INFORMATION FOR SEQ ID NO:842:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 406 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..406

(D) OTHER INFORMATION: / Ceres Seq. ID 1499075

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:842:

Met Gln Ile Pro Ser Arg Glu His Ser Phe Ile Leu Phe Leu Phe Ile

1	5	10	15
Ser Ala Phe Val Ile Gly Ala Ala Ser Val Pro Val Pro Asp Ser Asn			
20		25	30
Cys Tyr Ala Leu Asp Asn Ser Ser Arg Leu Val Asp Phe Ser Ser Trp			
35	40	45	
Ile Gly His Pro Phe Glu Tyr Asp Gly Lys Glu Phe Asp Leu Val Val			
50	55	60	
Arg Phe Cys Lys Asp Val Glu Thr Arg Gly Gln Ala Gly Tyr Val Asp			
65	70	75	80
Phe Gly Arg Phe Asp Pro Leu Ser Tyr Phe Val Ser Ser Ser Glu Asn			
85	90	95	
Phe Asp Phe Val Gln Gly Phe Tyr His Gly Asp Leu Ser Asn Cys Glu			
100	105	110	
Gln Ser Tyr Asp Lys Leu Gly Arg Thr Ala Gln Val Asn Ile Ile Cys			
115	120	125	
Gly Asn Cys Ser Asp Gly Arg Cys Lys Gly Gly Leu Gly Cys Ile Cys			
130	135	140	
Ser Val Thr Gln Asp Ser Thr Cys Arg Val Thr Val Asp Leu Ala Ile			
145	150	155	160
Pro Cys Glu Lys Pro Gly Pro Arg Val Phe Lys Gly Phe Thr Val Gly			
165	170	175	
Leu His Pro Arg Ser Trp Glu Ile Ile Tyr Asn Gly Met Thr Gln Phe			
180	185	190	
Gly Phe Asp Lys Pro Arg Arg Glu Phe Ser Phe Lys Thr Glu Gln Thr			
195	200	205	
His Leu Thr Leu Tyr Met Thr Ala Ile Ala Ser Leu Ser Thr Leu Val			
210	215	220	
Gly Lys Pro Ile Ile Lys Val Ser Pro Glu Asn Gly Leu Asp Val Lys			
225	230	235	240
Ile Ala Gly Ser Ser Leu Thr Gly Asn His Pro Thr Thr Leu Ser Pro			
245	250	255	
Ser Thr Leu Val Leu Asp Trp Asn Cys Glu Lys Ser Arg Arg Thr Pro			
260	265	270	
Tyr Glu Val Asn Val Thr Ile Pro Val Asp Gly Tyr Asp Pro Val Gln			
275	280	285	
Phe Phe Leu Thr Lys Leu Cys Glu Tyr Asn Gln Gly Asn Glu Gly Gly			
290	295	300	
Ser Ala Lys Gly Trp Ala Ile Phe Gly Val Phe Ser Cys Val Phe Leu			
305	310	315	320
Val Ala Ser Ala Leu Phe Cys Cys Gly Gly Phe Ile Tyr Lys Thr Arg			
325	330	335	
Val Glu Arg Val Arg Gly Thr Asp Ala Leu Pro Gly Met Ser Leu Leu			
340	345	350	
Ser Gly Leu Leu Glu Thr Val Ser Gly Ser Gly Gln Ser Tyr Ser Arg			
355	360	365	
Thr Glu Asp Ile Asn Asn Ala Phe Ala Asn Glu Val Ser Trp Asp Arg			
370	375	380	
Ser Ser Ala Ser Ser Thr Gln Ala Thr Thr Thr Gln Arg Pro Ser Glu			
385	390	395	400
Arg Thr Tyr Gly Ala Ile			
405			

(2) INFORMATION FOR SEQ ID NO:843:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..218

(D) OTHER INFORMATION: / Ceres Seq. ID 1499076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:843:

Met	Thr	Gln	Phe	Gly	Phe	Asp	Lys	Pro	Arg	Arg	Glu	Phe	Ser	Phe	Lys
1				5					10					15	
Thr	Glu	Gln	Thr	His	Leu	Thr	Leu	Tyr	Met	Thr	Ala	Ile	Ala	Ser	Leu
				20				25					30		
Ser	Thr	Leu	Val	Gly	Lys	Pro	Ile	Lys	Val	Ser	Pro	Glu	Asn	Gly	
				35			40				45				
Leu	Asp	Val	Lys	Ile	Ala	Gly	Ser	Ser	Leu	Thr	Gly	Asn	His	Pro	Thr
				50			55				60				
Thr	Leu	Ser	Pro	Ser	Thr	Leu	Val	Leu	Asp	Trp	Asn	Cys	Glu	Lys	Ser
65					70					75				80	
Arg	Arg	Thr	Pro	Tyr	Glu	Val	Asn	Val	Thr	Ile	Pro	Val	Asp	Gly	Tyr
				85				90					95		
Asp	Pro	Val	Gln	Phe	Phe	Leu	Thr	Lys	Leu	Cys	Glu	Tyr	Asn	Gln	Gly
				100				105					110		
Asn	Glu	Gly	Gly	Ser	Ala	Lys	Gly	Trp	Ala	Ile	Phe	Gly	Val	Phe	Ser
				115			120				125				
Cys	Val	Phe	Leu	Val	Ala	Ser	Ala	Leu	Phe	Cys	Cys	Gly	Gly	Phe	Ile
				130			135				140				
Tyr	Lys	Thr	Arg	Val	Glu	Arg	Val	Arg	Gly	Thr	Asp	Ala	Leu	Pro	Gly
145					150					155				160	
Met	Ser	Leu	Leu	Ser	Gly	Leu	Leu	Glu	Thr	Val	Ser	Gly	Ser	Gly	Gln
				165				170					175		
Ser	Tyr	Ser	Arg	Thr	Glu	Asp	Ile	Asn	Asn	Ala	Phe	Ala	Asn	Glu	Val
				180				185					190		
Ser	Trp	Asp	Arg	Ser	Ser	Ala	Ser	Ser	Thr	Gln	Ala	Thr	Thr	Thr	Gln
				195			200				205				
Arg	Pro	Ser	Glu	Arg	Thr	Tyr	Gly	Ala	Ile						
				210			215								

(2) INFORMATION FOR SEQ ID NO:844:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1358 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1358

(D) OTHER INFORMATION: / Ceres Seq. ID 1499077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:844:

agcacaataa	tactgtctaa	atgtctctct	actttctcat	cactgtgtctc	tctttctttt	60
tctttaccaa	atctctttct	cttctctcat	gggcatctga	aacccaaacc	ttgtctctct	120
tctacttcat	caagaatccc	tttatgaaca	cctacatca	gaccaaacc	gatccagcct	180
ctccggtagt	cgacaaatgt	tcggttcttg	acctccctga	gctggctctt	gactgcattc	240
ttgacctctt	tccacctct	ggactctgca	gcattggctag	ggtttgtagc	tccttgaggg	300
agagatgtgt	tagtgcattc	ctatgggaga	aacatttgaa	gaccaaattg	ggccaaattc	360
ttggccctgc	tgctcacaga	gagtggaat	gctatatctc	ctcttcacca	tatcatcttg	420
attctctctc	ctatcaaaat	gggaattctg	gttttgccaa	aatcatctct	ctgatccgat	480
ctctttcatc	cgttttccga	gaggataaac	aaaggagggg	atatgcattc	tctctgccac	540
ttgattccag	ctagagctgc	taacctctcc	ttgaaacagg	tcgttttttg	ttcccagctc	600
aagtgtacaa	ccgtgagaat	ggacatgtag	ggttcatggt	gtcatgctat	gatggggagc	660
tcagctatga	tactcacacg	gatacgttcc	aagccaggta	tcaccacatc	ggtgacgagc	720
catctgcgat	tgaaaaagggt	gtgacatggg	atagaataag	agcagctccc	attgatgcatt	780
caacctcatc	tctccatgta	tcagattctt	taaaagagtt	gaaacctgga	gacacatcat	840
aaatccagtc	gagaaggaaac	aaagagttcc	catatggatg	gtggatgtgt	ctgtgtccgc	900
actttggaat	ctgtgatgga	gatcataaac	attgccattg	ccatcttagt	gagacggtag	960
gtttggaatt	caaccagtag	acagtcggat	caaggtggag	aagaacagatg	atcatgagag	1020
atcataaaga	ggaaggtaac	gaagaagacg	ggttctatgg	aggaatccga	aagctaaatt	1080
gtaaagaaga	gattgcaatg	tggaacagtc	actggccttg	ctccatcttg	gaatagcatt	1140

aaagaagctt tgcgttaaca catggggaaa gatattacac atcactatac tgagagtagg 1200
ttgttaaat tagactctta ttctctttta tccaatgtat gggtgatcgt gaattatttg 1260
ttgggaataa agtctatagc tgaattattt gtgtcacttc gatttgagaa atattgtgtt 1320
gtatagggaa aacttaatac aattgatttg aatactcc

(2) INFORMATION FOR SEQ ID NO:845:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..371

(D) OTHER INFORMATION: / Ceres Seq. ID 1499078

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:845:

Met	Leu	Leu	Tyr	Phe	Leu	Ile	Thr	Cys	Leu	Ser	Phe	Phe	Phe	Phe	Thr
1			5						10				15		
Lys	Ser	Leu	Ser	Leu	Pro	Pro	Trp	Ala	Ser	Glu	Thr	Lys	Thr	Leu	Leu
		20						25				30			
Ser	Phe	Tyr	Phe	Ile	Lys	Asn	Pro	Phe	Met	Asn	Thr	Leu	His	Gln	Thr
		35				40					45				
Lys	His	Asp	Pro	Ala	Ser	Pro	Val	Ile	Asp	Gln	Met	Ser	Val	Leu	Asp
	50				55				60						
Leu	Pro	Glu	Leu	Ala	Leu	Asp	Cys	Ile	Leu	Asp	Leu	Leu	Pro	Pro	Ser
65				70					75				80		
Gly	Leu	Cys	Ser	Met	Ala	Arg	Val	Cys	Ser	Ser	Leu	Arg	Glu	Arg	Cys
		85						90				95			
Val	Ser	Asp	His	Leu	Trp	Glu	Lys	His	Leu	Lys	Thr	Lys	Trp	Gly	Lys
		100					105				110				
Ile	Leu	Gly	Pro	Ala	Ala	His	Arg	Glu	Trp	Gln	Cys	Tyr	Ile	Ser	Ser
		115				120					125				
Ser	Thr	Tyr	His	Leu	Asp	Ser	Pro	His	His	Gln	Thr	Gly	Asn	Leu	Gly
	130				135						140				
Phe	Ala	Lys	Ile	Ile	Ser	Leu	Ile	Arg	Ser	Leu	Ser	Ser	Val	Phe	Arg
145				150					155					160	
Glu	Asp	Lys	Gln	Arg	Arg	Gly	Tyr	Ala	Ser	Ser	Leu	Pro	Leu	Asp	Ser
		165						170					175		
Ser	Met	Ser	Cys	Tyr	Leu	Ser	Leu	Glu	Thr	Gly	Arg	Phe	Trp	Phe	Pro
		180						185				190			
Ala	Gln	Val	Tyr	Asn	Arg	Glu	Asn	Gly	His	Val	Gly	Phe	Met	Leu	Ser
		195				200					205				
Cys	Tyr	Asp	Ala	Glu	Leu	Ser	Tyr	Asp	Thr	His	Thr	Asp	Thr	Phe	Gln
	210					215					220				
Ala	Arg	Tyr	Pro	Pro	His	Gly	Arg	Arg	Ala	Ser	Ala	Ile	Glu	Lys	Gly
225				230					235					240	
Val	Thr	Trp	Asp	Arg	Ile	Arg	Ala	Ala	Pro	Ile	Asp	Ala	Ser	Pro	His
		245					250						255		
Leu	Leu	His	Val	Ser	Asp	Ser	Leu	Lys	Glu	Leu	Lys	Pro	Gly	Asp	His
		260					265					270			
Ile	Glu	Ile	Gln	Trp	Arg	Arg	Asn	Lys	Glu	Phe	Pro	Tyr	Gly	Trp	Trp
	275					280					285				
Tyr	Gly	Leu	Val	Arg	His	Leu	Glu	Ser	Cys	Asp	Gly	Asp	His	Asn	His
	290				295						300				
Cys	His	Cys	His	Leu	Ser	Glu	Thr	Val	Val	Leu	Glu	Phe	Asn	Gln	Tyr
305				310						315				320	
Thr	Val	Gly	Ser	Arg	Trp	Arg	Arg	Thr	Met	Ile	Met	Arg	Asp	His	Lys
		325						330					335		
Glu	Glu	Gly	Asn	Glu	Glu	Asp	Gly	Phe	Tyr	Gly	Gly	Ile	Arg	Lys	Leu
		340					345					350			
Asn	Cys	Lys	Glu	Glu	Ile	Ala	Met	Trp	Lys	Arg	His	Trp	Pro	Cys	Ser

355 360 365
Ile Leu Glu
370
(2) INFORMATION FOR SEQ ID NO:846:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 330 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..330
(D) OTHER INFORMATION: / Ceres Seq. ID 1499079
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:846:
Met Asn Thr Leu His Gln Thr Lys His Asp Pro Ala Ser Pro Val Ile
1 5 10 15
Asp Gln Met Ser Val Leu Asp Leu Pro Glu Leu Ala Leu Asp Cys Ile
20 25 30
Leu Asp Leu Leu Pro Pro Ser Gly Leu Cys Ser Met Ala Arg Val Cys
35 40 45
Ser Ser Leu Arg Glu Arg Cys Val Ser Asp His Leu Trp Glu Lys His
50 55 60
Leu Lys Thr Lys Trp Gly Lys Ile Leu Gly Pro Ala Ala His Arg Glu
65 70 75 80
Trp Gln Cys Tyr Ile Ser Ser Ser Thr Tyr His Leu Asp Ser Pro His
85 90 95
His Gln Thr Gly Asn Leu Gly Phe Ala Lys Ile Ile Ser Leu Ile Arg
100 105 110
Ser Leu Ser Ser Val Phe Arg Glu Asp Lys Gln Arg Arg Gly Tyr Ala
115 120 125
Ser Ser Leu Pro Leu Asp Ser Ser Met Ser Cys Tyr Leu Ser Leu Glu
130 135 140
Thr Gly Arg Phe Trp Phe Pro Ala Gln Val Tyr Asn Arg Glu Asn Gly
145 150 155 160
His Val Gly Phe Met Leu Ser Cys Tyr Asp Ala Glu Leu Ser Tyr Asp
165 170 175
Thr His Thr Asp Thr Phe Gln Ala Arg Tyr Pro Pro His Gly Arg Arg
180 185 190
Ala Ser Ala Ile Glu Lys Gly Val Thr Trp Asp Arg Ile Arg Ala Ala
195 200 205
Pro Ile Asp Ala Ser Pro His Leu Leu His Val Ser Asp Ser Leu Lys
210 215 220
Glu Leu Lys Pro Gly Asp His Ile Glu Ile Gln Trp Arg Arg Asn Lys
225 230 235 240
Glu Phe Pro Tyr Gly Trp Trp Tyr Gly Leu Val Arg His Leu Glu Ser
245 250 255
Cys Asp Gly Asp His Asn His Cys His Cys His Leu Ser Glu Thr Val
260 265 270
Val Leu Glu Phe Asn Gln Tyr Thr Val Gly Ser Arg Trp Arg Arg Thr
275 280 285
Met Ile Met Arg Asp His Lys Glu Glu Gly Asn Glu Glu Asp Gly Phe
290 295 300
Tyr Gly Gly Ile Arg Lys Leu Asn Cys Lys Glu Glu Ile Ala Met Trp
305 310 315 320
Lys Arg His Trp Pro Cys Ser Ile Leu Glu
325 330
(2) INFORMATION FOR SEQ ID NO:847:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 312 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..312
(D) OTHER INFORMATION: / Ceres Seq. ID 1499080
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:847:
Met Ser Val Leu Asp Leu Pro Glu Leu Ala Leu Asp Cys Ile Leu Asp
1 5 10 15
Leu Leu Pro Pro Ser Gly Leu Cys Ser Met Ala Arg Val Cys Ser Ser
20 25 30
Leu Arg Glu Arg Cys Val Ser Asp His Leu Trp Glu Lys His Leu Lys
35 40 45
Thr Lys Trp Gly Lys Ile Leu Gly Pro Ala Ala His Arg Glu Trp Gln
50 55 60
Cys Tyr Ile Ser Ser Ser Thr Tyr His Leu Asp Ser Pro His His Gln
65 70 75 80
Thr Gly Asn Leu Gly Phe Ala Lys Ile Ile Ser Leu Ile Arg Ser Leu
85 90 95
Ser Ser Val Phe Arg Glu Asp Lys Gln Arg Arg Gly Tyr Ala Ser Ser
100 105 110
Leu Pro Leu Asp Ser Ser Met Ser Cys Tyr Leu Ser Leu Glu Thr Gly
115 120 125
Arg Phe Trp Phe Pro Ala Gln Val Tyr Asn Arg Glu Asn Gly His Val
130 135 140
Gly Phe Met Leu Ser Cys Tyr Asp Ala Glu Leu Ser Tyr Asp Thr His
145 150 155 160
Thr Asp Thr Phe Gln Ala Arg Tyr Pro Pro His Gly Arg Arg Ala Ser
165 170 175
Ala Ile Glu Lys Gly Val Thr Trp Asp Arg Ile Arg Ala Ala Pro Ile
180 185 190
Asp Ala Ser Pro His Leu Leu His Val Ser Asp Ser Leu Lys Glu Leu
195 200 205
Lys Pro Gly Asp His Ile Glu Ile Gln Trp Arg Arg Asn Lys Glu Phe
210 215 220
Pro Tyr Gly Trp Trp Tyr Gly Leu Val Arg His Leu Glu Ser Cys Asp
225 230 235 240
Gly Asp His Asn His Cys His Cys His Leu Ser Glu Thr Val Val Leu
245 250 255
Glu Phe Asn Gln Tyr Thr Val Gly Ser Arg Trp Arg Arg Thr Met Ile
260 265 270
Met Arg Asp His Lys Glu Glu Gly Asn Glu Glu Asp Gly Phe Tyr Gly
275 280 285
Gly Ile Arg Lys Leu Asn Cys Lys Glu Glu Ile Ala Met Trp Lys Arg
290 295 300
His Trp Pro Cys Ser Ile Leu Glu
305 310
(2) INFORMATION FOR SEQ ID NO:848:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 470 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..470
(D) OTHER INFORMATION: / Ceres Seq. ID 1499085
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:848:
aaaacattac tcattcacaa aaccatctta aagcaactac acaaatcttg aaattttctc

atatttttcta tttactatat aaactttttaa tcaaatcaag attaactatg gctgaggagt 120
acaagaacaa cgtttcccag cacgagacac caacggtcgc aacagaggaa tcaccagcga 180
cgacaacaga ggttacggat cgtggattgt ttgatttctt ggggaagaag gaagaggaa 240
tgaaacctca agagacaacg acgctcgagt ctgagtgtcg atcataagge tcagatctct 300
gaaccggagt tagctgcgga sacgaggaag taaaggagaa caagattact ctgctagagg 360
agcttcaaga aagaccggag gaagatgagg agaacaagcc tagtgtcacc gaaaagcttc 420
accgatccaa cagctcttct tcctctctcg agcgatgaag aagagctggt

(2) INFORMATION FOR SEQ ID NO:849:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 1499086

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:849:

Asn Ile Thr His Ser Gln Asn His Leu Lys Ala Thr Thr Gln Ile Leu
1 5 10 15
Lys Phe Ser His Ile Phe Tyr Leu Leu Tyr Lys Leu Leu Ile Lys Ser
20 25 30
Arg Leu Thr Met Ala Glu Glu Tyr Lys Asn Asn Val Pro Glu His Glu
35 40 45
Thr Pro Thr Val Ala Thr Glu Glu Ser Pro Ala Thr Thr Thr Glu Val
50 55 60
Thr Asp Arg Gly Leu Phe Asp Phe Leu Gly Lys Lys Glu Glu Glu Val
65 70 75 80
Lys Pro Gln Glu Thr Thr Thr Leu Glu Ser Glu Cys Arg Ser
85 90

(2) INFORMATION FOR SEQ ID NO:850:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..59

(D) OTHER INFORMATION: / Ceres Seq. ID 1499087

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:850:

Met Ala Glu Glu Tyr Lys Asn Asn Val Pro Glu His Glu Thr Pro Thr
1 5 10 15
Val Ala Thr Glu Glu Ser Pro Ala Thr Thr Thr Glu Val Thr Asp Arg
20 25 30
Gly Leu Phe Asp Phe Leu Gly Lys Lys Glu Glu Glu Val Lys Pro Gln
35 40 45
Glu Thr Thr Thr Leu Glu Ser Glu Cys Arg Ser
50 55

(2) INFORMATION FOR SEQ ID NO:851:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 678 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..678

(D) OTHER INFORMATION: / Ceres Seq. ID 1499088

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:851:

cggkttgataa aggaaatatt aastccatgc caaacagaaag catgccagct tctccttato	60
ctactccagg ggctctgttta atgggagatg catttaacat gcgtcatcct ttgacgggtg	120
gaggaatgac ggttgacatta gctgacattg ttgtcctcgc taatctcctt agaccgctgc	180
gtgatcttag tgacggcgct agtctctgca aatatcttga atcatctttac actctgcgaa	240
agccagtggc agcaacaatc aacacccttg cgaatgctct ttaccaagtt tctctgtcat	300
cagaaaatga agcaagaaac gagatgaggg aagcttgctt cgattatctg ggactcgggg	360
gtatgtgcac aagtggacca gtatctttgc ttctgggttt gaacctctga ccataaacac	420
ttgttgcaca ttcttttgcg gttgcgggtt atggagtcac acggttgta atccattcc	480
ctccccaaaa acgaatctgg cttggagcta aattgatctc gggagcatcg gggataatat	540
ttccaataat aaaagcggaa ggagtttagc agatgttttt ccagcaact gtacctgcat	600
actactacaa agctcctaca gttggagaaa ccaaatgttc atagtccaa ataatctctg	660
tcacgagaaa tgcacatac	

(2) INFORMATION FOR SEQ ID NO:852:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..213

(D) OTHER INFORMATION: / Ceres Seq. ID 1499089

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:852:

Xaa Asp Lys Gly Asn Ile Xaa Ser Met Pro Asn Arg Ser Met Pro Ala	
1 5 10 15	
Ser Pro Tyr Pro Thr Pro Gly Ala Leu Leu Met Gly Asp Ala Phe Asn	
20 25 30	
Met Arg His Pro Leu Thr Gly Gly Met Thr Val Ala Leu Ala Asp	
35 40 45	
Ile Val Val Leu Arg Asn Leu Leu Arg Pro Leu Arg Asp Leu Ser Asp	
50 55 60	
Gly Ala Ser Leu Cys Lys Tyr Leu Glu Ser Phe Tyr Thr Leu Arg Lys	
65 70 75 80	
Pro Val Ala Ala Thr Ile Asn Thr Leu Ala Asn Ala Leu Tyr Gln Val	
85 90 95	
Phe Cys Ser Ser Glu Asn Glu Ala Arg Asn Glu Met Arg Glu Ala Cys	
100 105 110	
Phe Asp Tyr Leu Gly Leu Gly Gly Met Cys Thr Ser Gly Pro Val Ser	
115 120 125	
Leu Leu Ser Gly Leu Asn Pro Arg Pro Leu Thr Leu Val Cys His Phe	
130 135 140	
Phe Ala Val Ala Val Tyr Gly Val Ile Arg Leu Leu Ile Pro Phe Pro	
145 150 155 160	
Ser Pro Lys Arg Ile Trp Leu Gly Ala Lys Leu Ile Ser Gly Ala Ser	
165 170 175	
Gly Ile Ile Phe Pro Ile Ile Lys Ala Glu Gly Val Arg Gln Met Phe	
180 185 190	
Phe Pro Ala Thr Val Pro Ala Tyr Tyr Tyr Lys Ala Pro Thr Val Gly	
195 200 205	
Glu Thr Lys Cys Ser	
210	

(2) INFORMATION FOR SEQ ID NO:853:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..205

(D) OTHER INFORMATION: / Ceres Seq. ID 1499090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:853:

Met	Pro	Asn	Arg	Ser	Met	Pro	Ala	Ser	Pro	Tyr	Pro	Thr	Pro	Gly	Ala
1				5				10						15	
Leu	Leu	Met	Gly	Asp	Ala	Phe	Asn	Met	Arg	His	Pro	Leu	Thr	Gly	Gly
		20					25					30			
Gly	Met	Thr	Val	Ala	Leu	Ala	Asp	Ile	Val	Val	Leu	Arg	Asn	Leu	Leu
	35					40					45				
Arg	Pro	Leu	Arg	Asp	Leu	Ser	Asp	Gly	Ala	Ser	Leu	Cys	Lys	Tyr	Leu
	50				55						60				
Glu	Ser	Phe	Tyr	Thr	Leu	Arg	Lys	Pro	Val	Ala	Ala	Thr	Ile	Asn	Thr
	65				70				75					80	
Leu	Ala	Asn	Ala	Leu	Tyr	Gln	Val	Phe	Cys	Ser	Ser	Glu	Asn	Glu	Ala
				85				90						95	
Arg	Asn	Glu	Met	Arg	Glu	Ala	Cys	Phe	Asp	Tyr	Leu	Gly	Leu	Gly	Gly
		100					105					110			
Met	Cys	Thr	Ser	Gly	Pro	Val	Ser	Leu	Leu	Ser	Gly	Leu	Asn	Pro	Arg
		115					120					125			
Pro	Leu	Thr	Leu	Val	Cys	His	Phe	Phe	Ala	Val	Ala	Val	Tyr	Gly	Val
	130					135					140				
Ile	Arg	Leu	Leu	Ile	Pro	Phe	Pro	Ser	Pro	Lys	Arg	Ile	Trp	Leu	Gly
	145				150					155				160	
Ala	Lys	Leu	Ile	Ser	Gly	Ala	Ser	Gly	Ile	Ile	Phe	Pro	Ile	Ile	Lys
				165				170						175	
Ala	Glu	Gly	Val	Arg	Gln	Met	Phe	Phe	Pro	Ala	Thr	Val	Pro	Ala	Tyr
		180					185						190		
Tyr	Tyr	Lys	Ala	Pro	Thr	Val	Gly	Glu	Thr	Lys	Cys	Ser			
		195				200						205			

(2) INFORMATION FOR SEQ ID NO:854:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..200

(D) OTHER INFORMATION: / Ceres Seq. ID 1499091

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:854:

Met	Pro	Ala	Ser	Pro	Tyr	Pro	Thr	Pro	Gly	Ala	Leu	Leu	Met	Gly	Asp
1				5				10						15	
Ala	Phe	Asn	Met	Arg	His	Pro	Leu	Thr	Gly	Gly	Gly	Met	Thr	Val	Ala
		20					25					30			
Leu	Ala	Asp	Ile	Val	Val	Leu	Arg	Asn	Leu	Leu	Arg	Pro	Leu	Arg	Asp
		35				40					45				
Leu	Ser	Asp	Gly	Ala	Ser	Leu	Cys	Lys	Tyr	Leu	Glu	Ser	Phe	Tyr	Thr
	50				55						60				
Leu	Arg	Lys	Pro	Val	Ala	Ala	Thr	Ile	Asn	Thr	Leu	Ala	Asn	Ala	Leu
	65				70				75					80	
Tyr	Gln	Val	Phe	Cys	Ser	Ser	Glu	Asn	Glu	Ala	Arg	Asn	Glu	Met	Arg
			85				90						95		
Glu	Ala	Cys	Phe	Asp	Tyr	Leu	Gly	Leu	Gly	Gly	Met	Cys	Thr	Ser	Gly
		100					105					110			
Pro	Val	Ser	Leu	Leu	Ser	Gly	Leu	Asn	Pro	Arg	Pro	Leu	Thr	Leu	Val
		115				120						125			
Cys	His	Phe	Phe	Ala	Val	Ala	Val	Tyr	Gly	Val	Ile	Arg	Leu	Leu	Ile
	130						135					140			

Pro Phe Pro Ser Pro Lys Arg Ile Trp Leu Gly Ala Lys Leu Ile Ser
145 150 155 160
Gly Ala Ser Gly Ile Ile Phe Pro Ile Ile Lys Ala Glu Gly Val Arg
165 170 175
Gln Met Phe Phe Pro Ala Thr Val Pro Ala Tyr Tyr Tyr Lys Ala Pro
180 185 190
Thr Val Gly Glu Thr Lys Cys Ser
195 200

(2) INFORMATION FOR SEQ ID NO:855:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1146
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:855:

aattgcaaat caaatggatc gtcttaagct ttatttctcc gttttcgttt tgtctttctt 60
tatcgtctcg gtttcgtcgt ctgatgtcaa cgacggcgat gatctcgtga tccgtcaggt 120
ggttggttga gccgagcctc aggttttgac ctacagagat cacttttctc tcttcaagcg 180
gaagttcggg aaggtctacg cttccaacga ggagcatgac tatagattct cggtttgagt 240
tccgtaagaa gcaactgggg gttagaagtg gctttaagct tcctaaagat gccacaaggg 300
ctccgattct cctcaccacg aatctccctg aggattttga ttggagagat catggcgccc 360
ttactcccg tcaaaaatcag ggaacttgcg gctcttgctg gagtttcacg gccactggag 420
ctttggaagg tgctaaactc ctcgctacgc gcagactcgt cagcctcagc gaacaacgag 480
ctcgtcactg tgatcacgag tbtgatcccg aggaggcaga tttcctgcga ctctggttgc 540
aatggtggcg taatgaacag cgcttttgaa tacaccctca aaaccggagg gctcatgaaa 600
gaagaagact atccttaccac cggaaggagc ggcaagacct gcaagctaga caagtccaa 660
atcgttgcat ctgtctccaa ctctcagttt atctccattg atgaagaaca gattgctgca 720
aaccttgta agaacggacc tcttgctgta gccatcaacg ctggctatat gcagacttac 780
attggaggag tctcatgccc ttacatatgc accaggagcg tctcttattg 840
gttggtctat gagcgcgagc ttacgtctcg gctaggttca aggaagaagcc ttactggatc 900
atcaagaact cgtggggaga gacttggggg gaaaatgggt tctacaaaat ctgcaaaagg 960
cgtaacattt gtgtgttgga cagtatggtc tccactgttg cagccaccgt ctcaaccacc 1020
gccattaaag catctcgta ataatgttta attactttgg tgatttgat gagcgagctc 1080
tctttgcgct gctgactctc tctatttate tctgcttctt gcttgtaaat aaaatgcgct 1140
ctattg

(2) INFORMATION FOR SEQ ID NO:856:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..246
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:856:

Met Pro Thr Arg Leu Arg Phe Ser Leu Pro Lys Ile Ser Leu Arg Ile
1 5 10 15
Leu Ile Gly Glu Ile Met Ala Pro Leu Leu Pro Ser Lys Ile Arg Asp
20 25 30
Leu Ala Ala Leu Ala Gly Val Ser Ala Pro Leu Glu Leu Trp Lys Val
35 40 45
Leu Thr Ser Ser Leu Pro Ala Asp Ser Ser Ala Ser Ala Asn Asn Ser
50 55 60
Ser Ser Thr Val Ile Thr Ser Val Ile Pro Arg Arg Gln Ile Ser Cys

65	70	75	80
Asp Ser Gly Cys	Asn Gly Gly Leu Met	Asn Ser Ala Phe Glu Tyr Thr	
	85	90	95
Leu Lys Thr Gly	Gly Leu Met Lys Glu Glu Asp Tyr Pro Tyr Thr Gly		
	100	105	110
Lys Asp Gly Lys	Thr Cys Lys Leu Asp Lys Ser Lys Ile Val Ala Ser		
	115	120	125
Val Ser Asn Phe	Ser Val Ile Ser Ile Asp Glu Glu Gln Ile Ala Ala		
	130	135	140
Asn Leu Val Lys	Asn Gly Pro Leu Ala Val Ala Ile Asn Ala Gly Tyr		
	145	150	155
Met Gln Thr Tyr	Ile Gly Gly Val Ser Cys Pro Tyr Ile Cys Thr Arg		
	165	170	175
Arg Leu Asn His	Gly Val Leu Leu Val Gly Tyr Gly Ala Ala Gly Tyr		
	180	185	190
Ala Pro Ala Arg	Phe Lys Glu Lys Pro Tyr Trp Ile Ile Lys Asn Ser		
	195	200	205
Trp Gly Glu Thr	Trp Gly Glu Asn Gly Phe Tyr Lys Ile Cys Lys Gly		
	210	215	220
Arg Asn Ile Cys	Gly Val Asp Ser Met Val Ser Thr Val Ala Ala Thr		
	225	230	235
Val Ser Thr Thr	Ala His		240
	245		

(2) INFORMATION FOR SEQ ID NO:857:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..225

(D) OTHER INFORMATION: / Ceres Seq. ID 1499094

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:857:

Met Ala Pro Leu Leu Pro Ser Lys Ile Arg Asp Leu Ala Ala Leu Ala	
1	5 10 15
Gly Val Ser Ala Pro Leu Glu Leu Trp Lys Val Leu Thr Ser Ser Leu	
	20 25 30
Pro Ala Asp Ser Ser Ala Ser Ala Asn Asn Ser Ser Ser Thr Val Ile	
	35 40 45
Thr Ser Val Ile Pro Arg Arg Gln Ile Ser Cys Asp Ser Gly Cys Asn	
	50 55 60
Gly Gly Leu Met Asn Ser Ala Phe Glu Tyr Thr Leu Lys Thr Gly Gly	
	65 70 75 80
Leu Met Lys Glu Glu Asp Tyr Pro Tyr Thr Gly Lys Asp Gly Lys Thr	
	85 90 95
Cys Lys Leu Asp Lys Ser Lys Ile Val Ala Ser Val Ser Asn Phe Ser	
	100 105 110
Val Ile Ser Ile Asp Glu Glu Gln Ile Ala Ala Asn Leu Val Lys Asn	
	115 120 125
Gly Pro Leu Ala Val Ala Ile Asn Ala Gly Tyr Met Gln Thr Tyr Ile	
	130 135 140
Gly Gly Val Ser Cys Pro Tyr Ile Cys Thr Arg Arg Leu Asn His Gly	
	145 150 155 160
Val Leu Leu Val Gly Tyr Gly Ala Ala Gly Tyr Ala Pro Ala Arg Phe	
	165 170 175
Lys Glu Lys Pro Tyr Trp Ile Ile Lys Asn Ser Trp Gly Glu Thr Trp	
	180 185 190
Gly Glu Asn Gly Phe Tyr Lys Ile Cys Lys Gly Arg Asn Ile Cys Gly	
	195 200 205

Val Asp Ser Met Val Ser Thr Val Ala Ala Thr Val Ser Thr Thr Ala
210 215 220

His
225

(2) INFORMATION FOR SEQ ID NO:858:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..158

(D) OTHER INFORMATION: / Ceres Seq. ID 1499095

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:858:

Met	Asn	Ser	Ala	Phe	Glu	Tyr	Thr	Leu	Lys	Thr	Gly	Gly	Leu	Met	Lys
1				5					10				15		
Glu	Glu	Asp	Tyr	Pro	Tyr	Thr	Gly	Lys	Asp	Gly	Lys	Thr	Cys	Lys	Leu
			20					25					30		
Asp	Lys	Ser	Lys	Ile	Val	Ala	Ser	Val	Ser	Asn	Phe	Ser	Val	Ile	Ser
			35				40					45			
Ile	Asp	Glu	Gln	Ile	Ala	Ala	Asn	Leu	Val	Lys	Asn	Gly	Pro	Leu	
			50			55				60					
Ala	Val	Ala	Ile	Asn	Ala	Gly	Tyr	Met	Gln	Thr	Tyr	Ile	Gly	Gly	Val
65				70					75					80	
Ser	Cys	Pro	Tyr	Ile	Cys	Thr	Arg	Arg	Leu	Asn	His	Gly	Val	Leu	Leu
			85					90					95		
Val	Gly	Tyr	Gly	Ala	Ala	Gly	Tyr	Ala	Pro	Ala	Arg	Phe	Lys	Glu	Lys
			100					105					110		
Pro	Tyr	Trp	Ile	Ile	Lys	Asn	Ser	Trp	Gly	Glu	Thr	Trp	Gly	Glu	Asn
			115				120					125			
Gly	Phe	Tyr	Lys	Ile	Cys	Lys	Gly	Arg	Asn	Ile	Cys	Gly	Val	Asp	Ser
			130				135					140			
Met	Val	Ser	Thr	Val	Ala	Ala	Thr	Val	Ser	Thr	Thr	Ala	His		
145				150						155					

(2) INFORMATION FOR SEQ ID NO:859:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1854 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1854

(D) OTHER INFORMATION: / Ceres Seq. ID 1499100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:859:

aattcaccctt	cctccgtccc	cttcccctaa	tccccaaaac	acacagataa	aaatctctcc	60
ttttttcattc	gaagcatata	acacaaacacc	gacaaggaga	ttcctttaac	tatggcgaag	120
aaagcaagaa	ttgttataat	cggagctgga	atggctgtgtc	tcacggcggc	gaacaagctc	180
tacacaagct	ccaacaacac	cttcgagctc	tcagctgtcg	aaggcgggttc	tagaatcgcc	240
ggtaggatca	ataccctctga	gttctcatca	gagaagattg	agatgggtgc	cacgtggatc	300
cacggaatcg	gtggaagccc	tggttataga	atcgctaaag	agactgggttc	tttagtctct	360
gatgagccat	gggagtgat	ggattccacc	attgataaag	ctaagacctt	tgctgaaggt	420
gggttcgaga	ttgagccttc	cattgttgaa	tccatctctg	gtttgttcac	tgctctcatg	480
gaattagctc	aggggaagaa	gatctctcaa	tccgacgccg	atttgagtcg	tttggtctat	540
atttacgaaa	ctgccactag	ggttgtctct	aagggaagta	gtactagtgt	tggttcgttt	600
ttgaaatctg	ggtttgatgc	tattgggatg	tcaatcagca	atggaggaga	agaaggagtt	660
aaagggttatg	ggaaatggag	taggaagtca	cttgaagaag	ccatttttac	gatgtttgat	720
aacacacaga	ggacttacac	atctgctgat	gaactctcga	cgcttgattt	cgcgccggag	780

agtgagatc	agatgtttcc	aggagaagaa	atcactatag	ctaaaggcta	tcttagtggt	840
atctatcatt	tgacatctgt	gcttctctaa	gggttatcc	aattgaaatc	aaaggtcaag	900
aagatcgatg	ggcagagtaa	tgaagtgaag	ctgcatttct	cagatgggtc	tgtgtgtttt	960
gcagatcatg	ttattgttac	tgtctcttta	gggtgcttta	aagcagggat	tgagactgat	1020
gctgaattgt	ttagtcctcc	tttgctctgt	ttcaaatcag	acgctattag	aagactaggc	1080
tatggagttg	tcaacaagct	gttcgtcgag	atgtctcaaa	gaaagttccc	ctcttttgca	1140
cttggttttg	accggggaga	ttccgagttt	aggttcgtga	aaattccatg	gtggatgaga	1200
agaaccgcga	ccattaccoc	aatccatagc	aattcaaaag	tcttgctttc	ttggtttgca	1260
ggcaagaagc	ctctcgagct	tgagaaacct	accgatgagg	agatcaaaag	cgctgtcatg	1320
accactatct	cttgcttgac	aggcaaggaa	gttaagaatg	ataccgcaaa	gcccttgacc	1380
aatggctcat	tgaatgatga	tgatgaagcc	atgaagatta	caaaggtctt	gaagagcaaa	1440
tggggaaagt	atctctgttt	cagaggctcc	tattcgtatg	tagcggtttg	atcaaagcgg	1500
gatgacctag	acgcaatggc	tgagccattg	ccaaaagatta	ataagaaggt	tggtcaggtc	1560
aatggtcatg	atcaagccaa	ggttcatgag	cttcaagtcg	gtttgcagg	ggaagcaaca	1620
catagaacc	attactccac	aactcatggt	gcctactata	gtggtttaag	ggaagccaat	1680
aggcttctca	agcattacaa	atgtaatttt	tgagtgttaa	tttttaaaat	atgttctggt	1740
tttttttttt	gggtaaatgt	gtttagagaa	gcataaattag	ttttgtaaga	ttttttaatt	1800
gttaactctc	aatttttttt	ttactgtttt	ttactttttc	ttactacaaa	atcc	

(2) INFORMATION FOR SEQ ID NO:860:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 533 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..533

(D) OTHER INFORMATION: / Ceres Seq. ID 1499101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:860:

Met	Ala	Lys	Lys	Ala	Arg	Ile	Val	Ile	Ile	Gly	Ala	Gly	Met	Ala	Gly
1			5						10				15		
Leu	Thr	Ala	Ala	Asn	Lys	Leu	Tyr	Thr	Ser	Ser	Asn	Asn	Thr	Phe	Glu
			20					25					30		
Leu	Ser	Val	Val	Glu	Gly	Gly	Ser	Arg	Ile	Gly	Gly	Arg	Ile	Asn	Thr
			35				40					45			
Ser	Glu	Phe	Ser	Ser	Glu	Lys	Ile	Glu	Met	Gly	Ala	Thr	Trp	Ile	His
			50				55				60				
Gly	Ile	Gly	Gly	Ser	Pro	Val	Tyr	Arg	Ile	Ala	Lys	Glu	Thr	Gly	Ser
			65			70				75			80		
Leu	Val	Ser	Asp	Glu	Pro	Trp	Glu	Cys	Met	Asp	Ser	Thr	Ile	Asp	Lys
			85						90				95		
Ala	Lys	Thr	Phe	Ala	Glu	Gly	Gly	Phe	Glu	Ile	Glu	Pro	Ser	Ile	Val
			100					105				110			
Glu	Ser	Ile	Ser	Gly	Leu	Phe	Thr	Ala	Leu	Met	Glu	Leu	Ala	Gln	Gly
			115				120					125			
Lys	Glu	Ile	Ser	Gln	Ser	Asp	Ala	Asp	Leu	Ser	Arg	Leu	Ala	His	Ile
			130				135				140				
Tyr	Glu	Thr	Ala	Thr	Arg	Val	Cys	Ser	Lys	Gly	Ser	Ser	Thr	Ser	Val
			145			150				155				160	
Gly	Ser	Phe	Leu	Lys	Ser	Gly	Phe	Asp	Ala	Tyr	Trp	Asp	Ser	Ile	Ser
			165					170					175		
Asn	Gly	Gly	Glu	Glu	Gly	Val	Lys	Gly	Tyr	Gly	Lys	Trp	Ser	Arg	Lys
			180					185					190		
Ser	Leu	Glu	Glu	Ala	Ile	Phe	Thr	Met	Phe	Ser	Asn	Thr	Gln	Arg	Thr
			195				200					205			
Tyr	Thr	Ser	Ala	Asp	Glu	Leu	Ser	Thr	Leu	Asp	Phe	Ala	Ala	Glu	Ser
			210				215					220			
Glu	Tyr	Gln	Met	Phe	Pro	Gly	Glu	Glu	Ile	Thr	Ile	Ala	Lys	Gly	Tyr
			225			230				235				240	
Leu	Ser	Val	Ile	His	His	Leu	Ala	Ser	Val	Leu	Pro	Gln	Gly	Val	Ile

[illegible]

(2) INFORMATION FOR SEQ ID NO:861:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..520
(D) OTHER INFORMATION: / Ceres Seq. ID 1499102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:861:

Met	Ala	Gly	Leu	Thr	Ala	Ala	Asn	Lys	Leu	Tyr	Thr	Ser	Ser	Asn	Asn
1			5					10						15	
Thr	Phe	Glu	Leu	Ser	Val	Val	Glu	Gly	Gly	Ser	Arg	Ile	Gly	Gly	Arg
		20						25					30		
Ile	Asn	Thr	Ser	Glu	Phe	Ser	Ser	Glu	Lys	Ile	Glu	Met	Gly	Ala	Thr
		35					40					45			
Trp	Ile	His	Gly	Ile	Gly	Gly	Ser	Pro	Val	Tyr	Arg	Ile	Ala	Lys	Glu
	50					55					60				
Thr	Gly	Ser	Leu	Val	Ser	Asp	Glu	Pro	Trp	Glu	Cys	Met	Asp	Ser	Thr
65				70						75				80	
Ile	Asp	Lys	Ala	Lys	Thr	Phe	Ala	Glu	Gly	Gly	Phe	Glu	Ile	Glu	Pro
			85					90					95		

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..476

(D) OTHER INFORMATION: / Ceres Seq. ID 1499103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:862:

Met	Gly	Ala	Thr	Trp	Ile	His	Gly	Ile	Gly	Gly	Ser	Pro	Val	Tyr	Arg	
1				5				10						15		
Ile	Ala	Lys	Glu	Thr	Gly	Ser	Leu	Val	Ser	Asp	Glu	Pro	Trp	Glu	Cys	
		20					25						30			
Met	Asp	Ser	Thr	Ile	Asp	Lys	Ala	Lys	Thr	Phe	Ala	Glu	Gly	Gly	Phe	
		35				40						45				
Glu	Ile	Glu	Pro	Ser	Ile	Val	Glu	Ser	Ile	Ser	Gly	Leu	Phe	Thr	Ala	
	50					55				60						
Leu	Met	Glu	Leu	Ala	Gln	Gly	Lys	Glu	Ile	Ser	Gln	Ser	Asp	Ala	Asp	
	65				70				75					80		
Leu	Ser	Arg	Leu	Ala	His	Ile	Tyr	Glu	Thr	Ala	Thr	Arg	Val	Cys	Ser	
			85					90						95		
Lys	Gly	Ser	Ser	Thr	Ser	Val	Gly	Ser	Phe	Leu	Lys	Ser	Gly	Phe	Asp	
			100					105					110			
Ala	Tyr	Trp	Trp	Asp	Ser	Ile	Ser	Asn	Gly	Gly	Glu	Glu	Gly	Val	Lys	Gly
		115						120					125			
Tyr	Gly	Lys	Trp	Ser	Arg	Lys	Ser	Leu	Glu	Glu	Ala	Ile	Phe	Thr	Met	
	130					135					140					
Phe	Ser	Asn	Thr	Gln	Arg	Thr	Tyr	Thr	Ser	Ala	Asp	Glu	Leu	Ser	Thr	
	145				150					155				160		
Leu	Asp	Phe	Ala	Ala	Glu	Ser	Glu	Tyr	Gln	Met	Phe	Pro	Gly	Glu	Glu	
			165					170						175		
Ile	Thr	Ile	Ala	Lys	Gly	Tyr	Leu	Ser	Val	Ile	His	His	Leu	Ala	Ser	
			180					185					190			
Val	Leu	Pro	Gln	Gly	Val	Ile	Gln	Leu	Asn	Arg	Lys	Val	Thr	Lys	Ile	
		195				200						205				
Glu	Trp	Gln	Ser	Asn	Glu	Val	Lys	Leu	His	Phe	Ser	Asp	Gly	Ser	Val	
	210				215						220					
Val	Phe	Ala	Asp	His	Val	Ile	Val	Thr	Val	Ser	Leu	Gly	Val	Leu	Lys	
	225				230					235				240		
Ala	Gly	Ile	Glu	Thr	Asp	Ala	Glu	Leu	Phe	Ser	Pro	Pro	Leu	Pro	Asp	
			245					250						255		
Phe	Lys	Ser	Asp	Ala	Ile	Arg	Arg	Leu	Gly	Tyr	Gly	Val	Val	Asn	Lys	
		260				265							270			
Leu	Phe	Val	Glu	Met	Ser	Gln	Arg	Lys	Phe	Pro	Ser	Leu	Gln	Leu	Val	
		275				280						285				
Phe	Asp	Arg	Glu	Asp	Ser	Glu	Phe	Arg	Phe	Val	Lys	Ile	Pro	Trp	Trp	
	290					295					300					
Met	Arg	Arg	Thr	Ala	Thr	Ile	Thr	Pro	Ile	His	Ser	Asn	Ser	Lys	Val	
	305				310					315				320		
Leu	Leu	Ser	Trp	Phe	Ala	Gly	Lys	Glu	Ala	Leu	Glu	Leu	Glu	Lys	Leu	
			325					330						335		
Thr	Asp	Glu	Glu	Ile	Lys	Asp	Ala	Val	Met	Thr	Thr	Ile	Ser	Cys	Leu	
		340						345					350			
Thr	Gly	Lys	Glu	Val	Lys	Asn	Asp	Thr	Ala	Lys	Pro	Leu	Thr	Asn	Gly	
		355				360						365				
Ser	Leu	Asn	Asp	Asp	Asp	Glu	Ala	Met	Lys	Ile	Thr	Lys	Val	Leu	Lys	
	370					375					380					
Ser	Lys	Trp	Gly	Ser	Asp	Pro	Leu	Phe	Arg	Gly	Ser	Tyr	Ser	Tyr	Val	
		385			390					395				400		
Ala	Val	Gly	Ser	Ser	Gly	Asp	Asp	Leu	Asp	Ala	Met	Ala	Glu	Pro	Leu	
			405					410					415			
Pro	Lys	Ile	Asn	Lys	Lys	Val	Gly	Gln	Val	Asn	Gly	His	Asp	Gln	Ala	
		420					425						430			
Lys	Val	His	Glu	Leu	Gln	Val	Met	Phe	Ala	Gly	Glu	Ala	Thr	His	Arg	
		435				440						445				

Thr His Tyr Ser Thr Thr His Gly Ala Tyr Tyr Ser Gly Leu Arg Glu
450 455 460
Ala Asn Arg Leu Leu Lys His Tyr Lys Cys Asn Phe
465 470 475

(2) INFORMATION FOR SEQ ID NO:863:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1618 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..1618

- (D) OTHER INFORMATION: / Ceres Seq. ID 1499108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:863:

```
aaatacacagag  cagaaacctt  taagagaaga  tctaataaga  aagaagagga  aaaaaaagga  60
tggtttttctc  agttttccatt  ttgtcctctc  tcgtcctcgta  cttagtctct  tcgttactac  120
tcttctttctc  catcgagcag  ctctcttacc  tcgtcaaagaa  acgtaacctc  cctggctcct  180
tctttgtccc  tccgatcatc  ggaaacgccca  ttctactcgt  ccgtgatcct  acttctctct  240
gggtcaaagca  atccgacacg  gcaggcactt  cccctggcct  cgctgctaac  tacctcatcg  300
gcaaatctcat  catctacatc  agagacacag  agcttttctca  tcaaatattc  tccaacgttc  360
gtcttgaagc  ttttacacct  ctaggacatc  cttttggcaa  acaactattc  ggtgatcata  420
gcctaactcta  cttgtttggg  gaggatcaca  aaactgtttc  ccgtcacctt  gctcctaact  480
tcacccccc  ggcactctcc  acttaactgt  atctccaaca  aatagtatat  ctccgtcatc  540
tacgacagtg  ggaggaaga  ttctccggcg  gaactaagcc  ggtttctatg  cgagaccttg  600
tcgtgtaact  caatcttgag  acttctcaaa  cggttttctg  tggaccttac  ctgacaaggg  660
aagctaggaa  cagctctgt  actgattaca  atctgttcaa  tctcggtatc  atggcgctcc  720
cgatcaaacct  gcccgctttt  gcgttcaaca  aggcctcgcc  ggcggtaatg  aacctggaga  780
agacgccttc  cgctctgtcg  ggaaaatcca  aaaagaggat  ggctacagga  gaggagccaa  840
catgcttaat  cgatttttgg  atgcatcgat  tcgtcacgga  gatagaatcc  ggtaatccac  900
cgccgcttca  ctccgaagac  gaagccatcg  gcggtttgct  cttcgatttt  ctctttgcgc  960
cacaagacgc  gtgcagctca  tcaactcttt  gggcggtgac  gtttctagaa  tctcatccga  1020
aagtgcgag  caaagtgcag  gaggaagtgg  ccaagatttg  gtcaacctag  tctggccatc  1080
tgatcacgcg  cgatcagctc  gcggagatga  agtatactcg  cgctgtggca  cgtgaggtgg  1140
tgagatagc  accacccgca  actatgggtc  cacacattgc  tactaaatga  ttocctctta  1200
cagaatcgta  cactatccca  aaaggtacaa  tagtgtttcc  ctccgttttc  gacgcctcgt  1260
ttcaagggtt  tactgaacgc  aaccgggtcg  atccggacgc  gtttagtgag  acaaggcaag  1320
aggatacaagt  gttcaaagca  aactacctag  cttttggatg  ggtgacacac  caatgcgtag  1380
gccagcgtaa  cgcattgaac  caccctgtgc  tcttcatcgc  tatgttctca  tcgtgtgttg  1440
attcaagag  acttcaatcg  gcggttgcc  atgacatcat  atactgtccc  acgatctcgc  1500
caaaagacgc  gtgcacggtg  ttctgttcta  agcgcatcgt  aacgtatccg  aacctctgat  1560
ttgattttt  gttacaatt  attggtgatc  aaagtcaata  ctcatgagtg  tgattact
```

(2) INFORMATION FOR SEQ ID NO:864:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..499

- (D) OTHER INFORMATION: / Ceres Seq. ID 1499109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:864:

```
Met Val Phe Ser Val Ser Ile Phe Ala Ser Leu Ala Pro Tyr Leu Val
1 5 10 15
Ser Ser Leu Leu Leu Phe Phe Leu Ile Glu Gln Leu Ser Tyr Leu Val
20 25 30
Lys Lys Arg Asn Leu Pro Gly Pro Leu Phe Val Pro Pro Ile Ile Gly
35 40 45
```

Asn Ala Ile Ser Leu Val Arg Asp Pro Thr Ser Phe Trp Phe Lys Gln
50 55 60
Ser Asp Thr Ala Gly Thr Ser Pro Gly Leu Ala Asn Tyr Leu Ile
65 70 75 80
Gly Lys Phe Ile Ile Tyr Ile Arg Asp Thr Glu Leu Ser His Gln Ile
85 90 95
Phe Ser Asn Val Arg Leu Glu Ala Phe His Pro Leu Gly His Pro Phe
100 105 110
Gly Lys Gln Leu Phe Gly Asp His Ser Leu Ile Tyr Leu Phe Gly Glu
115 120 125
Asp His Lys Thr Val Arg Arg His Leu Ala Pro Asn Phe Thr Pro Lys
130 135 140
Ala Leu Ser Thr Tyr Ser Asp Leu Gln Gln Ile Val Met Leu Arg His
145 150 155 160
Leu Arg Gln Trp Glu Glu Ser Phe Ser Gly Gly Thr Lys Pro Val Ser
165 170 175
Met Arg Asp Leu Val Arg Glu Leu Asn Leu Glu Thr Ser Gln Thr Val
180 185 190
Phe Val Gly Pro Tyr Leu Asp Lys Glu Ala Arg Asn Thr Phe Cys Thr
195 200 205
Asp Tyr Asn Leu Phe Asn Leu Gly Ser Met Ala Leu Pro Ile Asn Leu
210 215 220
Pro Gly Phe Ala Phe Asn Lys Ala Arg Arg Ala Val Met Asn Leu Glu
225 230 235 240
Lys Thr Leu Ser Val Cys Ala Gly Lys Ser Lys Lys Arg Met Ala Thr
245 250 255
Gly Glu Glu Pro Thr Cys Leu Ile Asp Phe Trp Met His Ala Phe Val
260 265 270
Thr Glu Ile Glu Ser Gly Asn Pro Pro Leu His Ser Glu Asp Glu
275 280 285
Ala Ile Gly Gly Leu Leu Phe Asp Phe Leu Phe Ala Ala Gln Asp Ala
290 295 300
Ser Thr Ser Ser Leu Leu Trp Ala Val Thr Phe Leu Glu Ser His Pro
305 310 315 320
Lys Val Leu Ser Lys Val Arg Glu Glu Val Ala Lys Ile Trp Ser Pro
325 330 335
Gln Ser Gly His Leu Ile Thr Ala Asp Gln Leu Ala Glu Met Lys Tyr
340 345 350
Thr Arg Ala Val Ala Arg Glu Val Val Arg Tyr Arg Pro Pro Ala Thr
355 360 365
Met Val Pro His Ile Ala Thr Asn Asp Phe Pro Leu Thr Glu Ser Tyr
370 375 380
Thr Ile Pro Lys Gly Thr Ile Val Phe Pro Ser Val Phe Asp Ala Ser
385 390 395 400
Phe Gln Gly Phe Thr Glu Pro Asn Arg Phe Asp Pro Asp Arg Phe Ser
405 410 415
Glu Thr Arg Gln Glu Asp Gln Val Phe Lys Arg Asn Tyr Leu Ala Phe
420 425 430
Gly Trp Gly Ala His Gln Cys Val Gly Gln Arg Tyr Ala Leu Asn His
435 440 445
Leu Val Leu Phe Ile Ala Met Phe Ser Ser Leu Phe Asp Phe Lys Arg
450 455 460
Leu Gln Ser Asp Gly Cys Asp Asp Ile Ile Tyr Cys Pro Thr Ile Ser
465 470 475 480
Pro Lys Asp Gly Cys Thr Val Phe Leu Ser Lys Arg Ile Val Thr Tyr
485 490 495
Pro Asn Leu

(2) INFORMATION FOR SEQ ID NO:865:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 343 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..343
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499110
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:865:

Met	Leu	Arg	His	Leu	Arg	Gln	Trp	Glu	Glu	Ser	Phe	Ser	Gly	Gly	Thr
1				5				10						15	
Lys	Pro	Val	Ser	Met	Arg	Asp	Leu	Val	Arg	Glu	Leu	Asn	Leu	Glu	Thr
							20						30		
Ser	Gln	Thr	Val	Phe	Val	Gly	Pro	Tyr	Leu	Asp	Lys	Glu	Ala	Arg	Asn
							40					45			
Thr	Phe	Cys	Thr	Asp	Tyr	Asn	Leu	Phe	Asn	Leu	Gly	Ser	Met	Ala	Leu
							50				60				
Pro	Ile	Asn	Leu	Pro	Gly	Phe	Ala	Phe	Asn	Lys	Ala	Arg	Arg	Ala	Val
65							70			75					80
Met	Asn	Leu	Glu	Lys	Thr	Leu	Ser	Val	Cys	Ala	Gly	Lys	Ser	Lys	Lys
							85			90				95	
Arg	Met	Ala	Thr	Gly	Glu	Glu	Pro	Thr	Cys	Leu	Ile	Asp	Phe	Trp	Met
							100			105			110		
His	Ala	Phe	Val	Thr	Glu	Ile	Glu	Ser	Gly	Asn	Pro	Pro	Pro	Leu	His
							115			120			125		
Ser	Glu	Asp	Glu	Ala	Ile	Gly	Gly	Leu	Leu	Phe	Asp	Phe	Leu	Phe	Ala
							130					140			
Ala	Gln	Asp	Ala	Ser	Thr	Ser	Ser	Leu	Leu	Trp	Ala	Val	Thr	Phe	Leu
145							150			155					160
Glu	Ser	His	Pro	Lys	Val	Leu	Ser	Lys	Val	Arg	Glu	Glu	Val	Ala	Lys
							165			170				175	
Ile	Trp	Ser	Pro	Gln	Ser	Gly	His	Leu	Ile	Thr	Ala	Asp	Gln	Leu	Ala
							180			185			190		
Glu	Met	Lys	Tyr	Thr	Arg	Ala	Val	Ala	Arg	Glu	Val	Val	Arg	Tyr	Arg
							195			200			205		
Pro	Pro	Ala	Thr	Met	Val	Pro	His	Ile	Ala	Thr	Asn	Asp	Phe	Pro	Leu
							210					220			
Thr	Glu	Ser	Tyr	Thr	Ile	Pro	Lys	Gly	Thr	Ile	Val	Phe	Pro	Ser	Val
225							230			235					240
Phe	Asp	Ala	Ser	Phe	Gln	Gly	Phe	Thr	Glu	Pro	Asn	Arg	Phe	Asp	Pro
							245			250				255	
Asp	Arg	Phe	Ser	Glu	Thr	Arg	Gln	Glu	Asp	Gln	Val	Phe	Lys	Arg	Asn
							260			265			270		
Tyr	Leu	Ala	Phe	Gly	Trp	Gly	Ala	His	Gln	Cys	Val	Gly	Gln	Arg	Tyr
							275			280			285		
Ala	Leu	Asn	His	Leu	Val	Leu	Phe	Ile	Ala	Met	Phe	Ser	Ser	Leu	Phe
							290			295			300		
Asp	Phe	Lys	Arg	Leu	Gln	Ser	Asp	Gly	Cys	Asp	Asp	Ile	Ile	Tyr	Cys
305							310			315					320
Pro	Thr	Ile	Ser	Pro	Lys	Asp	Gly	Cys	Thr	Val	Phe	Leu	Ser	Lys	Arg
							325			330				335	
Ile	Val	Thr	Tyr	Pro	Asn	Leu									
							340								

(2) INFORMATION FOR SEQ ID NO:866:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 323 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..323
(D) OTHER INFORMATION: / Ceres Seq. ID 1499111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:866:

Met	Arg	Asp	Leu	Val	Arg	Glu	Leu	Asn	Leu	Glu	Thr	Ser	Gln	Thr	Val
1				5					10				15		
Phe	Val	Gly	Pro	Tyr	Leu	Asp	Lys	Glu	Ala	Arg	Asn	Thr	Phe	Cys	Thr
			20				25					30			
Asp	Tyr	Asn	Leu	Phe	Asn	Leu	Gly	Ser	Met	Ala	Leu	Pro	Ile	Asn	Leu
		35				40					45				
Pro	Gly	Phe	Ala	Phe	Asn	Lys	Ala	Arg	Arg	Ala	Val	Met	Asn	Leu	Glu
	50				55				60						
Lys	Thr	Leu	Ser	Val	Cys	Ala	Gly	Lys	Ser	Lys	Lys	Arg	Met	Ala	Thr
			70						75				80		
Gly	Glu	Glu	Pro	Thr	Cys	Leu	Ile	Asp	Phe	Trp	Met	His	Ala	Phe	Val
			85						90				95		
Thr	Glu	Ile	Glu	Ser	Gly	Asn	Pro	Pro	Pro	Leu	His	Ser	Glu	Asp	Glu
			100				105					110			
Ala	Ile	Gly	Gly	Leu	Leu	Phe	Asp	Phe	Leu	Phe	Ala	Ala	Gln	Asp	Ala
		115				120					125				
Ser	Thr	Ser	Ser	Leu	Leu	Trp	Ala	Val	Thr	Phe	Leu	Glu	Ser	His	Pro
		130			135						140				
Lys	Val	Leu	Ser	Lys	Val	Arg	Glu	Glu	Val	Ala	Lys	Ile	Trp	Ser	Pro
			145		150					155				160	
Gln	Ser	Gly	His	Leu	Ile	Thr	Ala	Asp	Gln	Leu	Ala	Glu	Met	Lys	Tyr
			165					170					175		
Thr	Arg	Ala	Val	Ala	Arg	Glu	Val	Val	Arg	Tyr	Arg	Pro	Pro	Ala	Thr
			180					185					190		
Met	Val	Pro	His	Ile	Ala	Thr	Asn	Asp	Phe	Pro	Leu	Thr	Glu	Ser	Tyr
		195					200					205			
Thr	Ile	Pro	Lys	Gly	Thr	Ile	Val	Phe	Pro	Ser	Val	Phe	Asp	Ala	Ser
		210				215					220				
Phe	Gln	Gly	Phe	Thr	Glu	Pro	Asn	Arg	Phe	Asp	Pro	Asp	Arg	Phe	Ser
		225			230					235				240	
Glu	Thr	Arg	Gln	Glu	Asp	Gln	Val	Phe	Lys	Arg	Asn	Tyr	Leu	Ala	Phe
			245					250					255		
Gly	Trp	Gly	Ala	His	Gln	Cys	Val	Gly	Gln	Arg	Tyr	Ala	Leu	Asn	His
			260					265					270		
Leu	Val	Leu	Phe	Ile	Ala	Met	Phe	Ser	Ser	Leu	Phe	Asp	Phe	Lys	Arg
		275					280					285			
Leu	Gln	Ser	Asp	Gly	Cys	Asp	Asp	Ile	Ile	Tyr	Cys	Pro	Thr	Ile	Ser
		290				295					300				
Pro	Lys	Asp	Gly	Cys	Thr	Val	Phe	Leu	Ser	Lys	Arg	Ile	Val	Thr	Tyr
			305		310					315				320	
Pro	Asn	Leu													

(2) INFORMATION FOR SEQ ID NO:867:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1451 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..1451
(D) OTHER INFORMATION: / Ceres Seq. ID 1499112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:867:

actcaactta	aactctttta	gtaacaatgg	tttctttctt	tttaaccaag	cttgtgttct	60
ttgtgtgtct	ctctctgtct	acattcacgg	acaaccttgt	ggctggaaaa	tctggcaaa	120
tgaagctcaa	tctttactac	gaatcacttt	gtcccggttg	tcaggaattc	atcgtcgatg	180

acctaggttaa	aatctttgac	tacgatctct	acacaatcac	tgatctcaag	ctgtttccat	240
tttgtaaatgc	cgaactctcc	gataatctga	ctgtcacttt	tttttttttt	ttttttgaga	300
gaaacaagag	caatggatat	gaacagacaa	gcacaccaca	tgagcttggt	gtattacaac	360
acaagctctt	ttttgcgctt	ctgctcaatc	acaacaactg	aagctctcac	cacaacaaca	420
gctaaggata	taaacagtcg	caagctgtca	aagatgaaga	agaccagaaa	cggtgctttg	480
tttgctatat	gagcttgcgc	tagcaactct	cctttcgacc	ggctctcttc	gtactgacgg	540
gggtattgtga	agatttgtct	gaagccactc	gtggccaata	gcactgcacc	aacagtttgt	600
gagtttaag	cggtgtttag	accactaatg	tgtagctctt	tgagctcttt	tgctatcttc	660
tggaactctta	cacctgtttg	tctgtgattg	tgaagctgag	attgtacttc	atgtttgatg	720
tcgctgactg	tttgcctcag	ttgcttagct	gggttctgag	gctttccgag	atctttagct	780
gtagcagctc	ctgcttctct	cagaactgac	acaagctctg	cgtttctcat	cttctcagag	840
acatcgactg	gcgtatctcc	agctttgttt	attgggttga	ggtttatgcc	ttcaaaaagt	900
accacaacacc	gtactatctt	aatacgcgcc	ttgtttgtgg	caataaagac	ttggcccgat	960
cagaataatc	aatactcggt	catacgggtg	gtcgaagcgc	atcacgaagc	gtgggaatca	1020
tggtttaaaa	actctggacg	tgagaagaca	atcaatgatt	gttaacaatg	tgatctttct	1080
agaagaactga	tacttgggta	cgcaacccaa	accaagaatt	tgaagccgac	acatgaatac	1140
gtaccatggg	tcacactcaa	cggaagccca	ctcgatgaca	gcgtacaaa	tacggatgat	1200
ctcgtagctc	aaatctgcaa	agcataccaa	ggaagagttg	ctctcccaaa	agtttgcgat	1260
tcacccgctc	caatgcttaa	gtcgcctgag	aggaaatgga	agcttcaagt	ctcttatgcc	1320
aataaagcta	ccaattatta	agtttaacta	caaacctcgt	attgaactaa	gatggattta	1380
agctttatgt	tataagtggg	atgatgaata	aaggcctggt	ctaaactttt	atggtttacga	1440
attgatgtat	t					

(2) INFORMATION FOR SEQ ID NO:868:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..124

(D) OTHER INFORMATION: / Ceres Seq. ID 1499113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:868:

Met Val Ser Ser Ser Leu Thr Lys Leu Val Phe Phe Gly Cys Leu Leu
1 5 10 15
Leu Leu Thr Phe Thr Asp Asn Leu Val Ala Gly Lys Ser Gly Lys Val
20 25 30
Lys Leu Asn Leu Tyr Tyr Glu Ser Leu Cys Pro Gly Cys Glu Phe
35 40 45
Ile Val Asp Asp Leu Gly Lys Ile Phe Asp Tyr Asp Leu Tyr Thr Ile
50 55 60
Thr Asp Leu Lys Leu Phe Pro Phe Gly Asn Ala Glu Leu Ser Asp Asn
65 70 75 80
Leu Thr Val Thr Phe Phe Phe Phe Phe Glu Arg Asn Lys Gly Asn
85 90 95
Gly Tyr Glu Gln Thr Ser Thr Pro His Glu Leu Val Asp Tyr Lys His
100 105 110
Lys Leu Leu Phe Arg Leu Leu Asn His Asn Asn
115 120

(2) INFORMATION FOR SEQ ID NO:869:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 151 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1499114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:869:

Met	Pro	Ser	Lys	Asp	Thr	Lys	His	Arg	Thr	Ile	Leu	Ile	Arg	Pro	Leu
1			5					10					15		
Phe	Val	Ala	Ile	Arg	Thr	Trp	Pro	Asp	Gln	Lys	Ser	Gln	Tyr	Ser	Phe
			20					25					30		
Ile	Arg	Cys	Val	Glu	Ser	Asp	Thr	Lys	Gly	Trp	Glu	Ser	Cys	Val	Lys
			35					40					45		
Asn	Ser	Gly	Arg	Glu	Lys	Ala	Ile	Asn	Asp	Cys	Tyr	Asn	Gly	Asp	Leu
			50					55					60		
Ser	Arg	Lys	Leu	Ile	Leu	Gly	Tyr	Ala	Thr	Lys	Thr	Lys	Asn	Leu	Lys
			65					70					75		
Pro	Pro	His	Glu	Tyr	Val	Pro	Trp	Val	Thr	Leu	Asn	Gly	Lys	Pro	Leu
			85										90		
Asp	Asp	Ser	Val	Gln	Ser	Thr	Asp	Asp	Leu	Val	Ala	Gln	Ile	Cys	Lys
			100										105		
Ala	Tyr	Lys	Gly	Lys	Val	Ala	Leu	Pro	Lys	Val	Cys	Asn	Ser	Ser	Ala
			115										120		
Ser	Met	Ser	Lys	Ser	Pro	Glu	Arg	Lys	Trp	Lys	Leu	Gln	Val	Ser	Tyr
			130										135		
Ala	Asn	Lys	Ala	Thr	Asn	Tyr							140		
			145										150		

(2) INFORMATION FOR SEQ ID NO:870:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1905 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1905
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:870:

acacaaacgcg	acccgaccgcg	aatctggccg	gtgagaaaat	ggagggtccaa	agcagcagca	60
acaatgggtg	tcactcttct	ttctccagtc	tcgcgctcta	ctcgaactct	ctttccgcga	120
cgctctctcg	cttatccgcg	cgcgctattt	ccgtctccac	ctcttccgag	gagatgagtc	180
gcgctgcgcg	cgtctccgcg	gaacagatgc	ccgctactct	ccggtgggtac	gatctcattg	240
gactcggaat	cgggggaatg	gtcggcgccg	gtgtctttgt	caccacggcg	cgtgctagtc	300
gtctcgacgc	cgtctcttca	attgtcgtct	cttacgccaat	cgccgggctc	tgccgtctcc	360
ttctcgcgtt	ctgttacacc	gaattcgccg	tccatctccc	ggctgcggcg	gggtcccttca	420
gctacatccg	tatcacattc	ggtagaattt	cagcatcttt	caccggagca	aattctgtaa	480
tggattacgt	aatgtcaaac	cggcgccgtt	cgagaagctt	caccgctatt	ttaggaacag	540
ctttcgggat	ctcaactctc	aagtggcgat	tcgtcgtctc	cgtgtttaccg	aaaggattca	600
acgagatgta	tccagtgcga	gttctcgtcg	ttctcgtaat	cacagtcaatc	atctgtgtga	660
gtacaagaga	gagttccaaa	gtgaacatga	taatgactgc	atttcacatc	gcattcataat	720
ttctcgtgat	cgtgatggga	ttcataaaag	gagattcaca	gaatctatcc	tcaccggcga	780
atccagagca	ccctcgggga	ttttttccgt	tcggcgccgc	gggagttttc	aacggagattc	840
ccatgggttta	cttaagctac	ataggatcac	acgcgctttc	aacctatggc	gaagaagttg	900
aaaatccggg	caaaagatac	cccgctgggt	tttcgggctc	cgctgcgaatc	gtcacccgttc	960
tttactgtct	cttcgcagtc	tctatgtcaa	tgcttctgcc	atacgatctg	atagatccgg	1020
aggcgcgggt	cttcgcggcg	ttcagaggat	cgaacggctg	ggaatgggtg	acgaaagtgg	1080
ttgggatagg	agcaagcttt	gggataatga	catcaacttt	ggtggcaaat	ttaggtcagg	1140
ctcgtctacat	gtgtgtcatt	ggacgggtcca	gagtgggtccc	cttttgggttc	gctaaagattc	1200
atcccaaaac	atctacgcga	gtcaacgcct	ccactttttc	ttggcatcttc	gtcacccgttc	1260
tttgcgtttt	caccgacatca	aacgtctctc	taaaacctcg	atccattgga	acactatttg	1320
tcctctacat	gggtgcgaac	cgtctcatct	tcagacgtta	cgtcccggtt	ggacccacca	1380
agccgtggcc	cacactctgc	ttctctcac	tattctccat	aacctctctc	gtcttcaccc	1440
tcactctgaa	acttgtgcgc	gaaggtaagc	ctaaagcttt	catgctcctg	ccaggtgcgg	1500
tggtggctat	agccatcgtg	ctgagctttc	agtcgctggg	tcgccaggtc	aggaacacctg	1560
agttgtgggg	aggtcccgct	atgcgttgga	cccgctgggt	gtcgatatct	ttgaacattt	1620
ttttgtctgg	ttcgttggtg	gcacccctct	acgtccgggt	tggattcttc	tcgggtttga	1680

tcgtgctcgt gtatttgttt tatggcgttc atgcgagttc tgaatgctgaa gcgaatggat 1740
cttttgggtg gaaagatgga caagtcataa aagagctaat tgaagtgtga aaagtattta 1800
tttagtttag ttttctaag catcatgaac caaaatgtaa ttaaactctc taattttttt 1860
tctacatgag ggggtttgaa atattaatga gaaaatatta aatgc

(2) INFORMATION FOR SEQ ID NO:871:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 595 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..595
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:871:

Thr	Asn	Arg	Pro	Asp	Pro	Asn	Leu	Ala	Gly	Glu	Lys	Met	Glu	Val	Gln
1				5					10					15	
Ser	Ser	Ser	Asn	Asn	Gly	Gly	His	Ser	Ser	Phe	Ser	Ser	Leu	Arg	Val
			20					25					30		
Tyr	Leu	Asn	Ser	Leu	Ser	Ala	Thr	Pro	Ser	Arg	Leu	Ser	Arg	Arg	Ala
	35					40					45				
Ile	Ser	Val	Ser	Thr	Ser	Ser	Asp	Glu	Met	Ser	Arg	Val	Arg	Ala	Val
	50					55					60				
Ser	Gly	Glu	Gln	Met	Arg	Arg	Thr	Leu	Arg	Trp	Tyr	Asp	Leu	Ile	Gly
	65				70				75				80		
Leu	Gly	Ile	Gly	Gly	Met	Val	Gly	Ala	Gly	Val	Phe	Val	Thr	Thr	Gly
			85					90					95		
Arg	Ala	Ser	Arg	Leu	Asp	Ala	Gly	Pro	Ser	Ile	Val	Val	Ser	Tyr	Ala
			100					105					110		
Ile	Ala	Gly	Leu	Cys	Ala	Leu	Leu	Ser	Ala	Phe	Cys	Tyr	Thr	Glu	Phe
		115				120						125			
Ala	Val	His	Leu	Pro	Val	Ala	Gly	Gly	Ala	Phe	Ser	Tyr	Ile	Arg	Ile
	130					135					140				
Thr	Phe	Gly	Glu	Phe	Pro	Ala	Phe	Phe	Thr	Gly	Ala	Asn	Leu	Val	Met
	145				150					155				160	
Asp	Tyr	Val	Met	Ser	Asn	Ala	Ala	Val	Ser	Arg	Ser	Phe	Thr	Ala	Tyr
			165						170				175		
Leu	Gly	Thr	Ala	Phe	Gly	Ile	Ser	Thr	Ser	Lys	Trp	Arg	Phe	Val	Val
		180						185					190		
Ser	Gly	Leu	Pro	Lys	Gly	Phe	Asn	Glu	Ile	Asp	Pro	Val	Ala	Val	Leu
		195				200						205			
Val	Val	Leu	Val	Ile	Thr	Val	Ile	Ile	Cys	Cys	Ser	Thr	Arg	Glu	Ser
		210				215					220				
Ser	Lys	Val	Asn	Met	Ile	Met	Thr	Ala	Phe	His	Ile	Ala	Phe	Ile	Phe
		225				230				235				240	
Phe	Val	Ile	Val	Met	Gly	Phe	Ile	Lys	Gly	Asp	Ser	Lys	Asn	Leu	Ser
			245					250					255		
Ser	Pro	Ala	Asn	Pro	Glu	His	Pro	Ser	Gly	Phe	Phe	Pro	Phe	Gly	Ala
		260						265					270		
Ala	Gly	Val	Phe	Asn	Gly	Ala	Ala	Met	Val	Tyr	Leu	Ser	Tyr	Ile	Gly
		275				280						285			
Tyr	Asp	Ala	Val	Ser	Thr	Met	Ala	Glu	Glu	Val	Glu	Asn	Pro	Val	Lys
		290				295					300				
Asp	Ile	Pro	Val	Gly	Val	Ser	Gly	Ser	Val	Ala	Ile	Val	Thr	Val	Leu
		305				310				315				320	
Tyr	Cys	Leu	Met	Ala	Val	Ser	Met	Ser	Met	Leu	Leu	Pro	Tyr	Asp	Leu
			325					330					335		
Ile	Asp	Pro	Glu	Ala	Pro	Phe	Ser	Ala	Ala	Phe	Arg	Gly	Ser	Asn	Gly
		340						345					350		
Trp	Glu	Trp	Val	Thr	Lys	Val	Val	Gly	Ile	Gly	Ala	Ser	Phe	Gly	Ile

355	360	365
Leu Thr Ser Leu Leu Val Ala Met Leu Gly Gln Ala Arg Tyr Met Cys		
370	375	380
Val Ile Gly Arg Ser Arg Val Val Pro Phe Trp Phe Ala Lys Ile His		
385	390	395
Pro Lys Thr Ser Thr Pro Val Asn Ala Ser Thr Phe Leu Gly Ile Phe		
405	410	415
Thr Ala Ala Leu Ala Leu Phe Thr Asp Leu Asn Val Leu Leu Asn Leu		
420	425	430
Val Ser Ile Gly Thr Leu Phe Val Phe Tyr Met Val Ala Asn Ala Leu		
435	440	445
Ile Phe Arg Arg Tyr Val Pro Val Gly Pro Thr Lys Pro Trp Pro Thr		
450	455	460
Leu Cys Phe Leu Thr Leu Phe Ser Ile Thr Ser Leu Val Phe Thr Leu		
465	470	475
Ile Trp Lys Leu Val Pro Glu Gly Lys Pro Lys Ala Phe Met Leu Gly		
485	490	495
Ala Ser Ala Val Val Ala Ile Ala Ile Val Leu Ser Phe Gln Cys Val		
500	505	510
Val Pro Gln Ala Arg Lys Pro Glu Leu Trp Gly Val Pro Phe Met Pro		
515	520	525
Trp Thr Pro Cys Val Ser Ile Phe Leu Asn Ile Phe Leu Leu Gly Ser		
530	535	540
Leu Asp Ala Pro Ser Tyr Val Arg Phe Gly Phe Phe Ser Gly Leu Ile		
545	550	555
Val Leu Val Tyr Leu Phe Tyr Gly Val His Ala Ser Ser Asp Ala Glu		
565	570	575
Ala Asn Gly Ser Phe Gly Val Lys Asp Gly Gln Val Met Lys Glu Leu		
580	585	590
Ile Glu Val		
595		

(2) INFORMATION FOR SEQ ID NO:872:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 583 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..583

(D) OTHER INFORMATION: / Ceres Seq. ID 1499117

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:872:

Met	Glu	Val	Gln	Ser	Ser	Asn	Asn	Gly	Gly	His	Ser	Ser	Phe	Ser
1		5					10					15		
Ser	Leu	Arg	Val	Tyr	Leu	Asn	Ser	Leu	Ser	Ala	Thr	Pro	Ser	Arg
		20					25					30		
Ser	Arg	Arg	Ala	Ile	Ser	Val	Ser	Thr	Ser	Ser	Asp	Glu	Met	Ser
		35					40				45			
Val	Arg	Ala	Val	Ser	Gly	Glu	Gln	Met	Arg	Arg	Thr	Leu	Arg	Trp
		50					55				60			
Asp	Leu	Ile	Gly	Leu	Gly	Ile	Gly	Gly	Met	Val	Gly	Ala	Gly	Val
65			70				75				80			
Val	Thr	Thr	Gly	Arg	Ala	Ser	Arg	Leu	Asp	Ala	Gly	Pro	Ser	Ile
			85				90				95			
Val	Ser	Tyr	Ala	Ile	Ala	Gly	Leu	Cys	Ala	Leu	Leu	Ser	Ala	Phe
			100				105				110			
Tyr	Thr	Glu	Phe	Ala	Val	His	Leu	Pro	Val	Ala	Gly	Gly	Ala	Phe
			115				120				125			
Tyr	Ile	Arg	Ile	Thr	Phe	Gly	Glu	Phe	Pro	Ala	Phe	Phe	Thr	Gly
			130				135				140			

Asn	Leu	Val	Met	Asp	Tyr	Val	Met	Ser	Asn	Ala	Ala	Val	Ser	Arg	Ser
145				150					155						160
Phe	Thr	Ala	Tyr	Leu	Gly	Thr	Ala	Phe	Gly	Ile	Ser	Thr	Ser	Lys	Trp
				165				170						175	
Arg	Phe	Val	Val	Ser	Gly	Leu	Pro	Lys	Gly	Phe	Asn	Glu	Ile	Asp	Pro
				180				185						190	
Val	Ala	Val	Leu	Val	Val	Leu	Val	Ile	Thr	Val	Ile	Ile	Cys	Cys	Ser
				195				200						205	
Thr	Arg	Glu	Ser	Ser	Lys	Val	Asn	Met	Ile	Met	Thr	Ala	Phe	His	Ile
				210				215						220	
Ala	Phe	Ile	Phe	Phe	Val	Ile	Val	Met	Gly	Phe	Ile	Lys	Gly	Asp	Ser
225				230						235				240	
Lys	Asn	Leu	Ser	Ser	Pro	Ala	Asn	Pro	Glu	His	Pro	Ser	Gly	Phe	Phe
				245				250						255	
Pro	Phe	Gly	Ala	Ala	Gly	Val	Phe	Asn	Gly	Ala	Ala	Met	Val	Tyr	Leu
				260				265						270	
Ser	Tyr	Ile	Gly	Tyr	Asp	Ala	Val	Ser	Thr	Met	Ala	Glu	Glu	Val	Glu
				275				280						285	
Asn	Pro	Val	Lys	Asp	Ile	Pro	Val	Gly	Val	Ser	Gly	Ser	Val	Ala	Ile
				290				295						300	
Val	Thr	Val	Leu	Tyr	Cys	Leu	Met	Ala	Val	Ser	Met	Ser	Met	Leu	Leu
305				310						315				320	
Pro	Tyr	Asp	Leu	Ile	Asp	Pro	Glu	Ala	Pro	Phe	Ser	Ala	Ala	Phe	Arg
				325						330				335	
Gly	Ser	Asn	Gly	Trp	Glu	Trp	Val	Thr	Lys	Val	Val	Gly	Ile	Gly	Ala
				340				345						350	
Ser	Phe	Gly	Ile	Leu	Thr	Ser	Leu	Leu	Val	Ala	Met	Leu	Gly	Gln	Ala
				355				360						365	
Arg	Tyr	Met	Cys	Val	Ile	Gly	Arg	Ser	Arg	Val	Val	Pro	Phe	Trp	Phe
				370				375						380	
Ala	Lys	Ile	His	Pro	Lys	Thr	Ser	Thr	Pro	Val	Asn	Ala	Ser	Thr	Phe
385				390										400	
Leu	Gly	Ile	Phe	Thr	Ala	Ala	Leu	Ala	Leu	Phe	Thr	Asp	Leu	Asn	Val
				405						410				415	
Leu	Leu	Asn	Leu	Val	Ser	Ile	Gly	Thr	Leu	Phe	Val	Phe	Tyr	Met	Val
				420						425				430	
Ala	Asn	Ala	Leu	Ile	Phe	Arg	Arg	Tyr	Val	Pro	Val	Gly	Pro	Thr	Lys
				435				440						445	
Pro	Trp	Pro	Thr	Leu	Cys	Phe	Leu	Thr	Leu	Phe	Ser	Ile	Thr	Ser	Leu
				450				455						460	
Val	Phe	Thr	Leu	Ile	Trp	Lys	Leu	Val	Pro	Glu	Gly	Lys	Pro	Lys	Ala
465				470						475				480	
Phe	Met	Leu	Gly	Ala	Ser	Ala	Val	Val	Ala	Ile	Ala	Ile	Val	Leu	Ser
				485						490				495	
Phe	Gln	Cys	Val	Val	Pro	Gln	Ala	Arg	Lys	Pro	Glu	Leu	Trp	Gly	Val
				500				505						510	
Pro	Phe	Met	Pro	Trp	Thr	Pro	Cys	Val	Ser	Ile	Phe	Leu	Asn	Ile	Phe
				515				520						525	
Leu	Leu	Gly	Ser	Leu	Asp	Ala	Pro	Ser	Tyr	Val	Arg	Phe	Gly	Phe	Phe
				530				535						540	
Ser	Gly	Leu	Ile	Val	Leu	Val	Tyr	Leu	Phe	Tyr	Gly	Val	His	Ala	Ser
545				550						555				560	
Ser	Asp	Ala	Glu	Ala	Asn	Gly	Ser	Phe	Gly	Val	Lys	Asp	Gly	Gln	Val
				565						570				575	
Met	Lys	Glu	Leu	Ile	Glu	Val									
				580											

(2) INFORMATION FOR SEQ ID NO:873:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 538 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..538

(D) OTHER INFORMATION: / Ceres Seq. ID 1499118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:873:

Met	Ser	Arg	Val	Arg	Ala	Val	Ser	Gly	Glu	Gln	Met	Arg	Arg	Thr	Leu
1				5					10					15	
Arg	Trp	Tyr	Asp	Leu	Ile	Gly	Leu	Gly	Ile	Gly	Gly	Met	Val	Gly	Ala
			20				25					30			
Gly	Val	Phe	Val	Thr	Thr	Gly	Arg	Ala	Ser	Arg	Leu	Asp	Ala	Gly	Pro
		35				40					45				
Ser	Ile	Val	Val	Ser	Tyr	Ala	Ile	Ala	Gly	Leu	Cys	Ala	Leu	Leu	Ser
	50				55					60					
Ala	Phe	Cys	Tyr	Thr	Glu	Phe	Ala	Val	His	Leu	Pro	Val	Ala	Gly	Gly
	65			70					75					80	
Ala	Phe	Ser	Tyr	Ile	Arg	Ile	Thr	Phe	Gly	Glu	Phe	Pro	Ala	Phe	Phe
			85					90					95		
Thr	Gly	Ala	Asn	Leu	Val	Met	Asp	Tyr	Val	Met	Ser	Asn	Ala	Ala	Val
			100				105					110			
Ser	Arg	Ser	Phe	Thr	Ala	Tyr	Leu	Gly	Thr	Ala	Phe	Gly	Ile	Ser	Thr
		115				120					125				
Ser	Lys	Trp	Arg	Phe	Val	Val	Ser	Gly	Leu	Pro	Lys	Gly	Phe	Asn	Glu
	130				135					140					
Ile	Asp	Pro	Val	Ala	Val	Leu	Val	Val	Leu	Val	Ile	Thr	Val	Ile	Ile
	145			150					155					160	
Cys	Cys	Ser	Thr	Arg	Glu	Ser	Ser	Lys	Val	Asn	Met	Ile	Met	Thr	Ala
			165					170					175		
Phe	His	Ile	Ala	Phe	Ile	Phe	Phe	Val	Ile	Val	Met	Gly	Phe	Ile	Lys
		180					185					190			
Gly	Asp	Ser	Lys	Asn	Leu	Ser	Ser	Pro	Ala	Asn	Pro	Glu	His	Pro	Ser
		195				200					205				
Gly	Phe	Phe	Pro	Phe	Gly	Ala	Ala	Gly	Val	Phe	Asn	Gly	Ala	Ala	Met
	210				215					220					
Val	Tyr	Leu	Ser	Tyr	Ile	Gly	Tyr	Asp	Ala	Val	Ser	Thr	Met	Ala	Glu
	225			230				235					240		
Glu	Val	Glu	Asn	Pro	Val	Lys	Asp	Ile	Pro	Val	Gly	Val	Ser	Gly	Ser
			245					250					255		
Val	Ala	Ile	Val	Thr	Val	Leu	Tyr	Cys	Leu	Met	Ala	Val	Ser	Met	Ser
		260				265					270				
Met	Leu	Leu	Pro	Tyr	Asp	Leu	Ile	Asp	Pro	Glu	Ala	Pro	Phe	Ser	Ala
	275					280					285				
Ala	Phe	Arg	Gly	Ser	Asn	Gly	Trp	Glu	Trp	Val	Thr	Lys	Val	Val	Gly
	290				295					300					
Ile	Gly	Ala	Ser	Phe	Gly	Ile	Leu	Thr	Ser	Leu	Leu	Val	Ala	Met	Leu
	305				310					315				320	
Gly	Gln	Ala	Arg	Tyr	Met	Cys	Val	Ile	Gly	Arg	Ser	Arg	Val	Val	Pro
			325						330				335		
Phe	Trp	Phe	Ala	Lys	Ile	His	Pro	Lys	Thr	Ser	Thr	Pro	Val	Asn	Ala
		340						345					350		
Ser	Thr	Phe	Leu	Gly	Ile	Phe	Thr	Ala	Ala	Leu	Ala	Leu	Phe	Thr	Asp
	355					360				365					
Leu	Asn	Val	Leu	Leu	Asn	Leu	Val	Ser	Ile	Gly	Thr	Leu	Phe	Val	Phe
	370				375					380					
Tyr	Met	Val	Ala	Asn	Ala	Leu	Ile	Phe	Arg	Arg	Tyr	Val	Pro	Val	Gly
	385			390					395				400		
Pro	Thr	Lys	Pro	Trp	Pro	Thr	Leu	Cys	Phe	Leu	Thr	Leu	Phe	Ser	Ile
			405					410					415		
Thr	Ser	Leu	Val	Phe	Thr	Leu	Ile	Trp	Lys	Leu	Val	Pro	Glu	Gly	Lys
		420				425						430			

Pro Lys Ala Phe Met Leu Gly Ala Ser Ala Val Val Ala Ile Ala Ile
435 440 445
Val Leu Ser Phe Gln Cys Val Val Pro Gln Ala Arg Lys Pro Glu Leu
450 455 460
Trp Gly Val Pro Phe Met Pro Trp Thr Pro Cys Val Ser Ile Phe Leu
465 470 475 480
Asn Ile Phe Leu Leu Gly Ser Leu Asp Ala Pro Ser Tyr Val Arg Phe
485 490 495
Gly Phe Phe Ser Gly Leu Ile Val Leu Val Tyr Leu Phe Tyr Gly Val
500 505 510
His Ala Ser Ser Asp Ala Glu Ala Asn Gly Ser Phe Gly Val Lys Asp
515 520 525
Gly Gln Val Met Lys Glu Leu Ile Glu Val
530 535

(2) INFORMATION FOR SEQ ID NO:874:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1279

(D) OTHER INFORMATION: / Ceres Seq. ID 1499119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:874:

aactgaattt gaagaaaaaa aaaaaaagaa atcataaaat gagaatcaat atgtttattca 60
tagtggcatt ctcatctttta gtctctgttc ggtcattacc gatgagacca actctaaagt 120
acgagtcatt cttaattttt ggcgattctt taagcgatac cggaactctt ttattatccg 180
gtgatgttga ctctccgaac attggaagac taccgtacgg acaaaccttt tttaaccggt 240
ccaccggctg ttgctctgac ggacgtctca tcactcgatt catcgctgag gctagtggac 300
taccgtacat tccaccgcat ctccaaagct tacggacgaa tgattcggtta gatttcaaga 360
gaggtgcmaa ttttgcggtg gctggagcaa cagcgaaacga atttagcttc tttaaaaaa 420
gaggtctttc agtaacattg ttgacaaaca agacactgga tattcaactt gattgtttca 480
agaagtgtgaa acccttctctg tgtaaaaaca agccagaatg tgacgcatat tttagaaaaa 540
ctctatttct cgtcggagaa attagtggaa acgattataa ctaccctctt ttggcatttc 600
gaagtttcaa acatgctatg gatttggtag catttggtat taacaaaatc atggacgtca 660
caagtgcatt gatagaggaa ggtgccatga cactaatagt tccaggaaac ctccaatcg 720
gtgttcttgc ggctctacta gagcggttta atgataatag tggatggctt tatgactcga 780
ggaaccaatg ctacatgcc a ttgaacaatt tggctaagct tcacaatgat aagctcaaga 840
aaggctctgc ggctctacta aaaaagtacc ctatgccaa aatttatatg gctgattatt 900
acagtcttgc catgcaattc ttcaactcac ctccaataa cggtttcaact ggaagtgttc 960
taaaaggcatg ttgtggagga ggagatggaa gatacaacgt gcaaccaaac gtgcggtgcy 1020
gagaaaaagg ttcaaccatt tcggaagatc catcaacgta cgcataattg gacggaattc 1080
acctcactga accgccttac cgccacattg caactggtct catctccgcg cgtttcacca 1140
tgctacttta taattaataa caattaaagt actcataagt tgtaactttt tttttaacac 1200
acaaactttt catataaact ctaattgaaa acctataaat cgatcatatt tatatcaagc 1260
tcgttcgaga gcataagcc

(2) INFORMATION FOR SEQ ID NO:875:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..384

(D) OTHER INFORMATION: / Ceres Seq. ID 1499120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:875:

Leu Asn Leu Lys Glu Lys Lys Lys Arg Asn His Lys Met Arg Ile Asn

1	5	10	15
Met Leu Phe Ile Val Ala Phe Ser Phe Leu Val Ser Val Arg Ser Leu			
20	25	30	
Pro Met Arg Pro Thr Leu Lys Tyr Glu Ser Ile Phe Asn Phe Gly Asp			
35	40	45	
Ser Leu Ser Asp Thr Gly Asn Phe Leu Leu Ser Gly Asp Val Asp Ser			
50	55	60	
Pro Asn Ile Gly Arg Leu Pro Tyr Gly Gln Thr Phe Phe Asn Arg Ser			
65	70	75	80
Thr Gly Arg Cys Ser Asp Gly Arg Leu Ile Ile Asp Phe Ile Ala Glu			
85	90	95	
Ala Ser Gly Leu Pro Tyr Ile Pro Pro Tyr Leu Gln Ser Leu Arg Thr			
100	105	110	
Asn Asp Ser Val Asp Phe Lys Arg Gly Ala Asn Phe Ala Val Ala Gly			
115	120	125	
Ala Thr Ala Asn Glu Phe Ser Phe Phe Lys Asn Arg Gly Leu Ser Val			
130	135	140	
Thr Leu Leu Thr Asn Lys Thr Leu Asp Ile Gln Leu Asp Trp Phe Lys			
145	150	155	160
Lys Leu Lys Pro Ser Leu Cys Lys Thr Lys Pro Glu Cys Glu Arg Tyr			
165	170	175	
Phe Arg Lys Ser Leu Phe Leu Val Gly Glu Ile Ser Gly Asn Asp Tyr			
180	185	190	
Asn Tyr Pro Leu Leu Ala Phe Arg Ser Phe Lys His Ala Met Asp Leu			
195	200	205	
Val Pro Phe Val Ile Asn Lys Ile Met Asp Val Thr Ser Ala Leu Ile			
210	215	220	
Glu Glu Gly Ala Met Thr Leu Ile Val Pro Gly Asn Leu Pro Ile Gly			
225	230	235	240
Cys Ser Ala Ala Leu Leu Glu Arg Phe Asn Asp Asn Ser Gly Trp Leu			
245	250	255	
Tyr Asp Ser Arg Asn Gln Cys Tyr Met Pro Leu Asn Asn Leu Ala Lys			
260	265	270	
Leu His Asn Asp Lys Leu Lys Lys Gly Leu Ala Ala Leu Arg Lys Lys			
275	280	285	
Tyr Pro Tyr Ala Lys Ile Ile Tyr Ala Asp Tyr Tyr Ser Ser Ala Met			
290	295	300	
Gln Phe Phe Asn Ser Pro Ser Lys Tyr Gly Phe Thr Gly Ser Val Leu			
305	310	315	320
Lys Ala Cys Cys Gly Gly Asp Gly Arg Tyr Asn Val Gln Pro Asn			
325	330	335	
Val Arg Cys Gly Glu Lys Gly Ser Thr Thr Cys Glu Asp Pro Ser Thr			
340	345	350	
Tyr Ala Asn Trp Asp Gly Ile His Leu Thr Glu Ala Ala Tyr Arg His			
355	360	365	
Ile Ala Thr Gly Leu Ile Ser Gly Arg Phe Thr Met Pro Thr Tyr Asn			
370	375	380	

(2) INFORMATION FOR SEQ ID NO:876:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..372

(D) OTHER INFORMATION: / Ceres Seq. ID 1499121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:876:

```

Met Arg Ile Asn Met Leu Phe Ile Val Ala Phe Ser Phe Leu Val Ser
1      5      10      15
Val Arg Ser Leu Pro Met Arg Pro Thr Leu Lys Tyr Glu Ser Ile Phe
20      25      30
Asn Phe Gly Asp Ser Leu Ser Asp Thr Gly Asn Phe Leu Leu Ser Gly
35      40      45
Asp Val Asp Ser Pro Asn Ile Gly Arg Leu Pro Tyr Gly Gln Thr Phe
50      55      60
Phe Asn Arg Ser Thr Gly Arg Cys Ser Asp Gly Arg Leu Ile Ile Asp
65      70      75      80
Phe Ile Ala Glu Ala Ser Gly Leu Pro Tyr Ile Pro Pro Tyr Leu Gln
85      90      95
Ser Leu Arg Thr Asn Asp Ser Val Asp Phe Lys Arg Gly Ala Asn Phe
100     105     110
Ala Val Ala Gly Ala Thr Ala Asn Glu Phe Ser Phe Phe Lys Asn Arg
115     120     125
Gly Leu Ser Val Thr Leu Leu Thr Asn Lys Thr Leu Asp Ile Gln Leu
130     135     140
Asp Trp Phe Lys Lys Leu Lys Pro Ser Leu Cys Lys Thr Lys Pro Glu
145     150     155     160
Cys Glu Arg Tyr Phe Arg Lys Ser Leu Phe Leu Val Gly Glu Ile Ser
165     170     175
Gly Asn Asp Tyr Asn Tyr Pro Leu Leu Ala Phe Arg Ser Phe Lys His
180     185     190
Ala Met Asp Leu Val Pro Phe Val Ile Asn Lys Ile Met Asp Val Thr
195     200     205
Ser Ala Leu Ile Glu Glu Gly Ala Met Thr Leu Ile Val Pro Gly Asn
210     215     220
Leu Pro Ile Gly Cys Ser Ala Ala Leu Leu Glu Arg Phe Asn Asp Asn
225     230     235     240
Ser Gly Trp Leu Tyr Asp Ser Arg Asn Gln Cys Tyr Met Pro Leu Asn
245     250     255
Asn Leu Ala Lys Leu His Asn Asp Lys Leu Lys Lys Gly Leu Ala Ala
260     265     270
Leu Arg Lys Lys Tyr Pro Tyr Ala Lys Ile Ile Tyr Ala Asp Tyr Tyr
275     280     285
Ser Ser Ala Met Gln Phe Phe Asn Ser Pro Ser Lys Tyr Gly Phe Thr
290     295     300
Gly Ser Val Leu Lys Ala Cys Cys Gly Gly Gly Asp Gly Arg Tyr Asn
305     310     315     320
Val Gln Pro Asn Val Arg Cys Gly Glu Lys Gly Ser Thr Thr Cys Glu
325     330     335
Asp Pro Ser Thr Tyr Ala Asn Trp Asp Gly Ile His Leu Thr Glu Ala
340     345     350
Ala Tyr Arg His Ile Ala Thr Gly Leu Ile Ser Gly Arg Phe Thr Met
355     360     365
Pro Thr Tyr Asn
370

```

(2) INFORMATION FOR SEQ ID NO:877:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 368 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..368

(D) OTHER INFORMATION: / Ceres Seq. ID 1499122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:877:

Met Leu Phe Ile Val Ala Phe Ser Phe Leu Val Ser Val Arg Ser Leu

1	5	10	15
Pro Met Arg Pro Thr Leu Lys Tyr Glu Ser Ile Phe Asn Phe Gly Asp	20	25	30
Ser Leu Ser Asp Thr Gly Asn Phe Leu Leu Ser Gly Asp Val Asp Ser	35	40	45
Pro Asn Ile Gly Arg Leu Pro Tyr Gly Gln Thr Phe Phe Asn Arg Ser	50	55	60
Thr Gly Arg Cys Ser Asp Gly Arg Leu Ile Ile Asp Phe Ile Ala Glu	65	70	75
Ala Ser Gly Leu Pro Tyr Ile Pro Pro Tyr Leu Gln Ser Leu Arg Thr	85	90	95
Asn Asp Ser Val Asp Phe Lys Arg Gly Ala Asn Phe Ala Val Ala Gly	100	105	110
Ala Thr Ala Asn Glu Phe Ser Phe Phe Lys Asn Arg Gly Leu Ser Val	115	120	125
Thr Leu Leu Thr Asn Lys Thr Leu Asp Ile Gln Leu Asp Trp Phe Lys	130	135	140
Lys Leu Lys Pro Ser Leu Cys Lys Thr Lys Pro Glu Cys Glu Arg Tyr	145	150	155
Phe Arg Lys Ser Leu Phe Leu Val Gly Glu Ile Ser Gly Asn Asp Tyr	165	170	175
Asn Tyr Pro Leu Leu Ala Phe Arg Ser Phe Lys His Ala Met Asp Leu	180	185	190
Val Pro Phe Val Ile Asn Lys Ile Met Asp Val Thr Ser Ala Leu Ile	195	200	205
Glu Glu Gly Ala Met Thr Leu Ile Val Pro Gly Asn Leu Pro Ile Gly	210	215	220
Cys Ser Ala Ala Leu Leu Glu Arg Phe Asn Asp Asn Ser Gly Trp Leu	225	230	235
Tyr Asp Ser Arg Asn Gln Cys Tyr Met Pro Leu Asn Asn Leu Ala Lys	245	250	255
Leu His Asn Asp Lys Leu Lys Lys Gly Leu Ala Ala Leu Arg Lys Lys	260	265	270
Tyr Pro Tyr Ala Lys Ile Ile Tyr Ala Asp Tyr Tyr Ser Ser Ala Met	275	280	285
Gln Phe Phe Asn Ser Pro Ser Lys Tyr Gly Phe Thr Gly Ser Val Leu	290	295	300
Lys Ala Cys Cys Gly Gly Gly Asp Gly Arg Tyr Asn Val Gln Pro Asn	305	310	315
Val Arg Cys Gly Glu Lys Gly Ser Thr Thr Cys Glu Asp Pro Ser Thr	325	330	335
Tyr Ala Asn Trp Asp Gly Ile His Leu Thr Glu Ala Ala Tyr Arg His	340	345	350
Ile Ala Thr Gly Leu Ile Ser Gly Arg Phe Thr Met Pro Thr Tyr Asn	355	360	365

(2) INFORMATION FOR SEQ ID NO:878:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1620
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:878:

ctctgcctct catctcttgt tctctccgcc catctctgct ctctttttatt ttcccagaaa
gttttttttt ttcccgaat tccgttaatc tcattgggggt ttccattgat agcaatggcg

60
120

acggcttttc	ctccactaa	gctcactgcc	acggttcttc	tgcatggatc	ccatgagaat	180
cgtctcttgc	tcccgatccg	attggtctct	cctctcttct	tctcctggatc	caccctgttc	240
ctctcccttc	gcagactcaa	ctactccaac	gccaccgcgt	gatctcccgt	cgtctctgtc	300
caggaagtgt	tcaaggagaa	gcaatccacc	aataatacca	gcctgttgat	aaccaaagag	360
gaaggattgg	agttgtatg	agatatgata	cttaggtagat	ctttcgaaaga	catgtgtgct	420
caaatgtatt	accgaggcaa	gatgtttggt	tttgttctact	tgtacaatgg	ccaagaggct	480
gtttctactg	gctttatcaa	gctccttacc	aagtctgact	ctgtcgttag	tacctaccgt	540
gacctgtctc	atgcctctag	caaagggtgc	tctgtctcgt	ctgttatgag	cagctctctc	600
ggcaaggtta	ctggatgctg	cagaggccaa	ggtggatcca	tgacatggtt	ctccaaagaa	660
cacaacatgc	ttggtggctt	tgcttttatt	ggtgaaggca	ttcctgtgcg	cactggtgct	720
gccttttagc	ccaagtacag	gaggggaagt	ttgaaacagg	attgtgatga	tgtcactgtc	780
gcctttttgc	gagatggaac	ttgtaacaac	ggacagttct	tcgagtgtct	caacatggct	840
gctctctata	aactgcctat	tatctttgtt	gtcgagaata	acttgtgggc	cattgggagt	900
tctcatctga	gagccacttc	tgaccocgag	atttggaaaga	aaggtctctg	atttgggagt	960
cctggtgttc	atgttgacgg	tatggatgtc	ttgaaggtca	gggaagtgcg	taaaagagct	1020
gtcactagag	ctagaagagg	agaaggtcca	accttgggtg	aagtgtgagc	ttatagattt	1080
agaggacact	ccttggctga	tcccgatgag	ctccgtgagt	ctgctgagaa	agccaaatac	1140
gcggctagag	accctaactgc	agcattgaag	aagtatttga	tagaagaacaa	gcgttgcaaa	1200
gaagcagatc	taaagtcaat	agagaaaaag	atagacagtt	ggtggaggaa	gcggttgagt	1260
ttgcagagc	tagtccacag	cccggtcgca	gtcagttgct	agagaatgtg	tttgcgtatc	1320
caaaaggatt	tgaattggga	cctgatggac	ggtacagatg	tgaggaccac	aagtttaccg	1380
aaggcacagc	tcaagtctga	gaagacaagt	ttaccataac	gctgtctact	gtctcttcga	1440
tgctttctata	tatctttata	agttaaatgc	tacagagaat	cagtttgaat	catttgcaat	1500
ttttgtcttt	tgtttggtgt	tactaaatta	tcacaaggtt	ctcttctgag	ttcgttgggt	1560
tttcatgtgt	taccacttac	cagagaattg	tatttttttt	tttaaagata	attattttgc	1620

(2) INFORMATION FOR SEQ ID NO:879:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 433 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..433

(D) OTHER INFORMATION: / Ceres Seq. ID 1499124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:879:

Leu	Cys	Leu	Ser	Ser	Leu	Val	Leu	Ser	Ala	His	Leu	Cys	Ser	Leu	Leu
1			5						10					15	
Phe	Ser	Gln	Lys	Val	Phe	Phe	Phe	Ser	Arg	Ile	Pro	Leu	Ile	Ser	Leu
			20						25				30		
Gly	Phe	Pro	Leu	Ile	Ala	Met	Ala	Thr	Ala	Phe	Ala	Pro	Thr	Lys	Leu
			35				40					45			
Thr	Ala	Thr	Val	Pro	Leu	His	Gly	Ser	His	Glu	Asn	Arg	Leu	Leu	Leu
			50				55				60				
Pro	Ile	Arg	Leu	Ala	Pro	Pro	Ser	Ser	Phe	Leu	Gly	Ser	Thr	Arg	Ser
			65				70			75				80	
Leu	Ser	Leu	Arg	Arg	Leu	Asn	His	Ser	Asn	Ala	Thr	Arg	Arg	Ser	Pro
			85						90					95	
Val	Val	Ser	Val	Gln	Glu	Val	Val	Lys	Glu	Lys	Gln	Ser	Thr	Asn	Asn
			100					105					110		
Thr	Ser	Leu	Leu	Ile	Thr	Lys	Glu	Glu	Gly	Leu	Glu	Leu	Tyr	Glu	Asp
			115				120						125		
Met	Ile	Leu	Gly	Arg	Ser	Phe	Glu	Asp	Met	Cys	Ala	Gln	Met	Tyr	Tyr
			130				135				140				
Arg	Gly	Lys	Met	Phe	Gly	Phe	Val	His	Leu	Tyr	Asn	Gly	Gln	Glu	Ala
			145				150				155			160	
Val	Ser	Thr	Gly	Phe	Ile	Lys	Leu	Leu	Thr	Lys	Ser	Asp	Ser	Val	Val
			165						170					175	
Ser	Thr	Tyr	Arg	Asp	His	Val	His	Ala	Leu	Ser	Lys	Gly	Val	Ser	Ala

Met	Ala	Thr	Ala	Phe	Ala	Pro	Thr	Lys	Leu	Thr	Ala	Thr	Val	Pro	Leu
1				5					10					15	
His	Gly	Ser	His	Glu	Asn	Arg	Leu	Leu	Leu	Pro	Ile	Arg	Leu	Ala	Pro
			20					25					30		
Pro	Ser	Ser	Phe	Leu	Gly	Ser	Thr	Arg	Ser	Leu	Ser	Leu	Arg	Arg	Leu
		35					40					45			
Asn	His	Ser	Asn	Ala	Thr	Arg	Arg	Ser	Pro	Val	Val	Ser	Val	Gln	Glu
		50				55					60				
Val	Val	Lys	Glu	Lys	Gln	Ser	Thr	Asn	Asn	Thr	Ser	Leu	Leu	Ile	Thr
65					70					75				80	
Lys	Glu	Glu	Gly	Leu	Glu	Leu	Tyr	Glu	Asp	Met	Ile	Leu	Gly	Arg	Ser
			85						90				95		
Phe	Glu	Asp	Met	Cys	Ala	Gln	Met	Tyr	Tyr	Arg	Gly	Lys	Met	Phe	Gly
			100					105					110		
Phe	Val	His	Leu	Tyr	Asn	Gly	Gln	Glu	Ala	Val	Ser	Thr	Gly	Phe	Ile
		115					120					125			

Lys Leu Leu Thr Lys Ser Asp Ser Val Val Ser Thr Tyr Arg Asp His
130 135 140
Val His Ala Leu Ser Lys Gly Val Ser Ala Arg Ala Val Met Ser Glu
145 150 155 160
Leu Phe Gly Lys Val Thr Gly Cys Cys Arg Gly Gln Gly Gly Ser Met
165 170 175
His Met Phe Ser Lys Glu His Asn Met Leu Gly Gly Phe Ala Phe Ile
180 185 190
Gly Glu Gly Ile Pro Val Ala Thr Gly Ala Ala Phe Ser Ser Lys Tyr
195 200 205
Arg Arg Glu Val Leu Lys Gln Asp Cys Asp Asp Val Thr Val Ala Phe
210 215 220
Phe Gly Asp Gly Thr Cys Asn Asn Gly Gln Phe Phe Glu Cys Leu Asn
225 230 235 240
Met Ala Ala Leu Tyr Lys Leu Pro Ile Ile Phe Val Val Glu Asn Asn
245 250 255
Leu Trp Ala Ile Gly Met Ser His Leu Arg Ala Thr Ser Asp Pro Glu
260 265 270
Ile Trp Lys Lys Gly Pro Ala Phe Gly Met Pro Gly Val His Val Asp
275 280 285
Gly Met Asp Val Leu Lys Val Arg Glu Val Ala Lys Glu Ala Val Thr
290 295 300
Arg Ala Arg Arg Gly Glu Gly Pro Thr Leu Val Glu Cys Glu Thr Tyr
305 310 315 320
Arg Phe Arg Gly His Ser Leu Ala Asp Pro Asp Glu Leu Arg Asp Ala
325 330 335
Ala Glu Lys Ala Lys Tyr Ala Ala Arg Asp Pro Ile Ala Ala Leu Lys
340 345 350
Lys Tyr Leu Ile Glu Asn Lys Leu Ala Lys Glu Ala Glu Leu Lys Ser
355 360 365
Ile Glu Lys Lys Ile Asp Ser Trp Trp Arg Lys Arg Leu Ser Leu Gln
370 375 380
Thr Leu Val His Ser Pro Val Ala Val Ser Cys
385 390 395

(2) INFORMATION FOR SEQ ID NO:881:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..305
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:881:

Met Ile Leu Gly Arg Ser Phe Glu Asp Met Cys Ala Gln Met Tyr Tyr
1 5 10 15
Arg Gly Lys Met Phe Gly Phe Val His Leu Tyr Asn Gly Gln Glu Ala
20 25 30
Val Ser Thr Gly Phe Ile Lys Leu Thr Lys Ser Asp Ser Val Val
35 40 45
Ser Thr Tyr Arg Asp His Val His Ala Leu Ser Lys Gly Val Ser Ala
50 55 60
Arg Ala Val Met Ser Glu Leu Phe Gly Lys Val Thr Gly Cys Cys Arg
65 70 75 80
Gly Gln Gly Lys Ser Met His Met Phe Ser Lys Glu His Asn Met Leu
85 90 95
Gly Gly Phe Ala Phe Ile Gly Glu Gly Ile Pro Val Ala Thr Gly Ala
100 105 110
Ala Phe Ser Ser Lys Tyr Arg Arg Glu Val Leu Lys Gln Asp Cys Asp

115	120	125
Asp Val Thr Val Ala Phe	Phe Gly Asp Gly Thr Cys Asn Asn Gly Gln	
130	135	140
Phe Phe Glu Cys Leu Asn Met Ala Ala Leu Tyr Lys Leu Pro Ile Ile		
145	150	155
Phe Val Val Glu Asn Asn Leu Trp Ala Ile Gly Met Ser His Leu Arg		
165	170	175
Ala Thr Ser Asp Pro Glu Ile Trp Lys Lys Gly Pro Ala Phe Gly Met		
180	185	190
Pro Gly Val His Val Asp Gly Met Asp Val Leu Lys Val Arg Glu Val		
195	200	205
Ala Lys Glu Ala Val Thr Arg Ala Arg Arg Gly Glu Gly Pro Thr Leu		
210	215	220
Val Glu Cys Glu Thr Tyr Arg Phe Arg Gly His Ser Leu Ala Asp Pro		
225	230	235
Asp Glu Leu Arg Asp Ala Ala Glu Lys Ala Lys Tyr Ala Ala Arg Asp		
245	250	255
Pro Ile Ala Ala Leu Lys Lys Tyr Leu Ile Glu Asn Lys Leu Ala Lys		
260	265	270
Glu Ala Glu Leu Lys Ser Ile Glu Lys Lys Ile Asp Ser Trp Trp Arg		
275	280	285
Lys Arg Leu Ser Leu Gln Thr Leu Val His Ser Pro Val Ala Val Ser		
290	295	300

Cys
305

(2) INFORMATION FOR SEQ ID NO:882:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1253 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1253

(D) OTHER INFORMATION: / Ceres Seq. ID 1499127

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:882:

aaacacatga	ccctaaatc	gagaggcttc	gttagggagaa	ggagaagcag	aagagtgttg	60
gtctctcgatt	gtcgactctca	acaattggcgt	agtcctcccca	aaatgcgtca	acctcgagct	120
tctctctgcgc	cgatatgttaa	ggatggtctcg	atcattgtga	ttggagggttg	cagggtccaag	180
aataatcgaga	cttgggggaga	gatttatgat	ctaaaagacca	atacttggggg	gcgaataactg	240
ctccaatcac	atgatcccac	agttcaaaaa	gcttacttga	atcgcttttaa	acctaaacttg	300
cagacgaatg	cttgctatgt	agagattgac	aaggtgtcgt	gcctgatatt	tttactccgat	360
gggaagctat	tttggcgtga	aaacaagcaa	gggtttgaga	gggtgtagtgt	tattttgggga	420
gatgatgagc	aagtgctctc	ttatcaactt	gtttcgggtg	caaacgcccgc	cggaggaggga	480
agagtgacag	tttgggtgaa	gtcgggggtta	aaagtctctg	atctctttaag	tggcactgag	540
acttggaat	gttacacaaa	tagtcgggtg	gcagagattt	cgtttgagag	aagagggttta	600
agagagcttt	ggggattctg	tgaattggtct	agagaggttg	ttaccgttga	tggatatgac	660
gataactcag	attctttttt	aaattctgct	attgtgacct	attgatcagt	gggactttat	720
cttacttgta	ctgtgggaat	tttgagtatg	attttaatag	ataaataaat	gtgattttgt	780
aaacaacatta	caacatagat	ctaaagcattc	aaggtgtttg	tggtgcctga	tggtctttga	840
tgaaggggag	gtttttctact	ttgatcaga	cttttgcctg	ctagtgaag	agagaataat	900
gggcacaaca	ttttgtttac	tcactgggaa	agataatgta	gagtggtctc	aaggaaaaaa	960
tggtgtggag	agtggtcaag	ggacttggat	tgccaaaacat	tggtgttcag	tttggtgggtg	1020
tacaatgttg	gatcacccct	atggtcgttaa	agtgacagatt	tcgcagagct	ttccaaggga	1080
atcatagaa	gctcaacgga	gttggtgttc	gaaccaaaagg	atgtatatatt	cgttccactt	1140
tcttcttgca	ctctgctaca	gtaacacatg	gattgttatg	ctctcatggg	agtggtacaaa	1200
ctcctagtga	tttggttttt	tatttgcct	ttggaatgct	taaagaatga	tat	

(2) INFORMATION FOR SEQ ID NO:883:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..234
(D) OTHER INFORMATION: / Ceres Seq. ID 1499128
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:883:
Lys His Met Thr Pro Lys Ser Arg Gly Phe Val Arg Arg Arg Ser
1 5 10 15
Arg Arg Val Leu Val Leu Asp Cys Arg Ser Gln Gln Trp Arg Ser Leu
20 25 30
Pro Lys Met Arg Gln Pro Arg Ala Ser Pro Ala Ala Tyr Val Lys Asp
35 40 45
Gly Leu Ile Ile Val Ile Gly Cys Arg Ser Lys Asn Ile Glu Thr
50 55 60
Trp Gly Glu Ile Tyr Asp Leu Lys Thr Asn Thr Trp Gly Arg Ile Leu
65 70 75 80
Leu Gln Ser His Asp Pro Thr Val Gln Asn Ala Tyr Leu Asn Arg Phe
85 90 95
Lys Pro Asn Leu Gln Thr Asn Ala Cys Tyr Val Glu Ile Asp Lys Val
100 105 110
Ser Cys Leu Ile Phe Leu Ser Asp Gly Lys Leu Phe Trp Arg Glu Thr
115 120 125
Lys Gln Gly Phe Glu Arg Cys Ser Val Ile Leu Gly Asp Asp Glu Gln
130 135 140
Val Ser Ser Tyr Gln Leu Val Ser Val Ala Asn Ala Ala Gly Gly Gly
145 150 155 160
Arg Val Thr Val Trp Trp Lys Ser Gly Leu Lys Val Leu Asp Leu Leu
165 170 175
Ser Gly Thr Glu Thr Trp Glu Cys Tyr Thr Asn Ser Arg Cys Ala Glu
180 185 190
Ile Ser Phe Glu Arg Arg Gly Leu Arg Glu Leu Trp Gly Phe Val Glu
195 200 205
Trp Ser Arg Glu Val Phe Thr Val Asp Gly Tyr Asp Asp Thr Tyr Asp
210 215 220
Phe Phe Leu Asn Ser Ala Ile Val Thr Tyr
225 230
(2) INFORMATION FOR SEQ ID NO:884:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 232 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..232
(D) OTHER INFORMATION: / Ceres Seq. ID 1499129
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:884:
Met Thr Pro Lys Ser Arg Gly Phe Val Arg Arg Arg Arg Ser Arg Arg
1 5 10 15
Val Leu Val Leu Asp Cys Arg Ser Gln Gln Trp Arg Ser Leu Pro Lys
20 25 30
Met Arg Gln Pro Arg Ala Ser Pro Ala Ala Tyr Val Lys Asp Gly Leu
35 40 45
Ile Ile Val Ile Gly Gly Cys Arg Ser Lys Asn Ile Glu Thr Trp Gly
50 55 60
Glu Ile Tyr Asp Leu Lys Thr Asn Thr Trp Gly Arg Ile Leu Leu Gln
65 70 75 80

Ser His Asp Pro Thr Val Gln Asn Ala Tyr Leu Asn Arg Phe Lys Pro
85 90 95
Asn Leu Gln Thr Asn Ala Cys Tyr Val Glu Ile Asp Lys Val Ser Cys
100 105 110
Leu Ile Phe Leu Ser Asp Gly Lys Leu Phe Trp Arg Glu Thr Lys Gln
115 120 125
Gly Phe Glu Arg Cys Ser Val Ile Leu Gly Asp Asp Glu Gln Val Ser
130 135 140
Ser Tyr Gln Leu Val Ser Val Ala Asn Ala Ala Gly Gly Gly Arg Val
145 150 155 160
Thr Val Trp Trp Lys Ser Gly Leu Lys Val Leu Asp Leu Leu Ser Gly
165 170 175
Thr Glu Thr Trp Glu Cys Tyr Thr Asn Ser Arg Cys Ala Glu Ile Ser
180 185 190
Phe Glu Arg Arg Gly Leu Arg Glu Leu Trp Gly Phe Val Glu Trp Ser
195 200 205
Arg Glu Val Phe Thr Val Asp Gly Tyr Asp Asp Thr Tyr Asp Phe Phe
210 215 220
Leu Asn Ser Ala Ile Val Thr Tyr
225 230

(2) INFORMATION FOR SEQ ID NO:885:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..200
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:885:

Met Arg Gln Pro Arg Ala Ser Pro Ala Ala Tyr Val Lys Asp Gly Leu
1 5 10 15
Ile Ile Val Ile Gly Gly Cys Arg Ser Lys Asn Ile Glu Thr Trp Gly
20 25 30
Glu Ile Tyr Asp Leu Lys Thr Asn Thr Trp Gly Arg Ile Leu Leu Gln
35 40 45
Ser His Asp Pro Thr Val Gln Asn Ala Tyr Leu Asn Arg Phe Lys Pro
50 55 60
Asn Leu Gln Thr Asn Ala Cys Tyr Val Glu Ile Asp Lys Val Ser Cys
65 70 75 80
Leu Ile Phe Leu Ser Asp Gly Lys Leu Phe Trp Arg Glu Thr Lys Gln
85 90 95
Gly Phe Glu Arg Cys Ser Val Ile Leu Gly Asp Asp Glu Gln Val Ser
100 105 110
Ser Tyr Gln Leu Val Ser Val Ala Asn Ala Ala Gly Gly Gly Arg Val
115 120 125
Thr Val Trp Trp Lys Ser Gly Leu Lys Val Leu Asp Leu Leu Ser Gly
130 135 140
Thr Glu Thr Trp Glu Cys Tyr Thr Asn Ser Arg Cys Ala Glu Ile Ser
145 150 155 160
Phe Glu Arg Arg Gly Leu Arg Glu Leu Trp Gly Phe Val Glu Trp Ser
165 170 175
Arg Glu Val Phe Thr Val Asp Gly Tyr Asp Asp Thr Tyr Asp Phe Phe
180 185 190
Leu Asn Ser Ala Ile Val Thr Tyr
195 200

(2) INFORMATION FOR SEQ ID NO:886:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1636 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1636
(D) OTHER INFORMATION: / Ceres Seq. ID 1499135
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:886:
ggagagtagaac atcgagacaaa agaagaaaag ctaaaaaaga gaaccccaaa gaatcgaata 60
tttattattt cgcccgcgag attctatttc tgatcattta caccctataa aagagtagag 120
ctttcgtgaa gccaccatgt gtggaggagc tataatctcc gatttcatac ctccgcgcag 180
gtccctccgc gtcactaacg agtttatctg gccggatctg aaaaacaaga tgaagcttc 240
aaagaagaga tcgaataaag gatccgattt ctctgatctt gacgatgatt tgaagctga 300
tttccaaagg tttaaggatg actcggcttt tgactgcgaa gacgatgatg atgtctctgt 360
caatgttaag cctttctctt tcaccgcaac tactaagccc gtactctccg ctttctgtct 420
cactgtata tatttggtag gtccagcata tgccaagaaa actgtagagt ccgctgagca 480
agctgagaaa tcttctaaga ggaagaggaa gaatcagtag cgagggatta ggcagcgtcc 540
ttggggaaaa tgggctgcgg agatccgtga tccgagaaaa ggctcccgag aatggcttgg 600
aacattcgac actgctgagg aagcagcaag agcttatgat gctgcagcac gcgaatccgc 660
tgccacgaaa gctaagggtga attttccoga ggagaagaac cctagcgtcg tatccagaa 720
acgtcctagt gctaagacta ataactctca gaaatcagtg gctaaaccaa acaaaacgct 780
aactttggtt cagcagccaa cacactctgag tcagcagtag tgcaacaact cctttgacaa 840
ctcttttggg gatatgagtt tcatggaaga gaagcctcag atgtacaaca atcagtttgg 900
gttaacaaac tcgtctgagt ctggaggtaa caatggatac cagtatttca gtccgatata 960
ggttcagtaac tccctgactg gtcttgagtt cgggtggagt gatcacggcc ctaaaacacc 1020
cgagatctct tcaatgcttg tcaataacaa cgaagcatca ttgtttgaag aacccaatgc 1080
agccaagaag ctcaaaccta actctgatga ctgacagcat ctgatggcat accttgacca 1140
cgcttctgtg gacacccacc tagaagtga agccatgctt ggcgcagatg ctggtgctgt 1200
gactcaggaa gaggaaaacc cagtggagct atgagctta gatgagatca ttctcatgct 1260
tgaaggagac ttttgaaagt acgatgggtt ccttagtttg taaataaagg tgtttggat 1320
gttctgttg ggggattgta caagtacac ctcaagctct atgcatttgt atctcatgag 1380
ctctctcttc atagagagtt tctcttttaa tttgtcgaa ataaaaaagg tgtgatgaag 1440
taaatagagg tataataata tctatctatt aagctctgtt ttgttcttct atttttgat 1500
tctctttcta tttaaaaagc agtttattag tctcttgagc tctcttttg atctttgta 1560
tagcgtatca tcacctctga aagtgtaag ttgtgacc ccaaacttgt ttacattat 1620
aataaagctt ctttgg
(2) INFORMATION FOR SEQ ID NO:887:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 379 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..379
(D) OTHER INFORMATION: / Ceres Seq. ID 1499136
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:887:
Met Cys Gly Gly Ala Ile Ile Ser Asp Phe Ile Pro Pro Pro Arg Ser
1 5 10 15
Leu Arg Val Thr Asn Glu Phe Ile Trp Pro Asp Leu Lys Asn Lys Val
20 25 30
Lys Ala Ser Lys Lys Arg Ser Asn Lys Arg Ser Asp Phe Phe Asp Leu
35 40 45
Asp Asp Asp Phe Glu Ala Asp Phe Gln Gly Phe Lys Asp Asp Ser Ala
50 55 60
Phe Asp Cys Glu Asp Asp Asp Val Phe Val Asn Val Lys Pro Phe
65 70 75 80
Val Phe Thr Ala Thr Lys Pro Val Ala Ser Ala Phe Val Ser Thr
85 90 95

Gly Ile Tyr Leu Val Gly Ser Ala Tyr Ala Lys Lys Thr Val Glu Ser
100 105 110
Ala Glu Gln Ala Glu Lys Ser Ser Lys Arg Lys Arg Lys Asn Gln Tyr
115 120 125
Arg Gly Ile Arg Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg
130 135 140
Asp Pro Arg Lys Gly Ser Arg Glu Trp Leu Gly Thr Phe Asp Thr Ala
145 150 155 160
Glu Glu Ala Ala Arg Ala Tyr Asp Ala Ala Arg Arg Ile Arg Gly
165 170 175
Thr Lys Ala Lys Val Asn Phe Pro Glu Glu Lys Asn Pro Ser Val Val
180 185 190
Ser Gln Lys Arg Pro Ser Ala Lys Thr Asn Asn Leu Gln Lys Ser Val
195 200 205
Ala Lys Pro Asn Lys Ser Val Thr Leu Val Gln Gln Pro Thr His Leu
210 215 220
Ser Gln Gln Tyr Cys Asn Asn Ser Phe Asp Asn Ser Phe Gly Asp Met
225 230 235 240
Ser Phe Met Glu Glu Lys Pro Gln Met Tyr Asn Asn Gln Phe Gly Leu
245 250 255
Thr Asn Ser Phe Asp Ala Gly Gly Asn Asn Gly Tyr Gln Tyr Phe Ser
260 265 270
Ser Asp Gln Gly Ser Asn Ser Phe Asp Cys Ser Glu Phe Gly Trp Ser
275 280 285
Asp His Gly Pro Lys Thr Pro Glu Ile Ser Ser Met Leu Val Asn Asn
290 295 300
Asn Glu Ala Ser Phe Val Glu Glu Thr Asn Ala Ala Lys Lys Leu Lys
305 310 315 320
Pro Asn Ser Asp Glu Ser Asp Asp Leu Met Ala Tyr Leu Asp Asn Ala
325 330 335
Leu Trp Asp Thr Pro Leu Glu Val Lys Ala Met Leu Gly Ala Asp Ala
340 345 350
Gly Ala Val Thr Gln Glu Glu Glu Asn Pro Val Glu Leu Trp Ser Leu
355 360 365
Asp Glu Ile Asn Phe Met Leu Glu Gly Asp Phe
370 375

(2) INFORMATION FOR SEQ ID NO:888:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 907 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..907

(D) OTHER INFORMATION: / Ceres Seq. ID 1499141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:888:

ctatctttgt	cgccgccaaa	cctctctcag	attctttctt	ttcttcgcag	atcgattttt	60
ttttgaagct	aaatctcaaa	aatggagaac	gacgcaggtc	aggctacaga	gctctacatt	120
tttgagattt	agcttcaaaa	acaaatccca	aagcttcaga	ggaagaagaa	gaagagagt	180
gaaacaatt	gcgtcgagca	ctctctcaat	cgcaacaaca	atccgttctt	cttctctctt	240
ctactccgct	tccatcattc	acttctcttc	caaaccaccc	gcaatcgaat	tcccatttgc	300
tctcagctct	ttctctagcc	accgtgcaat	caacctccgt	cttatctccg	ccgtcgaaagc	360
tccggagaaa	atcgagagaa	tcggatccga	aatctcatcc	ctaacctctg	aagaagctgc	420
tatctctgct	gaatatctcc	aagacaaaatt	cggtgtctcc	ccactctctt	tagccccccg	480
agcagcgccg	gttgctgctc	cagccgacgg	tggcgccggc	gctgtagtgg	aggagcaaac	540
agagttcgat	gtggttatca	atgaagttcc	cagcagttcc	cgtattgcag	tgattaaagc	600
tgtaggggct	ttaactagct	tggtgttgaa	ggaagctaa	gagctaatcg	aaggaattacc	660
aaagaagttt	aaagaagata	tcactaaaga	tgaagctgaa	gaagctaaga	agactcttga	720
agaagctggt	gctaagaagt	ccattgctta	agttttctta	acaatcgtaa	aaaaaaaaat	780

gtgatctttt cggaatttat gagtcttttt gttgtttagt atagtttggtg tttgagttgt 840
tgattcagct tttagaagaat tgggtgactt tgaatcaatt tggtttcgta ttacagtttt 900
agtcttc

(2) INFORMATION FOR SEQ ID NO:889:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..187

(D) OTHER INFORMATION: / Ceres Seq. ID 1499142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:889:

Met Ala Ser Thr Thr Leu Ser Ile Ala Thr Thr Ile Arg Ser Ser Ser
1 5 10 15
Pro Leu Thr Ser Ala Ser Thr His His Phe Leu Ser Lys Pro Thr Ala
20 25 30
Ile Glu Phe Pro Phe Arg Leu Ser Ser Ser Ser Ser His Arg Ala Ile
35 40 45
Asn Leu Arg Pro Ile Ser Ala Val Glu Ala Pro Glu Lys Ile Glu Lys
50 55 60
Ile Gly Ser Glu Ile Ser Ser Leu Thr Leu Glu Glu Ala Arg Ile Leu
65 70 75 80
Val Asp Tyr Leu Gln Asp Lys Phe Gly Val Ser Pro Leu Ser Leu Ala
85 90 95
Pro Ala Ala Ala Val Ala Val Ala Pro Ala Asp Gly Gly Ala Ala Ala
100 105 110
Val Val Glu Glu Gln Thr Glu Phe Asp Val Val Ile Asn Glu Val Pro
115 120 125
Ser Ser Ser Arg Ile Ala Val Ile Lys Ala Val Arg Ala Leu Thr Ser
130 135 140
Leu Ala Leu Lys Glu Ala Lys Glu Leu Ile Glu Gly Leu Pro Lys Lys
145 150 155 160
Phe Lys Glu Asp Ile Thr Lys Asp Glu Ala Glu Glu Ala Lys Lys Thr
165 170 175
Leu Glu Glu Ala Gly Ala Lys Val Ser Ile Ala
180 185

(2) INFORMATION FOR SEQ ID NO:890:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 674 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..674

(D) OTHER INFORMATION: / Ceres Seq. ID 1499147

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:890:

acataactcc aatgtccagc tcttgcaaac gcttagcctc aaaaggtctt aagctcactc 60
tggtctctgt ctccgacaaa cctctctctc catacaaaa agagcagcag tcaatcactg 120
tcttccccat ctccaacggc ttccaagaac gcgaggaacc attacaagac ctcgatgatt 180
acatggaagc agtagaaacc agcatcaaaa acaccttacc gaagttggtt gaagacatga 240
aactgtcggg aaatccacct agggctatcg tgtacgactc caccatgcc a tggcttcttg 300
atgtagctca tagttatgga ttgagcgggt cctgtttttt caccgaacct tggcttctga 360
cagctattta ctaccatgtt ttcaagggtt cgttctctgt accatctaca aagtacggtc 420
actgcagatt agcatcttcc ccttcgttcc cgatgctgac tgc aaatgat ttgcgcttct 480
tcctctgaga atcgtctctca taccgaata tactgaggat tgtgttggtat cagctctcaa 540
acattgatcg agtcgacata gtgtgtgcaa cactttcgat aaattggagg aaaagtgttg 600

aaatgggtca aagcttggtg ccagctctgaa tatkgaccaa cgggtccatc gatgtattag 660
acaacgactg tctg

(2) INFORMATION FOR SEQ ID NO:891:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..208
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:891:

Ile	Thr	Pro	Met	Ser	Gln	Phe	Cys	Lys	Arg	Leu	Ala	Ser	Lys	Gly	Leu
1				5				10						15	
Lys	Leu	Thr	Leu	Val	Leu	Val	Ser	Asp	Lys	Pro	Ser	Pro	Pro	Tyr	Lys
			20					25					30		
Thr	Glu	His	Asp	Ser	Ile	Thr	Val	Phe	Pro	Ile	Ser	Asn	Gly	Phe	Gln
			35				40				45				
Glu	Arg	Glu	Glu	Pro	Leu	Gln	Asp	Leu	Asp	Asp	Tyr	Met	Glu	Arg	Val
			50			55				60					
Glu	Thr	Ser	Ile	Lys	Asn	Thr	Leu	Pro	Lys	Leu	Val	Glu	Asp	Met	Lys
			65		70					75				80	
Leu	Ser	Gly	Asn	Pro	Pro	Arg	Ala	Ile	Val	Tyr	Asp	Ser	Thr	Met	Pro
			85					90						95	
Trp	Leu	Leu	Asp	Val	Ala	His	Ser	Tyr	Gly	Leu	Ser	Gly	Ala	Val	Phe
			100					105					110		
Phe	Thr	Gln	Pro	Trp	Leu	Val	Thr	Ala	Ile	Tyr	Tyr	His	Val	Phe	Lys
			115			120						125			
Gly	Ser	Phe	Ser	Val	Pro	Ser	Thr	Lys	Tyr	Gly	His	Ser	Thr	Leu	Ala
			130			135					140				
Ser	Phe	Pro	Ser	Phe	Pro	Met	Leu	Thr	Ala	Asn	Asp	Leu	Pro	Ser	Phe
			145			150				155				160	
Leu	Cys	Glu	Ser	Ser	Ser	Tyr	Pro	Asn	Ile	Leu	Arg	Ile	Val	Val	Asp
			165					170						175	
Gln	Leu	Ser	Asn	Ile	Asp	Arg	Val	Asp	Ile	Val	Cys	Ala	Thr	Leu	Ser
			180					185					190		
Ile	Asn	Trp	Arg	Lys	Ser	Val	Glu	Met	Gly	Gln	Ser	Leu	Trp	Pro	Val
			195			200						205			

(2) INFORMATION FOR SEQ ID NO:892:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..205
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:892:

Met	Ser	Gln	Phe	Cys	Lys	Arg	Leu	Ala	Ser	Lys	Gly	Leu	Lys	Leu	Thr
1				5				10					15		
Leu	Val	Leu	Val	Ser	Asp	Lys	Pro	Ser	Pro	Pro	Tyr	Lys	Thr	Glu	His
			20				25					30			
Asp	Ser	Ile	Thr	Val	Phe	Pro	Ile	Ser	Asn	Gly	Phe	Gln	Glu	Arg	Glu
			35			40				45					
Glu	Pro	Leu	Gln	Asp	Leu	Asp	Asp	Tyr	Met	Glu	Arg	Val	Glu	Thr	Ser

150	55	60
Ile Lys Asn Thr Leu Pro Lys Leu Val Glu Asp Met Lys Leu Ser Gly		
65	70	75
Asn Pro Pro Arg Ala Ile Val Tyr Asp Ser Thr Met Pro Trp Leu Leu		
	85	90
Asp Val Ala His Ser Tyr Gly Leu Ser Gly Ala Val Phe Phe Thr Gln		
	100	105
Pro Trp Leu Val Thr Ala Ile Tyr Tyr His Val Phe Lys Gly Ser Phe		
	115	120
Ser Val Pro Ser Thr Lys Tyr Gly His Ser Thr Leu Ala Ser Phe Pro		
	130	135
Ser Phe Pro Met Leu Thr Ala Asn Asp Leu Pro Ser Phe Leu Cys Glu		
145	150	155
Ser Ser Ser Tyr Pro Asn Ile Leu Arg Ile Val Val Asp Gln Leu Ser		
	165	170
Asn Ile Asp Arg Val Asp Ile Val Cys Ala Thr Leu Ser Ile Asn Trp		
	180	185
Arg Lys Ser Val Glu Met Gly Gln Ser Leu Trp Pro Val		
	195	200
		205

(2) INFORMATION FOR SEQ ID NO:893:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..148

(D) OTHER INFORMATION: / Ceres Seq. ID 1499150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:893:

Met Glu Arg Val Glu Thr Ser Ile Lys Asn Thr Leu Pro Lys Leu Val		
1	5	10
Glu Asp Met Lys Leu Ser Gly Asn Pro Pro Arg Ala Ile Val Tyr Asp		
	20	25
Ser Thr Met Pro Trp Leu Leu Asp Val Ala His Ser Tyr Gly Leu Ser		
	35	40
Gly Ala Val Phe Phe Thr Gln Pro Trp Leu Val Thr Ala Ile Tyr Tyr		
	50	55
His Val Phe Lys Gly Ser Phe Ser Val Pro Ser Thr Lys Tyr Gly His		
65	70	75
Ser Thr Leu Ala Ser Phe Pro Ser Phe Pro Met Leu Thr Ala Asn Asp		
	85	90
Leu Pro Ser Phe Leu Cys Glu Ser Ser Ser Tyr Pro Asn Ile Leu Arg		
	100	105
Ile Val Val Asp Gln Leu Ser Asn Ile Asp Arg Val Asp Ile Val Cys		
	115	120
Ala Thr Leu Ser Ile Asn Trp Arg Lys Ser Val Glu Met Gly Gln Ser		
	130	135
Leu Trp Pro Val		140
145		

(2) INFORMATION FOR SEQ ID NO:894:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1689 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1689

(D) OTHER INFORMATION: / Ceres Seq. ID 1499159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:894:

accgactctc	tctctctctc	tctccgtaac	aaaaaaaaatca	ccaatggcaa	aacaatatct	60
ctttgtactc	ctctcaatct	cctatctctt	atcactggag	ctcaccggcg	ccaccggagc	120
ctcacagacc	ggagcttcca	aaaaagccat	aaactctcat	caatcttctt	aaaaaacacc	180
cacataccct	gccttatgtg	tcactcact	ctccgtctac	gcaaacgaca	tccaaacaa	240
ccctaaagct	ttagctgaga	ccgctatagc	cgtgacacta	agccgagccc	aatccacgaa	300
gctctctgtc	tcgctcttaa	cacgtatgaa	gggtcttaag	aagcgcgagg	tcgaagccat	360
caagagattgc	gtcggaggaga	tgaacgatac	cgttgaccgt	tggacaaaat	ctgttcaaga	420
actgaagtgt	tgtggagtg	tcaaacagaa	gaagaggtcg	agttctgaag	agtcgggatt	480
ggagggaagag	tgaacacgaa	atgagatttt	acattgataa	acaaaacaaa	aaatacaata	540
cttttgcctc	aatcttgacg	gaaacttttt	tttttgctgc	ggaacatttc	ctttatttta	600
atataatggt	atgtgaaaat	gaattcatct	aaagacaaac	tgaaaaacat	gaacacagac	660
tctctttttt	tagcagatag	agagagacac	agagagaaaa	agagatggca	aacgaacacg	720
ctagttaaagt	agcgggttac	ttatctaacc	aagactcaag	acaccaaaa	agacatgttt	780
gcatctaaga	tatgcttatt	tgttgacaga	ttaataatac	tcagggtagt	ggcactgggt	840
gaacttggcc	gttgcctctc	gtgccagctc	caatggctcg	ggttggcgct	tcaaatcccg	900
ggtttggggac	aagcgtatca	tcgccaccag	ggagttgggt	gtgaggtccg	gcccttctgc	960
caccattata	tgatgggatt	ccccaccag	taagtggagc	tcgggtgaca	ggattgtaag	1020
ggtagaacgg	cttcttgcat	ttggaggaaa	gcaagaacct	tccaacaccg	ggaatgagaa	1080
tagtttggttt	ggctcattag	gttacaagaa	agtcagggtg	tttgacatca	gtggtcttag	1140
ggagacttggg	aacgtgacgt	agtcacacta	cttgctctac	agatcccaagc	actaggctta	1200
aaaccacgac	aatgactgcg	gaggtgataa	gtgaagaagc	cattaatattt	attttatttt	1260
gtttagaggg	agaaagctcg	tgtgtttgtt	tgaccaaaat	tgttcaagaa	ctgaagtgtt	1320
gtgggagtcg	caaagatcaa	gaccagtttg	cgtaccacat	tagtaatgct	cagacttgga	1380
ctagctggagc	tttgactgac	gagaacacct	gctccgagtg	gttctcgggt	cgggttatgg	1440
atggggaggt	caagaactcg	gttcgggcta	gaatcatgaa	cgtgggacat	gaacacagca	1500
acgctttgtc	cttgattaat	gcctttgcta	aaacttacta	atttaaaact	atattttgtc	1560
ctgtaaaaata	tatatataga	taaatgtaat	gtcttgctaa	gagtttgatg	tgatataatt	1620
ttttcgattt	tggtagtgtt	tttttgtttt	gtaacgtggt	ttataatagt	ataatgtgta	1680
ttttgagct						

(2) INFORMATION FOR SEQ ID NO:895:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..81

(D) OTHER INFORMATION: / Ceres Seq. ID 1499160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:895:

Thr	Asp	Ser	Leu	Ser	Leu	Ser	Leu	Arg	Asn	Lys	Lys	Ile	Thr	Asn	Gly
1			5					10						15	
Lys	Thr	Ile	Ser	Leu	Cys	Thr	Pro	Leu	Asn	Leu	Leu	Ser	Leu	Ile	Thr
			20					25				30			
Gly	Ala	His	Gly	Gly	His	Arg	Ser	Leu	Thr	Asp	Arg	Ser	Phe	Gln	Lys
			35					40				45			
Ser	His	Lys	Leu	His	Pro	Ile	Phe	Leu	Lys	Asn	His	His	Ile	Pro	Cys
			50					55				60			
Leu	Met	Cys	Pro	Leu	Thr	Leu	Arg	Leu	Arg	Lys	Arg	His	Pro	Asn	Lys
							70				75			80	
Pro															

(2) INFORMATION FOR SEQ ID NO:896:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1499161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:896:

Met Phe Ala Ser Lys Ile Cys Leu Phe Val Asp Arg Leu Ile Ile Leu
1 5 10 15
Arg Val Val Ala Leu Val Glu Leu Gly Arg Cys Phe Leu Cys Gln Leu
20 25 30
Gln Trp Ser Gly Leu Ala Leu Gln Ile Arg Gly Leu Gly Gln Ala Tyr
35 40 45
His Arg His Gln Gly Val Gly Cys Glu Val Arg Pro Leu Val His His
50 55 60
Tyr Met Met Gly Phe Pro His Gln
65 70

(2) INFORMATION FOR SEQ ID NO:897:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..109

(D) OTHER INFORMATION: / Ceres Seq. ID 1499162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:897:

Met Thr Ala Glu Val Ile Ser Glu Glu Ala Ile Asn Phe Ile Leu Phe
1 5 10 15
Cys Cys Arg Gly Glu Ser Ser Cys Val Cys Leu Thr Lys Ser Val Gln
20 25 30
Glu Leu Lys Leu Cys Gly Ser Ala Lys Asp Gln Asp Gln Phe Ala Tyr
35 40 45
His Ile Ser Asn Ala Gln Thr Trp Thr Ser Ala Ala Leu Thr Asp Glu
50 55 60
Asn Thr Cys Ser Asp Gly Phe Ser Gly Arg Val Met Asp Gly Arg Ile
65 70 75 80
Lys Asn Ser Val Arg Ala Arg Ile Met Asn Val Gly His Glu Thr Ser
85 90 95
Asn Ala Leu Ser Leu Ile Asn Ala Phe Ala Lys Thr Tyr
100 105

(2) INFORMATION FOR SEQ ID NO:898:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1367 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1367

(D) OTHER INFORMATION: / Ceres Seq. ID 1499163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:898:

gattttcact	ttcaaaattc	gttccgcttt	ttcttttttc	ggagaaagat	tcaatctttc	60
tgaatcatgt	actgaaatat	catcattcaa	acgaacagtg	ttctccattt	tgctgggaat	120
cagagtttct	gcttctctgt	aaaacccaaag	ctttctcttt	tataattttc	taatggcgct	180
aagagaagta	tcaacgatga	taagaaaaag	gtttatctct	gatcattctc	ttctttctc	240
tcctttaaga	accacgtctg	ttctcaaac	ctgtgtcccc	atagcctctc	ctccttctcc	300
gtacgattcc	actagcctct	ggcaagaagc	tgaatttggt	gggcatagat	gggtacagag	360
tgaccatgga	tggtgcacaag	aggcttttga	agagagaagt	gagttctctc	ttctaaaaat	420

gggtggagata	agtgaagtgcg	atgtgtacgt	agagactgtg	gtgtgtatgt	attgagatga	480
tcttaacaac	aagttagttg	gtgaaactgt	catcaaaatc	tgggttttcc	ttaaggtttc	540
ttcagctata	atgcttgacg	aggggaataa	gtattaccta	ctatggccgg	gtcagaagga	600
gctagcaatc	ccattccaa	gattccagct	atgtacagac	acaaaatag	caagatcact	660
gcaagaatc	tatctttttg	gtaaaaggaag	gatcttggtg	aatagggaga	ctcggttttc	720
ggatgaattg	tacagtgaact	actctacttt	gcaactgcaa	actaataatg	aaacagagag	780
aactcaacat	ggctcatttc	acttccgtgc	tccttccaaa	atcttctggc	gtaccgtctg	840
cggtatgatt	ccacacaaga	cgaagcgtgg	agctgctgca	ctagcacgtt	tgaaggtata	900
tgaaggtggt	cttactccat	atgacaagat	caagaggatg	gtcatccctg	atgctctcaa	960
gggtgttgagg	cttcaagctg	gtcacaataa	ctgtctgttg	ggccgtcttt	cttctgaagt	1020
gtgggtggagc	cattacagaca	ccatcaagga	gctggagaca	aagaggaagg	agagagccca	1080
cgtggtttac	gagcgaaaga	agcaacttaa	caaacttaga	gttaaggccg	agaaggtcgc	1140
tgaagagaag	ctcggagcac	agctcgatat	tcttgcgcca	gttaagtact	gagcttgcga	1200
gtagtattgt	tttttttttt	ggtaaggagc	ttgtcagtag	tagtttctct	ttgcagtgtt	1260
tgagcccaacc	caataccctt	ttacttttta	tcctttactt	aggtcttcta	tcgaaatttg	1320
tactcctaac	attttattct	tgagttttat	ttattatatt	gcgtgggc		

(2) INFORMATION FOR SEQ ID NO:899:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..100

(D) OTHER INFORMATION: / Ceres Seq. ID 1499164

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:899:

Met	Ala	Ser	Arg	Glu	Val	Ser	Thr	Met	Ile	Arg	Lys	Gly	Phe	Ile	Ser
1		5						10					15		
Asp	His	Ser	Leu	Ser	Phe	Ser	Pro	Leu	Arg	Thr	Thr	Ser	Val	Ser	Lys
		20						25				30			
Pro	Leu	Ser	Pro	Ile	Ala	Ser	Pro	Pro	Ser	Pro	Tyr	Asp	Ser	Thr	Ser
		35					40					45			
Leu	Trp	Gln	Glu	Ala	Glu	Phe	Gly	Gly	His	Arg	Trp	Val	Gln	Ser	Asp
	50					55					60				
His	Gly	Cys	Ala	Gln	Glu	Ala	Phe	Glu	Glu	Arg	Met	Glu	Ser	Leu	Ile
	65					70				75				80	
Leu	Lys	Met	Val	Glu	Ile	Ser	Glu	Cys	Asp	Val	Tyr	Val	Glu	Thr	Val
					85					90				95	
Val	Leu	Met	Tyr												
			100												

(2) INFORMATION FOR SEQ ID NO:900:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..92

(D) OTHER INFORMATION: / Ceres Seq. ID 1499165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:900:

Met	Ile	Arg	Lys	Gly	Phe	Ile	Ser	Asp	His	Ser	Leu	Ser	Phe	Ser	Pro
1			5						10				15		
Leu	Arg	Thr	Thr	Ser	Val	Ser	Lys	Pro	Leu	Ser	Pro	Ile	Ala	Ser	Pro
			20					25				30			
Pro	Ser	Pro	Tyr	Asp	Ser	Thr	Ser	Leu	Trp	Gln	Glu	Ala	Glu	Phe	Gly
			35				40					45			
Gly	His	Arg	Trp	Val	Gln	Ser	Asp	His	Gly	Cys	Ala	Gln	Glu	Ala	Phe

50 55 60
Glu Glu Arg Met Glu Ser Leu Ile Leu Lys Met Val Glu Ile Ser Glu
65 70 75 80
Cys Asp Val Tyr Val Glu Thr Val Val Leu Met Tyr
85 90

(2) INFORMATION FOR SEQ ID NO:901:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..115

- (D) OTHER INFORMATION: / Ceres Seq. ID 1499166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:901:

Met Ile Pro His Lys Thr Lys Arg Gly Ala Ala Leu Ala Arg Leu
1 5 10 15
Lys Val Tyr Glu Gly Val Pro Thr Pro Tyr Asp Lys Ile Lys Arg Met
20 25 30
Val Ile Pro Asp Ala Leu Lys Val Leu Arg Leu Gln Ala Gly His Lys
35 40 45
Tyr Cys Leu Leu Gly Arg Leu Ser Ser Glu Val Gly Trp Asn His Tyr
50 55 60
Asp Thr Ile Lys Glu Leu Glu Thr Lys Arg Lys Glu Arg Ala His Val
65 70 75 80
Val Tyr Glu Arg Lys Lys Gln Leu Asn Lys Leu Arg Val Lys Ala Glu
85 90 95
Lys Val Ala Glu Glu Lys Leu Gly Ala Gln Leu Asp Ile Leu Ala Pro
100 105 110
Val Lys Tyr
115

(2) INFORMATION FOR SEQ ID NO:902:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1368 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..1368

- (D) OTHER INFORMATION: / Ceres Seq. ID 1499185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:902:

aactgataaaa gtgataacgg agttggttgg aacgtgaac gcttataaaa ataaaccggt 60
ttaatttcac cggtttacct tcgccggtag atcatcagccg caatgtacat tctcgacacc 120
gagctcgat tcttcgccgt cagatttcca cgggtattca atctctctcc aacatctctc 180
cgtagacgat acttcacgt aagagctaatt ctctcattcc caaagcatca agctaagtat 240
cataaagagc ttgagggtcgc cattgatgct gttgatcgag cttgtcgtct ctgtgttgat 300
gtcaaaagat ctcttttttc ttctaaagag aagattgttg agaagaatga tcaaatccca 360
gttacaattg cagattttgg agtccaagct ttatgcagct tggagccttc gaaattgttt 420
ccttcaatac caattagttgc tgaggaagac tctcattttg tgcgtgctaa taaccttgta 480
agctctgtgg taagtgaagt caaatcaaaa gcaagcattg gagacaatca ctgtctgat 540
gctgatgtac ttgaagcaat tgatagaggt ggcaaaagatg cttacacggt ttgcaacaaa 600
ccagctactt attgggtttt ggaatccaatt gatggcacca ggggatttct taaaaggagat 660
gaggccttat atgtggttag attgcccctt gttgtagata atgaaattgt gctaggagtc 720
atgggttgtc caaactggcc aggagattct tcagatggat ctactggnaa cctaagtgc 780
tcgcataatg gctgtggaac gtggaccaag aagttacaaa atgtctctgg caatgtagcc 840
ggtagttgga taagggtgtt cgttgatgct tgtgttttaa tgacaagaag aagattttgt 900
atacaagaaa gccaaacctg ggaatcactt cctctctctg gtttcttcga cgcaagtact 960

(2) INFORMATION FOR SEO ID NO:903:

(A) LENGTH: 397 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..39

(D) OTHER INFORMATION: / Ceres Seq. ID 1499186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:903:

Met	Tyr	Ile	Leu	Asp	Thr	Gly	Ala	Arg	Phe	Ser	Ala	Val	Arg	Phe	Ser	
1				5												
Pro	Val	Phe	Asn	Pro	Pro	Pro	Thr	Ser	Leu	Arg	Arg	Arg	Tyr	Phe	Ile	
			20					25					30			
Val	Arg	Ala	Asn	Leu	Pro	Phe	Pro	Lys	His	Gln	Ala	Lys	Tyr	His	Lys	
		35					40					45				
Glu	Leu	Glu	Val	Ala	Ile	Asp	Ala	Val	Asp	Arg	Ala	Cys	Arg	Leu	Cys	
	50					55					60					
Val	Asp	Val	Lys	Arg	Ser	Leu	Phe	Ser	Ser	Lys	Glu	Lys	Ile	Val	Glu	
65				70					75						80	
Lys	Asn	Asp	Gln	Thr	Pro	Val	Thr	Ile	Ala	Asp	Phe	Gly	Val	Gln	Ala	
			85					90						95		
Leu	Val	Ser	Leu	Glu	Leu	Ser	Lys	Leu	Phe	Pro	Ser	Ile	Pro	Leu	Val	
		100						105					110			
Ala	Glu	Glu	Asp	Ser	His	Phe	Val	Arg	Ala	Asn	Asn	Leu	Val	Ser	Ser	
		115					120					125				
Val	Val	Ser	Glu	Val	Lys	Ser	Lys	Ala	Ser	Ile	Gly	Asp	Asn	His	Leu	
	130					135					140					
Ser	Asp	Ala	Asp	Val	Leu	Glu	Ala	Ile	Asp	Arg	Gly	Gly	Lys	Asp	Ala	
145				150					155					160		
Tyr	Thr	Phe	Cys	Asn	Lys	Pro	Ala	Thr	Tyr	Trp	Val	Leu	Asp	Pro	Ile	
			165					170						175		
Asp	Gly	Thr	Arg	Gly	Phe	Leu	Lys	Gly	Asp	Glu	Ala	Leu	Tyr	Val	Val	
		180						185						190		
Gly	Leu	Ala	Leu	Val	Val	Asp	Asn	Glu	Ile	Val	Leu	Gly	Val	Met	Gly	
		195					200					205				
Cys	Pro	Asn	Trp	Pro	Gly	Asp	Ser	Ser	Asp	Gly	Ser	Thr	Gly	Thr	Leu	
	210					215					220					
Met	Leu	Ser	His	Ile	Gly	Cys	Gly	Thr	Trp	Thr	Lys	Lys	Leu	Gln	Asn	
225				230						235				240		
Val	Ser	Gly	Asn	Val	Ala	Gly	Asp	Trp	Ile	Arg	Cys	Phe	Val	Asp	Ala	
			245						250					255		
Cys	Val	Leu	Met	Asn	Lys	Ala	Arg	Phe	Cys	Ile	Gln	Glu	Ser	Gln	Thr	
		260						265						270		
Trp	Glu	Ser	Leu	Pro	Leu	Ser	Gly	Phe	Phe	Asp	Ala	Ser	Thr	Val	Ser	
	275						280					285				
Glu	Asp	Leu	Lys	His	Lys	Glu	Ile	Leu	Leu	Leu	Pro	Thr	Cys	Cys	Gly	
	290					295					300					
Ser	Leu	Cys	Lys	Tyr	Leu	Met	Val	Ala	Ser	Gly	Arg	Ala	Ser	Val	Phe	
305				310						315				320		
Leu	Leu	Arg	Ala	Lys	Thr	Gln	Arg	Thr	Ile	Lys	Ser	Trp	Asp	His	Ala	
			325						330					335		

(2) INFORMATION FOR SEQ ID NO:904:

(A) LENGTH: 1063 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- ```
(A) NAME/KEY: -
(B) LOCATION: 1..1063
(D) OTHER INFORMATION: / Ceres Seq. ID 1499190
```

|            |             |            |             |             |             |      |
|------------|-------------|------------|-------------|-------------|-------------|------|
| ctcttcttct | ttcttcacgcc | gagatttctg | cgaactgtct  | agctcttacga | ccttaataaga | 60   |
| aacgacgcta | ttttcattct  | gcttgagctc | ttcatcgtgt  | ccacacagac  | gactctggac  | 120  |
| gtcgttttaa | gcgcaaaaac  | agaaaaaaag | actgacgttt  | atacatacta  | aataccgggt  | 180  |
| tggagtttgt | ctcttttgac  | tcagaaaagt | caaaagagag  | agagagagag  | agacatttct  | 240  |
| gtactcttct | gggttttttg  | tgtcgaaana | gaagctcaca  | gacaaaaaaa  | aaagcaatta  | 300  |
| tttttaggtt | tcaaaagaag  | caaaattttg | aactttcaga  | tgctgtgggt  | ggtgtgcttc  | 360  |
| tgaacaaata | agctttttct  | tgaactcttc | ttccaatttg  | gactcttacc  | tatctctctc  | 420  |
| ctcagctatg | gaattctctg  | gcagacgtct | aatgatgatg  | gagacaaacg  | ggaagtcttg  | 480  |
| ttctctgtga | gaagacgaca  | tcacaaccca | caagctctga  | ctcttttcca  | attccaaga   | 540  |
| gaggaagac  | aaggtttgag  | acagtttatt | agctcttcaa  | taacatagtt  | ccctctatgg  | 600  |
| aaagaccgac | actgcatacg  | ttcttttaga | cgcgatgcct  | caatagagtt  | ttcttcacga  | 660  |
| acaagtgaag | gtgcctaagt  | ctccgttatc | gcacaacgata | cctgatgcta  | cgcaggagga  | 720  |
| ctgtgagacg | tcacgcctga  | gaacaacgat | attatgtctt  | gttccaattg  | agaatacagt  | 780  |
| tggagtttgt | taagaacgca  | gcgcgtgagt | atggggcccc  | gttgaagact  | ctctataacc  | 840  |
| agctttcaag | gtcacatctc  | aaatacaact | tagatgacca  | attcgactaa  | tcaacctata  | 900  |
| cgaattttgt | gttaagcctt  | aaaaagaatt | accaatgttt  | attttctgta  | tgtagccttc  | 960  |
| gtaacatata | tagacagaga  | gcacatgatg | tgtggtttag  | actgctcatc  | gttggaagt   | 1020 |
| attgttata  | ttatttgact  | gcttaatgca | tccccttaet  | ttg         |             |      |

(2) INFORMATION FOR SEQ ID NO:905:

(A) LENGTH: 149 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..149  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499191

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Phe | Ser | Gly | Asp | Ala | Gly | Met | Met | Met | Glu | Asn | Lys | Arg | Asn |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Val | Cys | Ser | Leu | Gly | Glu | Ser | Ser | Ile | Lys | Arg | His | Lys | Ser | Asp | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Phe | Asn | Ser | Lys | Glu | Arg | Lys | Asp | Lys | Val | Gly | Glu | Arg | Ile | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Leu | Gln | Gln | Ile | Val | Ser | Pro | Tyr | Gly | Lys | Thr | Asp | Thr | Ala | Ser |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Leu | Leu | Asp | Ala | Met | His | Tyr | Ile | Glu | Phe | Leu | His | Glu | Gln | Val |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Lys | Val | Leu | Ser | Ala | Pro | Tyr | Leu | Gln | Thr | Ile | Pro | Asp | Ala | Thr | Gln |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     |     |     | 85  |     |     |     | 90  |     |     |     | 95  |     |     |     |     |
| Glu | Glu | Leu | Glu | Gln | Tyr | Ser | Leu | Arg | Asn | Arg | Gly | Leu | Cys | Leu | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Met | Glu | Asn | Thr | Val | Gly | Val | Ala | Gln | Ser | Asn | Gly | Ala | Asp | Ile |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Trp | Ala | Pro | Val | Lys | Thr | Pro | Leu | Ser | Pro | Ala | Phe | Ser | Val | Thr | Ser |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Gln | Ser | Pro | Phe | Arg |     |     |     |     |     |     |     |     |     |     |     |
| 145 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:906:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..141

(D) OTHER INFORMATION: / Ceres Seq. ID 1499192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:906:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Met | Glu | Asn | Lys | Arg | Asn | Val | Cys | Ser | Leu | Gly | Glu | Ser | Ser |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ile | Lys | Arg | His | Lys | Ser | Asp | Leu | Ser | Phe | Asn | Ser | Lys | Glu | Arg | Lys |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Asp | Lys | Val | Gly | Glu | Arg | Ile | Ser | Ala | Leu | Gln | Gln | Ile | Val | Ser | Pro |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Tyr | Gly | Lys | Thr | Asp | Thr | Ala | Ser | Val | Leu | Leu | Asp | Ala | Met | His | Tyr |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Ile | Glu | Phe | Leu | His | Glu | Gln | Val | Lys | Val | Leu | Ser | Ala | Pro | Tyr | Leu |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     | 80  |     |
| Gln | Thr | Ile | Pro | Asp | Ala | Thr | Gln | Glu | Glu | Leu | Glu | Gln | Tyr | Ser | Leu |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Arg | Asn | Arg | Gly | Leu | Cys | Leu | Val | Pro | Met | Glu | Asn | Thr | Val | Gly | Val |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Ala | Gln | Ser | Asn | Gly | Ala | Asp | Ile | Trp | Ala | Pro | Val | Lys | Thr | Pro | Leu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Pro | Ala | Phe | Ser | Val | Thr | Ser | Gln | Ser | Pro | Phe | Arg |     |     |     |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:907:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1499193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:907:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Glu | Asn | Lys | Arg | Asn | Val | Cys | Ser | Leu | Gly | Glu | Ser | Ser | Ile |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Lys | Arg | His | Lys | Ser | Asp | Leu | Ser | Phe | Asn | Ser | Lys | Glu | Arg | Lys | Asp |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Lys | Val | Gly | Glu | Arg | Ile | Ser | Ala | Leu | Gln | Gln | Ile | Val | Ser | Pro | Tyr |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Lys | Thr | Asp | Thr | Ala | Ser | Val | Leu | Leu | Asp | Ala | Met | His | Tyr | Ile |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Glu | Phe | Leu | His | Glu | Gln | Val | Lys | Val | Leu | Ser | Ala | Pro | Tyr | Leu | Gln |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     | 80  |     |

Thr Ile Pro Asp Ala Thr Gln Glu Glu Leu Glu Gln Tyr Ser Leu Arg  
85 90 95  
Asn Arg Gly Leu Cys Leu Val Pro Met Glu Asn Thr Val Gly Val Ala  
100 105 110  
Gln Ser Asn Gly Ala Asp Ile Trp Ala Pro Val Lys Thr Pro Leu Ser  
115 120 125  
Pro Ala Phe Ser Val Thr Ser Gln Ser Pro Phe Arg  
130 135 140

(2) INFORMATION FOR SEQ ID NO:908:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1819 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1819
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499194

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:908:

|             |             |            |             |             |             |      |
|-------------|-------------|------------|-------------|-------------|-------------|------|
| gtcttttggg  | gggtcttcgt  | caaagctctc | tcctttacgg  | tccttttctc  | cagcgcgatga | 60   |
| aataataaag  | gacacctgta  | tttattaaaa | tcactacatt  | ttccgtaaca  | aaaaaaatca  | 120  |
| aaactttggt  | tctcaatgaa  | cgggtcgggg | gaatcacgac  | tcggtgggtg  | tggtgggtgt  | 180  |
| gatgggttct  | ttggagttca  | gatccgacaa | acacgggatcg | taccggattt  | tctccagagc  | 240  |
| gtgaattcta  | agatgtgtaa  | attaggttac | aattacttta  | tctcaaatct  | cttgactctc  | 300  |
| tgttttatcc  | ctctgcgcgt  | tggtatctcc | gtcgaagcct  | ctcagatgaa  | cccagatgat  | 360  |
| ctcaaacagc  | tctggatcca  | ctcacaatac | aatctgggta  | gtatcatcat  | ctgttccagc  | 420  |
| attctagctc  | tcgggttaac  | gggtttatgt | acgacccgac  | ctagaccogt  | ttacttggtt  | 480  |
| gatttctctt  | gttatctccc  | acctgatcat | ctcaaaagctc | cttacgcctcg | gttcatggaa  | 540  |
| cattctagac  | tcaccggaga  | tttcgatgac | tctgctctcg  | agtttcaacg  | caagatccctt | 600  |
| gagcggttct  | gtttagggga  | agacacttgt | ccttgaagct  | atgcattatg  | ttccaccgag  | 660  |
| aattttcaatg | gcgtctgcta  | gagaagaagc | tgaacaagtc  | atgttttggtc | ctttagataa  | 720  |
| ccttttctcg  | aacactaatg  | tgaaaccaaa | ggatattgga  | atccttgttg  | tgaattgtag  | 780  |
| tctctttaat  | ccaactccct  | cggtatctgc | aatgattgtg  | aacaagtata  | agcttagagg  | 840  |
| taacattaga  | agctacaact  | taggcggtat | gggttgcaag  | gcgggagtta  | tcgtgttgga  | 900  |
| tcttgctaaa  | gacatgttgt  | tggtacatag | gaacacttat  | cggttgtgtg  | tttctaactga | 960  |
| gaacattact  | cagaatttgt  | attttggtaa | caagaatacg  | atgttgatag  | cgaactgctt  | 1020 |
| gtttccaggt  | ggtggctctg  | cggttttgct | atcgaacaag  | tcgaggggaca | agagacggtc  | 1080 |
| taagtacagg  | cttgtacatg  | tagtcaggac | tcaccgtgga  | gcagatgata  | aagctttccg  | 1140 |
| tttgttttgt  | caagagcagg  | atgatacagg | gagaacccgg  | gtttcgttgt  | cgaaagatct  | 1200 |
| aatggcgatt  | gcaggggaaa  | ctctcaaaac | caatatcact  | acattggggtc | ctcttgttct  | 1260 |
| accgataagt  | gagcagattc  | tctcttttat | gactctagtt  | gtgaagaagc  | tcttttaacg  | 1320 |
| taaagtgaaa  | ccgtatatcc  | cggatttcaa | acttgctttc  | gagcatcttc  | gtatccatgc  | 1380 |
| tggtggaaga  | gcgtgtgatc  | atgagttaga | gaagaatctg  | cagctttcac  | cagttcatgt  | 1440 |
| cgaggctctg  | aggatgactc  | ttcatcgatt | tggttaacaca | tcttcgagat  | ccatttggta  | 1500 |
| tgaattggct  | tacattgaag  | cgaagggaag | gatgcgaaga  | ggttaatcgt  | tttgccaagt  | 1560 |
| cgcggttgca  | agtggaattta | aatgtaaatg | cgcgattttg  | gaagcattaa  | ggcatgtgaa  | 1620 |
| accttcgaac  | aacagtcctt  | gtgaagattg | tattgacaag  | tatccggtaa  | ctttaagtta  | 1680 |
| ttagcttcgt  | ttgaggaact  | gttattgtgt | aacttcgaga  | ctaactocat  | gttggttttt  | 1740 |
| ttcttagaga  | agaaacccct  | agatttgatc | tctgacaatg  | tcaattgtgt  | tttgttttat  | 1800 |
| gtgttttggg  | gagtttgtg   |            |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:909:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..347

(D) OTHER INFORMATION: / Ceres Seq. ID 1499195

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:909:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | His | Tyr | Val | Pro | Pro | Arg | Ile | Ser | Met | Ala | Ala | Ala | Arg | Glu | Glu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ala | Glu | Gln | Val | Met | Phe | Gly | Ala | Leu | Asp | Asn | Leu | Phe | Ala | Asn | Thr |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Asn | Val | Lys | Pro | Lys | Asp | Ile | Gly | Ile | Leu | Val | Val | Asn | Cys | Ser | Leu |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Phe | Asn | Pro | Thr | Pro | Ser | Leu | Ser | Ala | Met | Ile | Val | Asn | Lys | Tyr | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Leu | Arg | Gly | Asn | Ile | Arg | Ser | Tyr | Asn | Leu | Gly | Gly | Met | Gly | Cys | Ser |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Gly | Val | Ile | Ala | Val | Asp | Leu | Ala | Lys | Asp | Met | Leu | Leu | Val | His |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Arg | Asn | Thr | Tyr | Ala | Val | Val | Val | Ser | Thr | Glu | Asn | Ile | Thr | Gln | Asn |
|     | 100 |     |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Trp | Tyr | Phe | Gly | Asn | Lys | Lys | Ser | Met | Leu | Ile | Pro | Asn | Cys | Leu | Phe |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Arg | Val | Gly | Gly | Ser | Ala | Val | Leu | Leu | Ser | Asn | Lys | Ser | Arg | Asp | Lys |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Arg | Arg | Ser | Lys | Tyr | Arg | Leu | Val | His | Val | Val | Arg | Thr | His | Arg | Gly |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Ala | Asp | Asp | Lys | Ala | Phe | Arg | Cys | Val | Tyr | Gln | Glu | Gln | Asp | Asp | Thr |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gly | Arg | Thr | Gly | Val | Ser | Leu | Ser | Lys | Asp | Leu | Met | Ala | Ile | Ala | Gly |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     |     | 190 |     |
| Glu | Thr | Leu | Lys | Thr | Asn | Ile | Thr | Thr | Leu | Gly | Pro | Leu | Val | Leu | Pro |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Ile | Ser | Glu | Gln | Ile | Leu | Phe | Phe | Met | Thr | Leu | Val | Val | Lys | Lys | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |
| Phe | Asn | Gly | Lys | Val | Lys | Pro | Tyr | Ile | Pro | Asp | Phe | Lys | Leu | Ala | Phe |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |     |
| Glu | His | Phe | Cys | Ile | His | Ala | Gly | Gly | Arg | Ala | Val | Ile | Asp | Glu | Leu |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Glu | Lys | Asn | Leu | Gln | Leu | Ser | Pro | Val | His | Val | Glu | Ala | Ser | Arg | Met |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     |     | 270 |     |
| Thr | Leu | His | Arg | Phe | Gly | Asn | Thr | Ser | Ser | Ser | Ser | Ile | Trp | Tyr | Glu |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     |     |     | 285 |     |
| Leu | Ala | Tyr | Ile | Glu | Ala | Lys | Gly | Arg | Met | Arg | Arg | Gly | Asn | Arg | Val |
|     | 290 |     |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |
| Trp | Gln | Ile | Ala | Phe | Gly | Ser | Gly | Phe | Lys | Cys | Asn | Ser | Ala | Ile | Trp |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     | 320 |     |
| Glu | Ala | Leu | Arg | His | Val | Lys | Pro | Ser | Asn | Asn | Ser | Pro | Cys | Glu | Asp |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Cys | Ile | Asp | Lys | Tyr | Pro | Val | Thr | Leu | Ser | Tyr |     |     |     |     |     |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:910:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 338 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..338

(D) OTHER INFORMATION: / Ceres Seq. ID 1499196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:910:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Ala | Arg | Glu | Glu | Ala | Glu | Gln | Val | Met | Phe | Gly | Ala | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Asp | Asn | Leu | Phe | Ala | Asn | Thr | Asn | Val | Lys | Pro | Lys | Asp | Ile | Gly | Ile |

|                         |                             |                     |
|-------------------------|-----------------------------|---------------------|
| 20                      | 25                          | 30                  |
| Leu Val Val Asn Cys Ser | Leu Phe Asn Pro Thr Pro Ser | Leu Ser Ala         |
| 35                      | 40                          | 45                  |
| Met Ile Val Asn Lys Tyr | Lys Leu Arg Gly Asn Ile Arg | Ser Tyr Asn         |
| 50                      | 55                          | 60                  |
| Leu Gly Gly Met Gly Cys | Ser Ala Gly Val Ile Ala Val | Asp Leu Ala         |
| 65                      | 70                          | 75                  |
| Lys Asp Met Leu Leu Val | His Arg Asn Thr Tyr Ala Val | Val Val Ser         |
| 85                      | 90                          | 95                  |
| Thr Glu Asn Ile Thr Gln | Asn Trp Tyr Phe Gly Asn Lys | Lys Ser Met         |
| 100                     | 105                         | 110                 |
| Leu Ile Pro Asn Cys Leu | Phe Arg Val Gly Gly Ser     | Ala Val Leu Leu     |
| 115                     | 120                         | 125                 |
| Ser Asn Lys Ser Arg Asp | Lys Arg Arg Ser Lys Tyr     | Arg Leu Val His     |
| 130                     | 135                         | 140                 |
| Val Val Arg Thr His Arg | Gly Ala Asp Asp Lys Ala     | Phe Arg Cys Val     |
| 145                     | 150                         | 155                 |
| Tyr Gln Glu Gln Asp     | Asp Thr Gly Arg Thr Gly     | Val Ser Leu Ser Lys |
| 165                     | 170                         | 175                 |
| Asp Leu Met Ala Ile Ala | Gly Glu Thr Leu Lys Thr     | Asn Ile Thr Thr     |
| 180                     | 185                         | 190                 |
| Leu Gly Pro Leu Val Leu | Pro Ile Ser Glu Gln Ile     | Leu Phe Phe Met     |
| 195                     | 200                         | 205                 |
| Thr Leu Val Val Lys Lys | Leu Phe Asn Gly Lys Val     | Lys Pro Tyr Ile     |
| 210                     | 215                         | 220                 |
| Pro Asp Phe Lys Leu Ala | Phe Glu His Phe Cys Ile     | His Ala Gly Gly     |
| 225                     | 230                         | 235                 |
| Arg Ala Val Ile Asp     | Glu Leu Glu Lys Asn Leu     | Gln Leu Ser Pro Val |
| 245                     | 250                         | 255                 |
| His Val Glu Ala Ser Arg | Met Thr Leu His Arg Phe     | Gly Asn Thr Ser     |
| 260                     | 265                         | 270                 |
| Ser Ser Ser Ile Trp Tyr | Glu Leu Ala Tyr Ile Glu     | Ala Lys Gly Arg     |
| 275                     | 280                         | 285                 |
| Met Arg Arg Gly Asn Arg | Val Trp Gln Ile Ala Phe     | Gly Ser Gly Phe     |
| 290                     | 295                         | 300                 |
| Lys Cys Asn Ser Ala Ile | Trp Glu Ala Leu Arg His     | Val Lys Pro Ser     |
| 305                     | 310                         | 315                 |
| Asn Asn Ser Pro Cys Glu | Asp Cys Ile Asp Lys Tyr     | Pro Val Thr Leu     |
| 325                     | 330                         | 335                 |

Ser Tyr

(2) INFORMATION FOR SEQ ID NO:911:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 327 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..327

(D) OTHER INFORMATION: / Ceres Seq. ID 1499197

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:911:

|                         |                         |                 |
|-------------------------|-------------------------|-----------------|
| Met Phe Gly Ala Leu Asp | Asn Leu Phe Ala Asn Thr | Asn Val Lys Pro |
| 1                       | 5                       | 10              |
| Lys Asp Ile Gly Ile Leu | Val Val Asn Cys Ser Leu | Phe Asn Pro Thr |
| 20                      | 25                      | 30              |
| Pro Ser Leu Ser Ala Met | Ile Val Asn Lys Tyr Lys | Leu Arg Gly Asn |
| 35                      | 40                      | 45              |
| Ile Arg Ser Tyr Asn Leu | Gly Gly Met Gly Cys Ser | Ala Gly Val Ile |
| 50                      | 55                      | 60              |



Ala Val Asp Leu Ala Lys Asp Met Leu Leu Val His Arg Asn Thr Tyr  
65 70 75 80  
Ala Val Val Val Ser Thr Glu Asn Ile Thr Gln Asn Trp Tyr Phe Gly  
85 90 95  
Asn Lys Lys Ser Met Leu Ile Pro Asn Cys Leu Phe Arg Val Gly Gly  
100 105 110  
Ser Ala Val Leu Leu Ser Asn Lys Ser Arg Asp Lys Arg Arg Ser Lys  
115 120 125  
Tyr Arg Leu Val His Val Val Arg Thr His Arg Gly Ala Asp Asp Lys  
130 135 140  
Ala Phe Arg Cys Val Tyr Gln Glu Gln Asp Asp Thr Gly Arg Thr Gly  
145 150 155 160  
Val Ser Leu Ser Lys Asp Leu Met Ala Ile Ala Gly Glu Thr Leu Lys  
165 170 175  
Thr Asn Ile Thr Thr Leu Gly Pro Leu Val Leu Pro Ile Ser Glu Gln  
180 185 190  
Ile Leu Phe Phe Met Thr Leu Val Val Lys Lys Leu Phe Asn Gly Lys  
195 200 205  
Val Lys Pro Tyr Ile Pro Asp Phe Lys Leu Ala Phe Glu His Phe Cys  
210 215 220  
Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu Leu Glu Lys Asn Leu  
225 230 235 240  
Gln Leu Ser Pro Val His Val Glu Ala Ser Arg Met Thr Leu His Arg  
245 250 255  
Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr Glu Leu Ala Tyr Ile  
260 265 270  
Glu Ala Lys Gly Arg Met Arg Arg Gly Asn Arg Val Trp Gln Ile Ala  
275 280 285  
Phe Gly Ser Gly Phe Lys Cys Asn Ser Ala Ile Trp Glu Ala Leu Arg  
290 295 300  
His Val Lys Pro Ser Asn Asn Ser Pro Cys Glu Asp Cys Ile Asp Lys  
305 310 315 320  
Tyr Pro Val Thr Leu Ser Tyr  
325

(2) INFORMATION FOR SEQ ID NO:912:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 976 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..976
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:912:

|             |            |             |             |             |             |     |
|-------------|------------|-------------|-------------|-------------|-------------|-----|
| acgtctgacg  | gaagtcggtt | cacttcaccc  | tgtgccgtgg  | ggatgttctg  | tcgtcacagt  | 60  |
| cggtcaagag  | atgtatgtaa | ttgggtgact  | cctagacata  | agacgtttac  | aggtaaatgac | 120 |
| ttctcatgat  | tgcgaactc  | acaaatttcg  | ctcgcttcgc  | agatgaaaaa  | gaggtcgttg  | 180 |
| caaaagcagcc | gccggaggtg | tcgacggaaa  | gattttacgta | atcggaggtt  | tcaggaggtt  | 240 |
| aaaacccgat  | gctgaatgga | ttgaagtgtt  | tgatctaaag  | acacagattt  | gggaatcttt  | 300 |
| gcctggtccg  | taccctaaaa | ctagtctcgt  | ttgcgagttg  | gacgcctatg  | tggtgatgga  | 360 |
| agagaagtta  | tacatgttgg | gttctaattt  | ttgttttggt  | tacgaaccaa  | aaagaaacgg  | 420 |
| tgaatgggac  | gcattccgtc | gagcaacccc  | attaaaagat  | ttgtggggaca | agacttgttg  | 480 |
| tgtggttagat | gatatttgtt | atcacgactga | tcctcggcgt  | actcttgagc  | atccaatagt  | 540 |
| cgtgtatcat  | ccaaaggaca | agacttggag  | acctgtgaaa  | ggatgaatcct | tggggagttt  | 600 |
| gcctagtatt  | ttcttttcta | agtctgaaaa  | tggcgaaatt  | tggttgaaa   | ttggtgattt  | 660 |
| tgggcagaaa  | caagagctat | gttactgtgt  | attgcattgg  | agaaaaagtt  | atttgttcgc  | 720 |
| taatgatcga  | gttggaaaaa | cgtgaaggag  | gtgagatttg  | ggggaaaggtt | gaatcactcg  | 780 |
| actgtgtgtt  | tggatacata | gacattgtgt  | cggttgggct  | ttgtcgatct  | ctgacattct  | 840 |
| gatgatacat  | gggtaggtat | cttgacagta  | cggttgatgt  | aatgagtatg  | acttttttgt  | 900 |

tgttcatgcc ttttcttttag cctcaagact tacttgcttt ttctcatgac ttattactc 960  
accttaacct ttgtgc

(2) INFORMATION FOR SEQ ID NO:913:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..229
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499199

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:913:

Arg Leu Thr Glu Val Gly Ser Leu Pro Pro Val Pro Trp Gly Cys Ser  
1 5 10 15  
Val Val Thr Val Gly Gln Glu Met Tyr Val Ile Gly Gly Leu Leu Asp  
20 25 30  
Ile Arg Arg Leu Gln Val Met Thr Leu Ile Asp Cys Arg Thr His Lys  
35 40 45  
Phe Arg Ser Leu Pro Ser Met Lys Arg Gly Arg Cys Lys Ala Ala Ala  
50 55 60  
Gly Val Val Asp Gly Lys Ile Tyr Val Ile Gly Phe Arg Met Arg  
65 70 75 80  
Lys Pro Asp Ala Glu Trp Ile Glu Val Phe Asp Leu Lys Thr Gln Ile  
85 90 95  
Trp Glu Ser Leu Pro Gly Pro Tyr Pro Lys Thr Ser Ser Cys Cys Glu  
100 105 110  
Leu Asp Ala Tyr Val Val Met Glu Glu Lys Leu Tyr Met Leu Gly Ser  
115 120 125  
Lys Phe Cys Leu Val Tyr Glu Pro Lys Arg Asn Gly Glu Trp Asp Ala  
130 135 140  
Ser Val Gly Ala Thr Pro Leu Lys Asp Leu Trp Asp Lys Thr Cys Cys  
145 150 155 160  
Val Val Asp Asp Met Leu Tyr Thr Thr Asp Pro Arg Arg Thr Leu Gly  
165 170 175  
His Pro Ile Val Val Tyr His Pro Lys Asp Lys Thr Trp Arg Pro Val  
180 185 190  
Lys Gly Glu Ser Leu Gly Ser Leu Pro Ser Tyr Phe Phe Ser Lys Ser  
195 200 205  
Glu Asn Gly Glu Phe Trp Trp Lys Val Gly Asp Phe Gly Gln Lys Gln  
210 215 220  
Glu Leu Cys Tyr Trp  
225

(2) INFORMATION FOR SEQ ID NO:914:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..206
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:914:

Met Tyr Val Ile Gly Gly Leu Leu Asp Ile Arg Arg Leu Gln Val Met  
1 5 10 15  
Thr Leu Ile Asp Cys Arg Thr His Lys Phe Arg Ser Leu Pro Ser Met  
20 25 30  
Lys Arg Gly Arg Cys Lys Ala Ala Ala Gly Val Val Asp Gly Lys Ile

(2) INFORMATION FOR SEO ID NO:915:

{A} LENGTH: 191 amino acids

(C) STRANDEDNESS:

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..191

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:915:

Thr Leu Ile Asp Cys Arg Thr His Lys Phe A

(2) INFORMATION FOR SEO ID NO:916:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1255 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1255

(D) OTHER INFORMATION: / Ceres Seq. ID 1499206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:916:

| (x17) Seq   |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| atcagcgaaa  | atggcgggaa  | gaggaggagaa | aagccgcgcga | ggcgctgtgac | cggtgtgaagt | 60   |
| tcggagcgtg  | atctcggcgtg | ggacgtgtgag | gtgcgcgtgct | cgctgatcgt  | ggcttcgaag  | 120  |
| gcgcgtggagc | acgtggaggcg | cgctgcttcgg | aagaaacgaa  | atgggtgtcca | gtccacaaac  | 180  |
| taggtgtcgt  | agtgctgtgac | aataaaaaaa  | cgaagatcga  | cgagatcatc  | cttcacattc  | 240  |
| tcocagtaaa  | ggaagtaccaa | atcatagatc  | atctggttgg  | acctacgttg  | aaagacaggg  | 300  |
| ttatgaagat  | catctgcgtgt | cagaaacaaa  | ccagagcgtgg | tcaagaagct  | agattcaagg  | 360  |
| ctcttttgtt  | tgttgtgtgat | ggtaatgttc  | ttcttggttt  | gggtgtcaag  | cgcttcaagg  | 420  |
| gaagtgtcaac | tgccatctaga | ggagctatta  | ttcttctgaa  | gctttctgtg  | gtcccggtga  | 480  |
| gaagagggtta | ttgggggaat  | aagatgtgga  | agcacacaa   | tgtgccttgt  | agaggttaagt | 540  |
| gtaaatgtgt  | ttctgttact  | gtgagaaagt  | ttcctgtctc  | gagaggtgtt  | ggatattgtg  | 600  |
| ctcttaggtg  | tcctaagaag  | gttcttcagt  | tcgctgtggt  | tgatgatgtt  | ttaacctctt  | 660  |
| ctagaggtatc | taccaaaaca  | ctcggaaaact | ttgttaaggc  | gacattcgat  | gttcctacaa  | 720  |
| agacatctag  | gttctctaca  | ccagagttct  | ggaaagagac  | tacattctcc  | agatcgccct  | 780  |
| accaagaagca | cactgatttc  | ctgtctgata  | aggctcttca  | ggccgcacaa  | gtttgtcaagg | 840  |
| agggtagaag  | acaagactta  | gacctctcatg | agatgagctt  | gtgtttatag  | gttctgtcag  | 900  |
| tggcgaatat  | ctttatcttt  | tctgtgcatg  | tttcttggtt  | gtctttatag  | tttttgatat  | 960  |
| tggagattca  | attacaagga  | taatactatt  | tagttatggt  | tggggtttatg | tacgaatttt  | 1020 |
| ataatgagtg  | tgccataatt  | taactataaaa | agaaaaaaaa  | agaaaaaaag  | agtgtttgat  | 1080 |
| gcactgtgtg  | tgtacttaatt | taattagtga  | cattttaagc  | aaatgtgtgt  | tggaaaaggt  | 1140 |
| tgctgtcaat  | aaattatgat  | atgggtgcga  | taagaagcgg  | aagatctgtg  | gactgttgct  | 1200 |
| tgtctacatc  | tatttatgta  | ttccgcatac  | tgttgttgta  | ttgttataat  | ttatt       |      |

(2) INFORMATION FOR SEQ ID NO:917:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 285 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..28

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:917:

Arg Lys Trp Arg Lys Glu Glu Glu Lys Ala A

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|--|
| 1   | Arg | Gly | Asp | Phe | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |    |  |
| Arg | Gly | Asp | Phe | 20  | Gly | Arg | Gly | Phe | Gly | Gly | Arg | Gly | Gly | Arg | Gly | Arg |     |    |  |
| Gly | Arg | Asp | Arg | 35  | Gly | Pro | Arg | Gly | 25  | Gly | Arg | Arg | Gly | 30  | Gly | Arg | Ala |    |  |
| Ser | Glu | Glu | Thr | Lys | Trp | Val | Pro | Val | 40  | Thr | Lys | Leu | Gly | 45  | Arg | Leu | Val |    |  |
| Ala | Asp | Asn | Lys | Ile | 70  | Thr | Lys | Leu | Glu | Gln | Ile | Tyr | Leu | His | Ser | Leu | 80  |    |  |
| Pro | Val | Lys | Glu | Tyr | 85  | Gln | Ile | Ile | Asp | His | 90  | Leu | Val | Gly | Pro | Thr | Leu | 95 |  |
| Lys | Asp | Glu | Val | Met | 100 | Lys | Ile | Met | Pro | Val | Gln | Lys | Gln | Thr | Arg | Ala |     |    |  |
| Gly | Gln | Arg | Thr | Arg | Phe | Lys | Ala | Phe | 105 | Val | Val | Val | Gly | 110 | Asp | Gly | Asn |    |  |
| Gly | His | Val | Gly | Leu | Gly | Val | Lys | Arg | Ser | Lys | Glu | Val | Ala | 115 | Thr | Ala |     |    |  |
| Ile | Arg | Gly | Ala | Ile | Ile | Leu | Ala | Lys | Leu | Ser | Val | Val | Pro | 120 | Val | Arg | 160 |    |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Gly | Tyr | Trp | Gly | Asn | Lys | Ile | Gly | Lys | Pro | His | Thr | Val | Pro | Cys |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Lys | Val | Thr | Gly | Lys | Cys | Gly | Ser | Val | Thr | Val | Arg | Met | Val | Pro | Ala |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Pro | Arg | Gly | Ser | Gly | Ile | Val | Ala | Ala | Arg | Val | Pro | Lys | Lys | Val | Leu |
|     |     |     | 195 |     |     |     |     | 200 |     |     |     | 205 |     |     |     |
| Gln | Phe | Ala | Gly | Ile | Asp | Val | Phe | Thr | Ser | Ser | Arg | Gly | Ser | Thr |     |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Lys | Thr | Leu | Gly | Asn | Phe | Val | Lys | Ala | Thr | Phe | Asp | Cys | Leu | Gln | Lys |
|     | 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Thr | Tyr | Gly | Phe | Leu | Thr | Pro | Glu | Phe | Trp | Lys | Glu | Thr | Arg | Phe | Ser |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Arg | Ser | Pro | Tyr | Gln | Glu | His | Thr | Asp | Phe | Leu | Ser | Thr | Lys | Ala | Leu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Gln | Ala | Ala | Lys | Val | Val | Thr | Glu | Gly | Glu | Glu | Gln | Ala |     |     |     |
|     |     |     | 275 |     |     |     |     | 280 |     |     |     | 285 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:918:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..185

(D) OTHER INFORMATION: / Ceres Seq. ID 1499208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:918:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Ile | Met | Pro | Val | Gln | Lys | Gln | Thr | Arg | Ala | Gly | Gln | Arg | Thr |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Arg | Phe | Lys | Ala | Phe | Val | Val | Val | Gly | Asp | Gly | Asn | Gly | His | Val | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Gly | Val | Lys | Arg | Ser | Lys | Glu | Val | Ala | Thr | Ala | Ile | Arg | Gly | Ala |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Ile | Leu | Ala | Lys | Leu | Ser | Val | Val | Pro | Val | Arg | Arg | Gly | Tyr | Trp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Asn | Lys | Ile | Gly | Lys | Pro | His | Thr | Val | Pro | Cys | Lys | Val | Thr | Gly |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Lys | Cys | Gly | Ser | Val | Thr | Val | Arg | Met | Val | Pro | Ala | Pro | Arg | Gly | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Gly | Ile | Val | Ala | Ala | Arg | Val | Pro | Lys | Lys | Val | Leu | Gln | Phe | Ala | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Asp | Asp | Val | Phe | Thr | Ser | Ser | Arg | Gly | Ser | Thr | Lys | Thr | Leu | Gly |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asn | Phe | Val | Lys | Ala | Thr | Phe | Asp | Cys | Leu | Gln | Lys | Thr | Tyr | Gly | Phe |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Thr | Pro | Glu | Phe | Trp | Lys | Glu | Thr | Arg | Phe | Ser | Arg | Ser | Pro | Tyr |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Gln | Glu | His | Thr | Asp | Phe | Leu | Ser | Thr | Lys | Ala | Leu | Gln | Ala | Ala | Lys |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Val | Val | Thr | Glu | Gly | Glu | Glu | Gln | Ala |     |     |     |     |     |     |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:919:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..182

(D) OTHER INFORMATION: / Ceres Seq. ID 1499209

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:919:

```
Met Pro Val Gln Lys Gln Thr Arg Ala Gly Gln Arg Thr Arg Phe Lys
1 5 10 15
Ala Phe Val Val Val Gly Asp Gly Asn Gly His Val Gly Leu Gly Val
20 25 30
Lys Arg Ser Lys Glu Val Ala Thr Ala Ile Arg Gly Ala Ile Ile Leu
35 40 45
Ala Lys Leu Ser Val Val Pro Val Arg Arg Gly Tyr Trp Gly Asn Lys
50 55 60
Ile Gly Lys Pro His Thr Val Pro Cys Lys Val Thr Gly Lys Cys Gly
65 70 75 80
Ser Val Thr Val Arg Met Val Pro Ala Pro Arg Gly Ser Gly Ile Val
85 90 95
Ala Ala Arg Val Pro Lys Lys Val Leu Gln Phe Ala Gly Ile Asp Asp
100 105 110
Val Phe Thr Ser Ser Arg Gly Ser Thr Lys Thr Leu Gly Asn Phe Val
115 120 125
Lys Ala Thr Phe Asp Cys Leu Gln Lys Thr Tyr Gly Phe Leu Thr Pro
130 135 140
Glu Phe Trp Lys Glu Thr Arg Phe Ser Arg Ser Pro Tyr Gln Glu His
145 150 155 160
Thr Asp Phe Leu Ser Thr Lys Ala Leu Gln Ala Ala Lys Val Val Thr
165 170 175
Glu Gly Glu Glu Gln Ala
180
```

(2) INFORMATION FOR SEQ ID NO:920:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1170 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1170

(D) OTHER INFORMATION: / Ceres Seq. ID 1499210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:920:

```
aagtgttagc tgcgtgcgct gttgtttctc ctccatttct ctatctttct ctctcgtctc 60
ttctcgaatc tctgtatata tcttcttctt ctccaagtga aaaatggcgc atggtgaggga 120
tattcagcca cttgtctgtg acaatggaac tggaaatggtg aaggctgggt ttgctggtga 180
tgatgcgccg agagcagtg tcccaagtat tgttggtcgt acaaccggta ttgtgctcga 240
ttctgtgatg ggtgtgtctc acactgtgcc aatctacgar gggtatgctc ttctcatcgc 300
tatctctcgt cttgatcttg cgggtcgagg tctcacagac tcaatcatga agattctcac 360
tgagagaggt tacatgttca ccactaccgc agaacgggaa atgttccgtg acataaaggga 420
gaaaactgtk tatgtgcctc ttgaactacga gcaagagcta gagacagcca agagcatttc 480
ttcagtgagg aargaacac gagcttctct atggacaagt cataaccatc ggagctgaga 540
gatyccgttg tctctgaggt ctgttcacgc catcgctcat cggaatggaa gctctctggaa 600
tccatgaaac aacttacaac tccatcatga aatgtgatgt cgatatacgg aaggwtctct 660
atggaacatc cgttctcaat ggtggttcca ccattgtccc aggaatttgt gaacctatga 720
gcaaagagat caccgtctct gcacctagca gcatgaagat caaggttggtt gcaccggcag 780
agagaaaaaa cagtgtcttg atcggaggat caatccttgc atccctcagc accctccaac 840
agatgtggat ttcaaagagt gagtacgatg agtcaggttc atcgatttgt ccacaggaaat 900
gtttctaagt gtgtcttctc ttatctggtt cgtggtgggt agtttgttac aaaaaaatct 960
attttcccta gttgagatgg gaattgaact atctgttggt atgtggattt ttttttctt 1020
tttctcttta gaaccttatg gttgtgtcaa gaagtcttgt gtactttagt tttatatctc 1080
tgttttatct cttctatttt ctttaggatg cttgtgatga tgctgttttt tttgtccctc 1140
aagcaaaaaa atatcatatt atattggcc
```

(2) INFORMATION FOR SEQ ID NO:921:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..135  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499211  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:921:  
Met Ala Asp Gly Glu Asp Ile Gln Pro Leu Val Cys Asp Asn Gly Thr  
1 5 10 15  
Gly Met Val Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val  
20 25 30  
Phe Pro Ser Ile Val Gly Arg Thr Thr Gly Ile Val Leu Asp Ser Gly  
35 40 45  
Asp Gly Val Ser His Thr Val Pro Ile Tyr Xaa Gly Tyr Ala Leu Pro  
50 55 60  
His Ala Ile Leu Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp Ser  
65 70 75 80  
Leu Met Lys Ile Leu Thr Glu Arg Gly Tyr Met Phe Thr Thr Thr Ala  
85 90 95  
Glu Arg Glu Ile Val Arg Asp Ile Lys Glu Lys Leu Xaa Tyr Val Ala  
100 105 110  
Leu Asp Tyr Glu Gln Glu Leu Glu Thr Ala Lys Ser Ser Ser Val  
115 120 125  
Glu Xaa Glu Leu Arg Ala Ser  
130 135

(2) INFORMATION FOR SEQ ID NO:922:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..118

(D) OTHER INFORMATION: / Ceres Seq. ID 1499212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:922:

Met Val Lys Ala Gly Phe Ala Gly Asp Asp Ala Pro Arg Ala Val Phe  
1 5 10 15  
Pro Ser Ile Val Gly Arg Thr Thr Gly Ile Val Leu Asp Ser Gly Asp  
20 25 30  
Gly Val Ser His Thr Val Pro Ile Tyr Xaa Gly Tyr Ala Leu Pro His  
35 40 45  
Ala Ile Leu Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp Ser Leu  
50 55 60  
Met Lys Ile Leu Thr Glu Arg Gly Tyr Met Phe Thr Thr Thr Ala Glu  
65 70 75 80  
Arg Glu Ile Val Arg Asp Ile Lys Glu Lys Leu Xaa Tyr Val Ala Leu  
85 90 95  
Asp Tyr Glu Gln Glu Leu Glu Thr Ala Lys Ser Ser Ser Ser Val Glu  
100 105 110  
Xaa Glu Leu Arg Ala Ser  
115

(2) INFORMATION FOR SEQ ID NO:923:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..107  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1499213  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:923:  
Met Glu Ala Pro Gly Ile His Glu Thr Tyr Asn Ser Ile Met Lys  
1          5          10          15  
Cys Asp Val Asp Ile Arg Lys Xaa Leu Tyr Gly Asn Ile Val Leu Ser  
          20          25          30  
Gly Gly Ser Thr Met Phe Pro Gly Ile Ala Asp Arg Met Ser Lys Glu  
          35          40          45  
Ile Thr Ala Leu Ala Pro Ser Ser Met Lys Ile Lys Val Val Ala Pro  
          50          55          60  
Pro Glu Arg Lys Tyr Ser Val Trp Ile Gly Gly Ser Ile Leu Ala Ser  
65          70          75          80  
Leu Ser Thr Phe Gln Gln Met Trp Ile Ser Lys Ser Glu Tyr Asn Glu  
          85          90          95  
Ser Gly Pro Ser Ile Val His Arg Lys Cys Phe  
          100          105

(2) INFORMATION FOR SEQ ID NO:924:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1107 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1107

(D) OTHER INFORMATION: / Ceres Seq. ID 1499214

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:924:

aaatttcgtt gtmcagagaa gaagcaaaaag agagaaacat ccgaccgcga atctgcacctg 60  
aaaacccgga agaatacgaaa aatgggggaaa gatggtctga cgcacgatca ggtctcgtctg 120  
atgaaggaag ccttcacgtct cttcgacacc gatggcgagc gcaaaatcgc accgtcaagag 180  
ctcgggatcc tcatcgatct tctcgccgga aaccgcaccc aagccacgt gaaatccata 240  
atcgatccg agaattctct ttaccggttt gatttcaaca gattctcga tctcatcgcg 300  
aaacatctga agacgggaacc ttctgatcgc cagctccgtg acgcattcaa agtgctcgat 360  
aaggaaggtta ccgggttcgt tgctgtggcg gatctgaggc atattctgac cagtatcga 420  
gagaagctgg agcctaataga gtctgatgag tggatcaagg aggtggatgt tggatccgat 480  
ggaaagatcc ggtacttctg taatgatgtc cgcaattgcc ggctcctacg gctacatagc 540  
tccagagatc cggatatacat tgaaggtaga tgagaagagc gatgtgtata gtttcggtgt 600  
tgttctctca gaactcatca ccgggaaaaa acccgtcgga gaatttggcg acggcggtga 660  
tattgttcaa tgggtgagaa cgaatgacga ttcaaatata gattgtgtgc tcaaaataat 720  
cgatctttaga ctctcttcag ttccagttca cgaggtaaca cactgttctt acgttgcggt 780  
gctctgtggt gaagaacaaag cgggtggagag gccgacgatg cgtgaagtcg ttacagattct 840  
cactgagatc ccaaaatctc ctcttctgaa cgagcaagcg gccggaatcag acgtgactga 900  
gaaagctccg gcgattaatg aatcgtcgcc ggattcagga agtccacggc atctctttaag 960  
taattagact ttccggcgat tgggttttgt cattgagggg caaattgttc ttctaaattt 1020  
tctgttcacc gaagtcctgg tagtggagtt aattacttaa tttagccggtt gttgtctggt 1080  
tcgggttaag gcacaatta ttggttt

(2) INFORMATION FOR SEQ ID NO:925:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide



(B) LOCATION: 1..166

(D) OTHER INFORMATION: / Ceres Seq. ID 1499215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:925:

Lys Phe Arg Cys Xaa Glu Lys Lys Gln Lys Arg Glu Thr Ser Asp Pro  
1 5 10 15  
Glu Ser Asp Leu Lys Thr Arg Lys Asn Arg Lys Met Gly Lys Asp Gly  
20 25 30  
Leu Ser Asp Asp Gln Val Ser Ser Met Lys Glu Ala Phe Met Leu Phe  
35 40 45  
Asp Thr Asp Gly Asp Gly Lys Ile Ala Pro Ser Glu Leu Gly Ile Leu  
50 55 60  
Met Arg Ser Leu Gly Gly Asn Pro Thr Gln Ala Gln Leu Lys Ser Ile  
65 70 75 80  
Ile Ala Ser Glu Asn Leu Ser Ser Pro Phe Asp Phe Asn Arg Phe Leu  
85 90 95  
Asp Leu Met Ala Lys His Leu Lys Thr Glu Pro Phe Asp Arg Gln Leu  
100 105 110  
Arg Asp Ala Phe Lys Val Leu Asp Lys Glu Gly Thr Gly Phe Val Ala  
115 120 125  
Val Ala Asp Leu Arg His Ile Leu Thr Ser Ile Gly Glu Lys Leu Glu  
130 135 140  
Pro Asn Glu Phe Asp Glu Trp Ile Lys Glu Val Asp Val Gly Ser Asp  
145 150 155 160  
Gly Lys Ile Arg Tyr Phe  
165

(2) INFORMATION FOR SEQ ID NO:926:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..176

(D) OTHER INFORMATION: / Ceres Seq. ID 1499216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:926:

Met Ser Ser Met Ser Gly Ser Arg Arg Trp Met Leu Asp Pro Met Glu  
1 5 10 15  
Arg Ser Gly Thr Ser Glu Cys Met Ser Ala Ile Ala Gly Ser Tyr Gly  
20 25 30  
Tyr Ile Ala Pro Glu Tyr Ala Tyr Thr Leu Lys Val Asp Glu Lys Ser  
35 40 45  
Asp Val Tyr Ser Phe Gly Val Val Leu Leu Glu Leu Ile Thr Gly Lys  
50 55 60  
Lys Pro Val Gly Glu Phe Gly Asp Gly Val Asp Ile Val Gln Trp Val  
65 70 75 80  
Arg Ser Met Thr Asp Ser Asn Lys Asp Cys Val Leu Lys Val Ile Asp  
85 90 95  
Leu Arg Leu Ser Ser Val Pro Val His Glu Val Thr His Val Phe Tyr  
100 105 110  
Val Ala Leu Leu Cys Val Glu Glu Gln Ala Val Glu Arg Pro Thr Met  
115 120 125  
Arg Glu Val Val Gln Ile Leu Thr Glu Ile Pro Lys Ile Pro Leu Ser  
130 135 140  
Lys Gln Gln Ala Ala Glu Ser Asp Val Thr Glu Lys Ala Pro Ala Ile  
145 150 155 160  
Asn Glu Ser Ser Pro Asp Ser Gly Ser Pro Pro Asp Leu Leu Ser Asn  
165 170 175

(2) INFORMATION FOR SEQ ID NO:927:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..173  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:927:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Gly | Ser | Arg | Arg | Trp | Met | Leu | Asp | Pro | Met | Glu | Arg | Ser | Gly |
| 1   | Thr | Ser | Glu | Cys | Met | Ser | Ala | Ile | Ala | Gly | Ser | Tyr | Gly | Tyr | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Glu | Tyr | Ala | Tyr | Thr | Leu | Lys | Val | Asp | Glu | Lys | Ser | Asp | Val | Tyr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Phe | Gly | Val | Val | Leu | Leu | Glu | Leu | Ile | Thr | Gly | Lys | Lys | Pro | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Glu | Phe | Gly | Asp | Gly | Val | Asp | Ile | Val | Gln | Trp | Val | Arg | Ser | Met |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Thr | Asp | Ser | Asn | Lys | Asp | Cys | Val | Leu | Lys | Val | Ile | Asp | Leu | Arg | Leu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ser | Ser | Val | Pro | Val | His | Glu | Val | Thr | His | Val | Phe | Tyr | Val | Ala | Leu |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Leu | Cys | Val | Glu | Glu | Gln | Ala | Val | Glu | Arg | Pro | Thr | Met | Arg | Glu | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Gln | Ile | Leu | Thr | Glu | Ile | Pro | Lys | Ile | Pro | Leu | Ser | Lys | Gln | Gln |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Ala | Glu | Ser | Asp | Val | Thr | Glu | Lys | Ala | Pro | Ala | Ile | Asn | Glu | Ser |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Pro | Asp | Ser | Gly | Ser | Pro | Pro | Asp | Leu | Leu | Ser | Asn |     |     |     |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:928:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1663 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1663  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499218

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:928:

|         |          |             |            |            |             |             |            |    |
|---------|----------|-------------|------------|------------|-------------|-------------|------------|----|
| agc     | aaaaat   | gtc         | atacaat    | taaaaggctg | tccaaatg    | gcatattcc   | acacaagttg | 60 |
| tgt     | tgcacgc  | tcagacaaga  | aaggcgtgtg | tcaatgtgtg | atattctcca  | ttctctcatc  | 120        |    |
| caaat   | ttccga   | cataactatc  | ctagccgcga | tttgtttctc | acatttcaaa  | accctcagca  | 180        |    |
| gctt    | ccaaaac  | tcttcgcgat  | tcttcctcac | gtctgcattt | ctctcgtctc  | catttttaata | 240        |    |
| gttttt  | tcttc    | tcggaatcac  | aaatcttcgg | cttctgtgtc | ttctggcggt  | gtgtgtgtgtg | 300        |    |
| tgtgaat | ggtc     | cttgttcagc  | ggatttccaa | ttctctccc  | agtatatcgga | attggcaaca  | 360        |    |
| acg     | caggagac | cttttttgact | ctattttgtg | tttacctatc | aaataactgac | cttctctctc  | 420        |    |
| tct     | cccccttt | acagagaagg  | actctgttga | gagatataca | agggatacaat | ggcgtgtacaa | 480        |    |
| atgcg   | ttgaa    | ccaacgcgcc  | catcgctcac | attctccatc | ccatttgaag  | ataagtgctt  | 540        |    |
| tgt     | tatgggaa | acagcatatt  | catcgacgct | gcctgagcgt | aagaagatct  | tggcagtgct  | 600        |    |
| gaaga   | gagaa    | agagtataag  | gatgcgaagg | tgggtgat   | tgccaggagat | atgtgtatct  | 660        |    |
| tgt     | tgggca   | ctggccaggag | atctcgagct | tttgactctt | aaagctgtca  | gagttaatca  | 720        |    |
| aagt    | cgcat    | cttttcgttt  | acagcagagc | tgtctccaat | gatgtctgtc  | agtttgtgtc  | 780        |    |
| tct     | gatgct   | agactctctt  | attctggcga | taagctgtgt | tatcatatga  | gaactcagga  | 840        |    |
| tcagat  | ttcat    | gaactactcc  | taaatttttc | caagcgtgtg | ccactgtgtc  | tacgcgttaa  | 900        |    |

|            |            |             |             |            |            |      |
|------------|------------|-------------|-------------|------------|------------|------|
| aggtggagat | cctctggtct | tgtgacgggg  | cggcgaagaa  | atggactttc | tgcaacagca | 960  |
| agggattcga | gttcaagtta | taccagggat  | aactgcggcg  | tcggggatag | cagcagagtt | 1020 |
| ggggattcca | ctaacacatc | gaggtgttgc  | aactagtgtg  | aggtttctca | ctggctattc | 1080 |
| aaggaagga  | gggacagacc | ctctgtttgt  | tcgacagaat  | gcagctgacc | cggatacaac | 1140 |
| acttctcgtt | tatatgggtt | tggaacattt  | acctctctct  | gcacaaaaac | taatggacca | 1200 |
| tggtctccct | cttgatacac | cagctgtttgc | ggttgaacct  | ggaaccactc | ctctacagcg | 1260 |
| tacagttttt | gctgagctta | aagattttgc  | aactgagatt  | cagtcagctg | gatttggtgc | 1320 |
| accaacactc | atcatcatag | ggaaagtctg  | tgagctctca  | ctttatggcg | cacattgcac | 1380 |
| gaaagaatcc | tcctgctctg | tagagaccgc  | gtagatatct  | cactcttatt | ttacggcgct | 1440 |
| gtggcttcca | tcgacattac | ggtgaagttt  | taggagctat  | ggagctatga | aggttgagac | 1500 |
| gtgagagatg | taataaaca  | aaaggaagac  | tgatagtttc  | ttatgacgtg | tccttcaatt | 1560 |
| tgttgaggac | aattgtaagt | gcaatgttaa  | tgtaataaac  | aagtattcaa | tcagtgccac | 1620 |
| tgtagtaaat | ttttccacca | caagatgatg  | tcctttaaacc | ttt        |            |      |

(2) INFORMATION FOR SEQ ID NO:929:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 369 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..369

(D) OTHER INFORMATION: / Ceres Seq. ID 1499219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:929:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Leu | Val | Gln | Arg | Ile | Pro | Ile | Ser | Ser | Ser | Ser | Ile | Arg | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Trp | Gln | Gln | Ala | Arg | Thr | Asn | Leu | Thr | Pro | Ile | Cys | Cys | Leu | His | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Thr | Ala | Ser | Ser | Ser | Ser | Ser | Pro | Phe | Thr | Glu | Lys | His | Ser | Val |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Arg | Tyr | Gln | Arg | Asp | Gln | Trp | Leu | Tyr | Lys | Ala | Val | Glu | Pro | Thr |
|     |     |     | 50  |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Pro | Pro | Ser | Thr | Pro | Ser | Pro | Ser | Pro | Phe | Glu | Asp | Glu | Val | Phe | Val |
|     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Arg | Glu | Asn | Asp | Ile | Ala | Ser | Gln | Leu | Pro | Glu | Leu | Lys | Lys | Leu | Leu |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ala | Val | Leu | Lys | Glu | Lys | Arg | Val | Lys | Gly | Cys | Lys | Gly | Gly | Asp | Cys |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Gly | Pro | Gly | Asp | Val | Tyr | Leu | Val | Gly | Thr | Gly | Pro | Gly | Asp | Pro | Glu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Leu | Thr | Leu | Lys | Ala | Val | Arg | Val | Ile | Gln | Ser | Ala | Asp | Leu | Leu |
|     |     |     | 130 |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Leu | Tyr | Asp | Arg | Leu | Val | Ser | Asn | Asp | Val | Leu | Glu | Leu | Val | Ala | Pro |
|     |     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     | 160 |     |
| Asp | Ala | Arg | Leu | Leu | Tyr | Val | Gly | Lys | Thr | Ala | Gly | Tyr | His | Ser | Arg |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     | 175 |     |     |
| Thr | Gln | Glu | Glu | Ile | His | Glu | Leu | Leu | Leu | Asn | Phe | Ala | Glu | Ala | Gly |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Thr | Val | Val | Arg | Leu | Lys | Gly | Gly | Asp | Pro | Leu | Val | Phe | Gly | Arg |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gly | Gly | Glu | Glu | Met | Asp | Phe | Leu | Gln | Gln | Gln | Gly | Ile | Arg | Val | Gln |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Val | Ile | Pro | Gly | Ile | Thr | Ala | Ala | Ser | Gly | Ile | Ala | Ala | Glu | Leu | Gly |
|     |     |     | 225 |     |     | 230 |     |     |     | 235 |     |     |     | 240 |     |
| Ile | Pro | Leu | Thr | His | Arg | Gly | Val | Ala | Thr | Ser | Val | Arg | Phe | Leu | Thr |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Gly | His | Ser | Arg | Lys | Gly | Gly | Thr | Asp | Pro | Leu | Phe | Val | Ala | Glu | Asn |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Ala | Ala | Asp | Pro | Asp | Thr | Thr | Leu | Val | Val | Tyr | Met | Gly | Leu | Gly | Thr |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |

Leu Pro Ser Leu Ala Gln Lys Leu Met Asp His Gly Leu Pro Ser Asp  
290 295 300  
Thr Pro Ala Val Ala Val Glu Arg Gly Thr Thr Pro Leu Gln Arg Thr  
305 310 315 320  
Val Phe Ala Glu Leu Lys Asp Phe Ala Thr Glu Ile Gln Ser Ala Gly  
325 330 335  
Leu Val Ser Pro Thr Leu Ile Ile Ile Gly Lys Val Val Glu Leu Ser  
340 345 350  
Pro Leu Trp Pro His Cys Thr Lys Glu Ser Ser Cys Leu Val Glu Thr  
355 360 365  
Arg

(2) INFORMATION FOR SEQ ID NO:930:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1526

(D) OTHER INFORMATION: / Ceres Seq. ID 1499220

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:930:

|            |             |             |             |             |             |      |
|------------|-------------|-------------|-------------|-------------|-------------|------|
| aaaacacgag | tctaatgtt   | gctgttgatt  | taagtaaaact | tcagaaacct  | agaagtaagg  | 60   |
| gagtcagagg | tagaggagg   | gtaaggaaaa  | ctgacagtat  | aggtaataag  | agttccaagg  | 120  |
| tagcggaacc | agccaaaaag  | gcgacaaaag  | aaaacagggt  | ttgggatgat  | gcggctccca  | 180  |
| aacaatcgaa | attggacttc  | acggattcca  | tcgatgaaaa  | tgggaacaat  | gatcatgtag  | 240  |
| atattgtg   | tgctgaccaa  | ggagaaagta  | tgatggacaa  | ggaagaggtt  | ttcagcagtg  | 300  |
| atagtgaag  | tgaagatgat  | gacgaaccag  | gaagtgatga  | gaagcctgct  | caggctaaga  | 360  |
| aaaaggagat | gttttctct   | gttttccaga  | gtattactgg  | gaaagcgaat  | cttgaagaag  | 420  |
| cagacccctg | accggcggtg  | aaagctctga  | aggaacggct  | catgaccaag  | aatgtggcag  | 480  |
| aagagattgc | tgagaagctt  | tgccaatcag  | tggaaagctag | tcttgaagga  | aagaaattgt  | 540  |
| catctttcac | caggatctct  | tcaaccgttc  | aggcagcgat  | ggaggatgct  | ctgtgttcga  | 600  |
| tattgactcc | aagacgctcc  | attgatatat  | taagagatgt  | tcatgctgcc  | aaagaacaga  | 660  |
| ggaaacctta | tgtgtgttgg  | ttgtttggag  | tcaatggagt  | tgggaatacc  | accaatctcg  | 720  |
| ctaaagtggc | gtattggcct  | cagcagcata  | aggtoagtgt  | aatgatggct  | gcttgtgaca  | 780  |
| ctttccggtc | tggagctgtt  | gagcagttac  | ggactcatgc  | tcgtagggtt  | cagataccga  | 840  |
| tattgaaaa  | gggttatgaa  | aaggatccag  | cagtagtggc  | taaaagaagc  | atacaagaag  | 900  |
| caactcgaaa | tggatccgat  | gtcgttctgt  | ttgacacagc  | tggtcgagat  | caggataaatg | 960  |
| aacctttgat | gagagacact  | tcaaaagtcca | tcaaccttaa  | tcagccggac  | tgtgtcttgt  | 1020 |
| ttgtttgtga | agctcttgtt  | ggaacacgat  | cagtagacca  | gctctcgaag  | tcaatcaga   | 1080 |
| aactttcgga | ctctctcgact | ctcgggaacc  | caagaactgat | cgatggaatc  | ttactgacaa  | 1140 |
| agtttctaac | cattgacgac  | aaggtcggag  | cagcgttgct  | tatgttttac  | atcatcgagat | 1200 |
| accgggttat | gttcgtgggt  | tgtggccagt  | cttacactga  | cttgaagaag  | cttaattgtca | 1260 |
| aagccatagt | caagacactt  | ctcaagtgat  | ctcctcttca  | tcatacatcat | catcatcatc  | 1320 |
| actatcatca | ttaccatcta  | ctatcaacaa  | tcaatgtcct  | atccatcatg  | ctgtgtgttt  | 1380 |
| tggtttttta | tttgaagacg  | gtttctcttt  | ggaagtgttg  | tgttttcttt  | aaaactcaaa  | 1440 |
| agactggagt | cgcataaaat  | accatcccat  | gactttatat  | gatgcaacgt  | aacttttgtt  | 1500 |
| ttaaattaaa | gattataat   | catgtc      |             |             |             |      |

(2) INFORMATION FOR SEQ ID NO:931:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..428

(D) OTHER INFORMATION: / Ceres Seq. ID 1499221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:931:

Asn Thr Ser Ser Asn Val Ala Val Asp Leu Ser Lys Leu Gln Lys Leu  
1 5 10 15  
Arg Ser Lys Gly Val Arg Gly Arg Gly Val Arg Lys Thr Asp Ser  
20 25 30  
Ile Gly Asn Lys Ser Ser Lys Val Ala Glu Pro Ala Lys Lys Ala Thr  
35 40 45  
Lys Lys Asn Arg Val Trp Asp Asp Ala Ala Pro Lys Gln Ser Lys Leu  
50 55 60  
Asp Phe Thr Asp Ser Ile Asp Glu Asn Gly Asn Asn Asp His Val Asp  
65 70 75 80  
Ile Val Ala Ala Asp Gln Gly Glu Ser Met Met Asp Lys Glu Glu Val  
85 90 95  
Phe Ser Ser Asp Ser Glu Ser Glu Asp Asp Glu Pro Gly Ser Asp  
100 105 110  
Glu Lys Pro Ala Gln Ala Lys Lys Lys Gly Trp Phe Ser Ser Val Phe  
115 120 125  
Gln Ser Ile Thr Gly Lys Ala Asn Leu Glu Arg Thr Asp Leu Gly Pro  
130 135 140  
Ala Leu Lys Ala Leu Lys Glu Arg Leu Met Thr Lys Asn Val Ala Glu  
145 150 155 160  
Glu Ile Ala Glu Lys Leu Cys Glu Ser Val Glu Ala Ser Leu Glu Gly  
165 170 175  
Lys Lys Leu Ser Ser Phe Thr Arg Ile Ser Ser Thr Val Gln Ala Ala  
180 185 190  
Met Glu Asp Ala Leu Val Arg Ile Leu Thr Pro Arg Arg Ser Ile Asp  
195 200 205  
Ile Leu Arg Asp Val His Ala Ala Lys Glu Gln Arg Lys Pro Tyr Val  
210 215 220  
Val Val Phe Val Gly Val Asn Gly Val Gly Lys Ser Thr Asn Leu Ala  
225 230 235 240  
Lys Val Ala Tyr Trp Leu Gln Gln His Lys Val Ser Val Met Met Ala  
245 250 255  
Ala Cys Asp Thr Phe Arg Ser Gly Ala Val Glu Gln Leu Arg Thr His  
260 265 270  
Ala Arg Arg Leu Gln Ile Pro Ile Phe Glu Lys Gly Tyr Glu Lys Asp  
275 280 285  
Pro Ala Val Val Ala Lys Glu Ala Ile Gln Glu Ala Thr Arg Asn Gly  
290 295 300  
Ser Asp Val Val Leu Val Asp Thr Ala Gly Arg Met Gln Asp Asn Glu  
305 310 315 320  
Pro Leu Met Arg Ala Leu Ser Lys Leu Ile Asn Leu Asn Gln Pro Asp  
325 330 335  
Leu Val Leu Phe Val Gly Glu Ala Leu Val Gly Asn Asp Ala Val Asp  
340 345 350  
Gln Leu Ser Lys Phe Asn Gln Lys Leu Ser Asp Leu Ser Thr Ser Gly  
355 360 365  
Asn Pro Arg Leu Ile Asp Gly Ile Leu Leu Thr Lys Phe Asp Thr Ile  
370 375 380  
Asp Asp Lys Val Gly Ala Ala Leu Ser Met Val Tyr Ile Ser Gly Ser  
385 390 395 400  
Pro Val Met Phe Val Gly Cys Gly Gln Ser Tyr Thr Asp Leu Lys Lys  
405 410 415  
Leu Asn Val Lys Ala Ile Val Lys Thr Leu Leu Lys  
420 425

(2) INFORMATION FOR SEQ ID NO:932:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..339

(D) OTHER INFORMATION: / Ceres Seq. ID 1499222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:932:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Asp | Lys | Glu | Glu | Val | Phe | Ser | Ser | Asp | Ser | Glu | Ser | Glu | Asp |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |     |
| Asp | Asp | Glu | Pro | Gly | Ser | Asp | Glu | Lys | Pro | Ala | Gln | Ala | Lys | Lys | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Gly | Trp | Phe | Ser | Ser | Val | Phe | Gln | Ser | Ile | Thr | Gly | Lys | Ala | Asn | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Glu | Arg | Thr | Asp | Leu | Gly | Pro | Ala | Leu | Lys | Ala | Leu | Lys | Glu | Arg | Leu |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Met | Thr | Lys | Asn | Val | Ala | Glu | Glu | Ile | Ala | Glu | Lys | Leu | Cys | Glu | Ser |
|     |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Val | Glu | Ala | Ser | Leu | Glu | Gly | Lys | Lys | Leu | Ser | Ser | Phe | Thr | Arg | Ile |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Ser | Ser | Thr | Val | Gln | Ala | Ala | Met | Glu | Asp | Ala | Leu | Val | Arg | Ile | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Pro | Arg | Arg | Ser | Ile | Asp | Ile | Leu | Arg | Asp | Val | His | Ala | Ala | Lys |
|     |     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |     |     |
| Glu | Gln | Arg | Lys | Pro | Tyr | Val | Val | Val | Phe | Val | Gly | Val | Asn | Gly | Val |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Gly | Lys | Ser | Thr | Asn | Leu | Ala | Lys | Val | Ala | Tyr | Trp | Leu | Gln | Gln | His |
|     |     |     | 145 |     |     |     | 150 |     |     |     | 155 |     |     |     | 160 |
| Lys | Val | Ser | Val | Met | Met | Ala | Ala | Cys | Asp | Thr | Phe | Arg | Ser | Gly | Ala |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Val | Glu | Gln | Leu | Arg | Thr | His | Ala | Arg | Arg | Leu | Gln | Ile | Pro | Ile | Phe |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Glu | Lys | Gly | Tyr | Glu | Lys | Asp | Pro | Ala | Val | Val | Ala | Lys | Glu | Ala | Ile |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gln | Glu | Ala | Thr | Arg | Asn | Gly | Ser | Asp | Val | Val | Leu | Val | Asp | Thr | Ala |
|     |     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Gly | Arg | Met | Gln | Asp | Asn | Glu | Pro | Leu | Met | Arg | Ala | Leu | Ser | Lys | Leu |
|     |     |     | 225 |     |     |     | 230 |     |     |     | 235 |     |     |     | 240 |
| Ile | Asn | Leu | Asn | Gln | Pro | Asp | Leu | Val | Leu | Phe | Val | Gly | Glu | Ala | Leu |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Val | Gly | Asn | Asp | Ala | Val | Asp | Gln | Leu | Ser | Lys | Phe | Asn | Gln | Lys | Leu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ser | Asp | Leu | Ser | Thr | Ser | Gly | Asn | Pro | Arg | Leu | Ile | Asp | Gly | Ile | Leu |
|     |     |     | 275 |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Leu | Thr | Lys | Phe | Asp | Thr | Ile | Asp | Asp | Lys | Val | Gly | Ala | Ala | Leu | Ser |
|     |     |     | 290 |     |     |     | 295 |     |     |     | 300 |     |     |     |     |
| Met | Val | Tyr | Ile | Ser | Gly | Ser | Pro | Val | Met | Phe | Val | Gly | Cys | Gly | Gln |
|     |     |     | 305 |     |     | 310 |     |     |     | 315 |     |     |     |     | 320 |
| Ser | Tyr | Thr | Asp | Leu | Lys | Lys | Leu | Asn | Val | Lys | Ala | Ile | Val | Lys | Thr |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |     |
| Leu | Leu | Lys |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:933:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 338 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..338

(D) OTHER INFORMATION: / Ceres Seq. ID 1499223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:933:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Lys | Glu | Glu | Val | Phe | Ser | Ser | Asp | Ser | Glu | Ser | Glu | Asp | Asp |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Glu | Pro | Gly | Ser | Asp | Glu | Lys | Pro | Ala | Gln | Ala | Lys | Lys | Lys | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Trp | Phe | Ser | Ser | Val | Phe | Gln | Ser | Ile | Thr | Gly | Lys | Ala | Asn | Leu | Glu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Thr | Asp | Leu | Gly | Pro | Ala | Leu | Lys | Ala | Leu | Lys | Glu | Arg | Leu | Met |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Thr | Lys | Asn | Val | Ala | Glu | Glu | Ile | Ala | Glu | Lys | Leu | Cys | Glu | Ser | Val |
|     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Glu | Ala | Ser | Leu | Glu | Gly | Lys | Lys | Leu | Ser | Ser | Phe | Thr | Arg | Ile | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Thr | Val | Gln | Ala | Ala | Met | Glu | Asp | Ala | Leu | Val | Arg | Ile | Leu | Thr |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Arg | Arg | Ser | Ile | Asp | Ile | Leu | Arg | Asp | Val | His | Ala | Ala | Lys | Glu |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Gln | Arg | Lys | Pro | Tyr | Val | Val | Val | Phe | Val | Gly | Val | Asn | Gly | Val | Gly |
|     |     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Lys | Ser | Thr | Asn | Leu | Ala | Lys | Val | Ala | Tyr | Trp | Leu | Gln | Gln | His | Lys |
|     |     |     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     | 160 |
| Val | Ser | Val | Met | Met | Ala | Ala | Cys | Asp | Thr | Phe | Arg | Ser | Gly | Ala | Val |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Glu | Gln | Leu | Arg | Thr | His | Ala | Arg | Arg | Leu | Gln | Ile | Pro | Ile | Phe | Glu |
|     |     |     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Lys | Gly | Tyr | Glu | Lys | Asp | Pro | Ala | Val | Val | Ala | Lys | Glu | Ala | Ile | Gln |
|     |     |     |     | 195 |     |     |     | 200 |     |     |     | 205 |     |     |     |
| Glu | Ala | Thr | Arg | Asn | Gly | Ser | Asp | Val | Val | Leu | Val | Asp | Thr | Ala | Gly |
|     |     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Arg | Met | Gln | Asp | Asn | Glu | Pro | Leu | Met | Arg | Ala | Leu | Ser | Lys | Leu | Ile |
|     |     |     |     | 225 |     |     | 230 |     |     | 235 |     |     |     | 240 |     |
| Asn | Leu | Asn | Gln | Pro | Asp | Leu | Val | Leu | Phe | Val | Gly | Glu | Ala | Leu | Val |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gly | Asn | Asp | Ala | Val | Asp | Gln | Leu | Ser | Lys | Phe | Asn | Gln | Lys | Leu | Ser |
|     |     |     |     | 260 |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Asp | Leu | Ser | Thr | Ser | Gly | Asn | Pro | Arg | Leu | Ile | Asp | Gly | Ile | Leu | Leu |
|     |     |     |     | 275 |     |     |     | 280 |     |     |     | 285 |     |     |     |
| Thr | Lys | Phe | Asp | Thr | Ile | Asp | Asp | Lys | Val | Gly | Ala | Ala | Leu | Ser | Met |
|     |     |     |     | 290 |     |     | 295 |     |     |     |     | 300 |     |     |     |
| Val | Tyr | Ile | Ser | Gly | Ser | Pro | Val | Met | Phe | Val | Gly | Cys | Gly | Gln | Ser |
|     |     |     |     | 305 |     |     |     | 310 |     |     | 315 |     |     |     | 320 |
| Tyr | Thr | Asp | Leu | Lys | Lys | Leu | Asn | Val | Lys | Ala | Ile | Val | Lys | Thr | Leu |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |

Leu Lys

(2) INFORMATION FOR SEQ ID NO:934:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..521
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:934:

|            |            |            |            |            |             |     |
|------------|------------|------------|------------|------------|-------------|-----|
| attgtgatga | atcatcatga | gcagtgactt | catacttgat | attacgggtg | agaggccact  | 60  |
| ataaaaagca | ggcgctctct | cgaagaagaa | gaagaagaag | taacaaattg | gtggaaatca  | 120 |
| gaagttgaat | oggagaataa | caacgatgac | gacgaacaag | caggtcatat | tcaaaagacca | 180 |
| cgtgagvgwr | ttccctaagg | aatccgattt | caatttcacc | accaccacgg | tcgaacttag  | 240 |

ggttccggaa ggttctaaaat cggttcttgt gaagaatctc tacctgtcat gcgatacctta 300  
tatgcggctc cgcattggga aacctgatcc ctctctgtct cttgctcaag cttacgctcc 360  
cggcaagcca atctatgggt atggagtgtc tagagtata gaatctgggc atccagatta 420  
caagaaaggt gatttacctt ggggaatagt tggatktgag gagtatatgt ttattacacc 480  
aatggctcac atgcatttca agatccaaca tacagatgtt c

(2) INFORMATION FOR SEQ ID NO:935:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1499225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:935:

Met Thr Thr Asn Lys Gln Val Ile Phe Lys Asp His Val Xaa Xaa Phe  
1 5 10 15  
Pro Lys Glu Ser Asp Phe Asn Phe Thr Thr Thr Thr Val Glu Leu Arg  
20 25 30  
Val Pro Glu Gly Ser Lys Ser Val Leu Val Lys Asn Leu Tyr Leu Ser  
35 40 45  
Cys Asp Pro Tyr Met Arg Ser Arg Met Gly Lys Pro Asp Pro Ser Ser  
50 55 60  
Ala Leu Ala Gln Ala Tyr Ala Pro Gly Lys Pro Ile Tyr Gly Tyr Gly  
65 70 75 80  
Val Ser Arg Val Ile Glu Ser Gly His Pro Asp Tyr Lys Lys Gly Asp  
85 90 95  
Leu Leu Trp Gly Ile Val Gly Xaa Glu Glu Tyr Ser Val Ile Thr Pro  
100 105 110  
Met Ala His Met His Phe Lys Ile Gln His Thr Asp Val  
115 120 125

(2) INFORMATION FOR SEQ ID NO:936:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..73

(D) OTHER INFORMATION: / Ceres Seq. ID 1499226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:936:

Met Arg Ser Arg Met Gly Lys Pro Asp Pro Ser Ser Ala Leu Ala Gln  
1 5 10 15  
Ala Tyr Ala Pro Gly Lys Pro Ile Tyr Gly Tyr Gly Val Ser Arg Val  
20 25 30  
Ile Glu Ser Gly His Pro Asp Tyr Lys Lys Gly Asp Leu Leu Trp Gly  
35 40 45  
Ile Val Gly Xaa Glu Glu Tyr Ser Val Ile Thr Pro Met Ala His Met  
50 55 60  
His Phe Lys Ile Gln His Thr Asp Val  
65 70

(2) INFORMATION FOR SEQ ID NO:937:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..69  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1499227  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:937:  
Met Gly Lys Pro Asp Pro Ser Ser Ala Leu Ala Gln Ala Tyr Ala Pro  
1                  5                  10                  15  
Gly Lys Pro Ile Tyr Gly Tyr Gly Val Ser Arg Val Ile Glu Ser Gly  
                  20                  25                  30  
His Pro Asp Tyr Lys Lys Gly Asp Leu Leu Trp Gly Ile Val Gly Xaa  
                  35                  40                  45  
Glu Glu Tyr Ser Val Ile Thr Pro Met Ala His Met His Phe Lys Ile  
                  50                  55                  60  
Gln His Thr Asp Val  
65

(2) INFORMATION FOR SEQ ID NO:938:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 1721 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..1721  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:938:

aaaaaatcca gccatcgccct cgaagaaaaa acctcccaaa tctgagaaat cggaaaagat 60  
gaccacacc gaacacctaa atctgctcga tgaatcgag tctctgtct ccgatacgct 120  
tcaagtggta tcttacaat ggcctgagtcg aaatttctcg ctttcatcaa atactgcca 180  
gaggttgctc aaggatttta tagagaaaca tgggaagggt ttggaagttg tatataattg 240  
gtccggatgt ctaagaacg gaccttcgca ttaccacgca aggccttgct ctagtaccga 300  
acttccagaa gttagaaga agttcaatgg aaaaatttca gtacatatct acagtggtta 360  
agctagtatt ccaatggatc cagcagccat atggaaacat gagttgttac aagcagaaga 420  
actcttcagg cagccttctg ccaactgataa ttgtttgaaa ggcaacagtt ttgttggegt 480  
ctccaattct tgtgtgaagc gcaatataga gggagccat gaaaaagtta ccgccccgcg 540  
aactgaaagt gtgagaacta caggacaatc taaaagttag tcaaattttc aaaatagtag 600  
agtgccgtca aaccagggaa agaattttcca gcactcaagc tctaattgtg gccatcaggc 660  
taagagtga tctattgtcg ctccagctaa aaatcggtct gcgaaatcct ctttggtataa 720  
agaaaaagct ttctatgtcg ccgctaataa aaagaatgga cagggcgaga agagcgtgat 780  
tggaactggt ggtttgttga aaaatatgtg gggccgtgtg cctgtgaaaa cagaagatga 840  
ttctccaaca gtatagtgta aaaaatcatat tactaatcat tcggaacccc aaaaacttct 900  
tcatgatgct gacaagaagg gaggcagcga tgatgagact cgagacgcga atttcatgat 960  
agcgctctaa gataacagaa aaagaaagggt gatatttgat ttttcagatg acgagtatga 1020  
agatgtaatc agcttagcat ctcatagtag tccaaagggtt aattcacgtc cagatgtcga 1080  
actcagttcg gaagattcag gtccagagaa cctgacgcga gatgtttctc cagagaataa 1140  
atctgaggaa ccagaggcca gcaaagaaga caggcaaac actgctctct ttgatgcttc 1200  
tacgactttg tcaacggaga agatccagcg cattggttct gaagctgaag tgaatccctc 1260  
aaagagaaga actactgcag ttctagtct gccgaaaagg aaaaaggtgt tgaagtcaag 1320  
gattgatgat cgtgggagag aagtaactga ggtagtgtg gaggagacag aaacgaacgc 1380  
aaagagaaga gaggcacta atacaagtaa gaagttagat ttggtgcaaa ccgcaaatgc 1440  
tgtaacagg gcggttgca cagaagaagg tccggccatt ggaacacag cagcgacaaa 1500  
cgcagagga aaagcgggaa gcaagaaagg aggaacgctc aaagatccaa agcaagggaa 1560  
tataatgtcc ttcttcaaga aagtttaaaa aggcctcttt ttgtatatta ttgtttgcta 1620  
agtttgagtt gaggatatta taggaaatc agaacttggaa tctcatctgc tgatgtttct 1680  
gatccattgt gtctaagaaa aaaacttttg agccgtttct c

(2) INFORMATION FOR SEQ ID NO:939:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 528 amino acids  
    (B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..528  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1499229  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:939:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Asn | Ser | Ala | Ile | Ala | Ser | Lys | Lys | Lys | Pro | Pro | Lys | Ser | Glu | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Glu | Lys | Met | Thr | His | Thr | Glu | Thr | Leu | Asn | Leu | Leu | Asp | Glu | Ile |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Glu | Ser | Leu | Val | Ser | Asp | Gln | Leu | Gln | Val | Val | Ser | Tyr | Lys | Trp | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Arg | Asn | Phe | Ser | Leu | Ser | Ser | Asn | Thr | Ala | Lys | Arg | Leu | Leu | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Phe | Ile | Glu | Lys | His | Gly | Lys | Gly | Leu | Glu | Val | Val | Tyr | Ile | Val |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Gly | Leu | Leu | Lys | Asn | Gly | Pro | Ser | Asp | Tyr | His | Ala | Arg | Leu | Ala |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Ser | Ser | Thr | Glu | Leu | Pro | Glu | Val | Glu | Lys | Glu | Phe | Asn | Gly | Lys | Tyr |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Val | His | Ile | Tyr | Ser | Val | Gln | Ala | Ser | Ile | Pro | Met | Asp | Pro | Ala |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Ile | Trp | Asn | Thr | Glu | Phe | Val | Gln | Ala | Glu | Glu | Leu | Phe | Arg | Gln |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Pro | Ser | Ala | Thr | Asp | Asn | Cys | Leu | Lys | Gly | Asn | Ser | Phe | Cys | Gly | Val |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Ser | Asn | Ser | Cys | Val | Lys | Arg | Asn | Ile | Glu | Gly | Ala | Thr | Glu | Asn | Val |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Thr | Ala | Pro | Arg | Thr | Glu | Ser | Val | Arg | Thr | Thr | Gly | Gln | Ser | Lys | Ser |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Ser | Asn | Phe | Gln | Asn | Ser | Thr | Val | Pro | Ser | Asn | Gln | Gly | Lys | Asn |
|     | 195 |     |     |     |     |     |     | 200 |     |     |     | 205 |     |     |     |
| Phe | Gln | His | Ser | Ser | Ser | Asn | Val | Gly | His | Gln | Ala | Lys | Ser | Glu | Ser |
|     | 210 |     |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |
| Ile | Ala | Ala | Pro | Ala | Lys | Asn | Arg | Ser | Ala | Lys | Ser | Ser | Leu | Asp | Lys |
|     | 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     | 240 |     |
| Glu | Lys | Ala | Phe | His | Val | Pro | Ala | Asn | Lys | Lys | Asn | Gly | Gln | Gly | Glu |
|     |     |     | 245 |     |     |     |     |     |     | 250 |     |     |     | 255 |     |
| Lys | Ser | Val | Thr | Gly | Thr | Gly | Gly | Leu | Leu | Lys | Asn | Met | Trp | Gly | Arg |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Val | Pro | Val | Lys | Thr | Glu | Asp | Asp | Ser | Pro | Thr | Val | Asp | Val | Lys | Asn |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| His | Ile | Thr | Asn | His | Ser | Glu | Pro | Gln | Lys | Pro | Ser | His | Asp | Ala | Asp |
|     | 290 |     |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |
| Lys | Lys | Gly | Gly | Ser | Asp | Asp | Glu | Thr | Arg | Asp | Ala | Asn | Phe | Met | Arg |
|     | 305 |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |
| Ala | Pro | Lys | Asp | Asn | Arg | Lys | Arg | Lys | Val | Ile | Phe | Asp | Phe | Ser | Asp |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Asp | Glu | Tyr | Glu | Asp | Val | Ile | Ser | Leu | Ala | Ser | His | Ser | Ser | Pro | Lys |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Val | Asn | Ser | Arg | Pro | Asp | Val | Glu | Leu | Ser | Ser | Glu | Asp | Ser | Gly | Pro |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Glu | Lys | Pro | Asp | Ala | Asp | Val | Ser | Pro | Glu | Ile | Lys | Ser | Glu | Glu | Pro |
|     | 370 |     |     |     |     | 375 |     |     |     |     |     | 380 |     |     |     |
| Glu | Ala | Ser | Lys | Glu | Asp | Arg | Gln | Asn | Thr | Ala | Ser | Val | Asp | Ala | Ser |
|     | 385 |     |     |     |     | 390 |     |     |     | 395 |     |     |     | 400 |     |
| Thr | Thr | Leu | Ser | Thr | Glu | Lys | Ile | Gln | Ala | Ile | Gly | Ser | Glu | Ala | Glu |
|     |     |     |     |     | 405 |     |     |     | 410 |     |     |     |     | 415 |     |
| Val | Asn | Pro | Ser | Lys | Arg | Arg | Thr | Thr | Ala | Val | Pro | Ser | Ser | Pro | Lys |

| (X1) SEQUENCE DESCRIPTION |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|---------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met                       | Thr | His | Thr | Glu | Thr | Leu | Asn | Leu | Leu | Asp | Glu | Ile | Glu | Ser | Leu |
| 1                         |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Val                       | Ser | Asp | Gln | Leu | Gln | Val | Val | Ser | Tyr | Lys | Trp | Leu | Ser | Arg | Asn |
|                           |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe                       | Ser | Leu | Ser | Ser | Asn | Thr | Ala | Lys | Arg | Leu | Leu | Lys | Asp | Phe | Ile |
|                           |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu                       | Lys | His | Gly | Lys | Gly | Leu | Glu | Val | Val | Tyr | Ile | Val | Ser | Gly | Leu |
|                           |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu                       | Lys | Asn | Gly | Pro | Ser | Asp | Tyr | His | Ala | Arg | Leu | Ala | Ser | Ser | Thr |
| 65                        |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| Glu                       | Leu | Pro | Glu | Val | Glu | Lys | Glu | Phe | Asn | Gly | Lys | Tyr | Ser | Val | His |
|                           |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile                       | Tyr | Ser | Val | Gln | Ala | Ser | Ile | Pro | Met | Asp | Pro | Ala | Ala | Ile | Trp |
|                           |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn                       | Thr | Glu | Phe | Val | Gln | Ala | Glu | Glu | Leu | Phe | Arg | Gln | Pro | Ser | Ala |
|                           |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr                       | Asp | Asn | Cys | Leu | Lys | Gly | Asn | Ser | Phe | Cys | Gly | Val | Ser | Asn | Ser |
|                           |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Cys                       | Val | Lys | Arg | Asn | Ile | Glu | Gly | Ala | Thr | Glu | Asn | Val | Thr | Ala | Pro |
| 145                       |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Arg                       | Thr | Glu | Ser | Val | Arg | Thr | Thr | Gly | Gln | Ser | Lys | Ser | Ser | Ser | Asn |
|                           |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Phe                       | Gln | Asn | Ser | Thr | Val | Pro | Ser | Asn | Gln | Gly | Lys | Asn | Phe | Gln | His |
|                           |     |     |     | 180 |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser                       | Ser | Ser | Asn | Val | Gly | His | Gln | Ala | Lys | Ser | Glu | Ser | Ile | Ala | Ala |
|                           |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Pro                       | Ala | Lys | Asn | Arg | Ser | Ala | Lys | Ser | Ser | Leu | Asp | Lys | Glu | Lys | Ala |
|                           |     |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Phe                       | His | Val | Pro | Ala | Asn | Lys | Lys | Asn | Gly | Gln | Gly | Glu | Lys | Ser | Val |
| 225                       |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     | 240 |
| Thr                       | Gly | Thr | Gly | Gly | Leu | Leu | Lys | Asn | Met | Trp | Gly | Arg | Val | Pro | Val |
|                           |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Lys                       | Thr | Glu | Asp | Asp | Ser | Pro | Thr | Val | Asp | Val | Lys | Asn | His | Ile | Thr |
|                           |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |

Asn His Ser Glu Pro Gln Lys Pro Ser His Asp Ala Asp Lys Lys Gly  
275 280 285  
Gly Ser Asp Asp Glu Thr Arg Asp Ala Asn Phe Met Arg Ala Pro Lys  
290 295 300  
Asp Asn Arg Lys Arg Lys Val Ile Phe Asp Phe Ser Asp Asp Glu Tyr  
305 310 315 320  
Glu Asp Val Ile Ser Leu Ala Ser His Ser Ser Pro Lys Val Asn Ser  
325 330 335  
Arg Pro Asp Val Glu Leu Ser Ser Glu Asp Ser Gly Pro Glu Lys Pro  
340 345 350  
Asp Ala Asp Val Ser Pro Glu Ile Lys Ser Glu Glu Pro Glu Ala Ser  
355 360 365  
Lys Glu Asp Arg Gln Asn Thr Ala Ser Val Asp Ala Ser Thr Thr Leu  
370 375 380  
Ser Thr Glu Lys Ile Gln Ala Ile Gly Ser Glu Ala Glu Val Asn Pro  
385 390 395 400  
Ser Lys Arg Arg Thr Thr Ala Val Pro Ser Ser Pro Lys Arg Lys Lys  
405 410 415  
Val Leu Lys Ser Arg Ile Asp Asp Arg Gly Arg Glu Val Thr Glu Val  
420 425 430  
Val Trp Glu Glu Thr Glu Thr Asn Ala Lys Lys Lys Glu Asp Thr Asn  
435 440 445  
Thr Ser Lys Lys Leu Asp Asp Gly Lys Thr Ala Asn Ala Val Asn Arg  
450 455 460  
Ala Val Ala Gln Lys Lys Ser Pro Ala Ile Gly Asn Thr Ala Ala Thr  
465 470 475 480  
Asn Ala Gly Gly Lys Ala Gly Ser Lys Lys Gly Gly Asn Val Lys Asp  
485 490 495  
Pro Lys Gln Gly Asn Ile Met Ser Phe Phe Lys Lys Val  
500 505

(2) INFORMATION FOR SEQ ID NO:941:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..404
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:941:

Met Asp Pro Ala Ala Ile Trp Asn Thr Glu Phe Val Gln Ala Glu Glu  
1 5 10 15  
Leu Phe Arg Gln Pro Ser Ala Thr Asp Asn Cys Leu Lys Gly Asn Ser  
20 25 30  
Phe Cys Gly Val Ser Asn Ser Cys Val Lys Arg Asn Ile Glu Gly Ala  
35 40 45  
Thr Glu Asn Val Thr Ala Pro Arg Thr Glu Ser Val Arg Thr Thr Gly  
50 55 60  
Gln Ser Lys Ser Ser Ser Asn Phe Gln Asn Ser Thr Val Pro Ser Asn  
65 70 75 80  
Gln Gly Lys Asn Phe Gln His Ser Ser Ser Asn Val Gly His Gln Ala  
85 90 95  
Lys Ser Glu Ser Ile Ala Ala Pro Ala Lys Asn Arg Ser Ala Lys Ser  
100 105 110  
Ser Leu Asp Lys Glu Lys Ala Phe His Val Pro Ala Asn Lys Lys Asn  
115 120 125  
Gly Gln Gly Glu Lys Ser Val Thr Gly Thr Gly Gly Leu Leu Lys Asn  
130 135 140  
Met Trp Gly Arg Val Pro Val Lys Thr Glu Asp Asp Ser Pro Thr Val

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| 145                                                             | 150 | 155 | 160 |
| Asp Val Lys Asn His Ile Thr Asn His Ser Glu Pro Gln Lys Pro Ser |     |     |     |
|                                                                 | 165 | 170 | 175 |
| His Asp Ala Asp Lys Lys Gly Gly Ser Asp Asp Glu Thr Arg Asp Ala |     |     |     |
|                                                                 | 180 | 185 | 190 |
| Asn Phe Met Arg Ala Pro Lys Asp Asn Arg Lys Arg Lys Val Ile Phe |     |     |     |
|                                                                 | 195 | 200 | 205 |
| Asp Phe Ser Asp Asp Glu Tyr Glu Asp Val Ile Ser Leu Ala Ser His |     |     |     |
|                                                                 | 210 | 215 | 220 |
| Ser Ser Pro Lys Val Asn Ser Arg Pro Asp Val Glu Leu Ser Ser Glu |     |     |     |
|                                                                 | 225 | 230 | 235 |
| Asp Ser Gly Pro Glu Lys Pro Asp Ala Asp Val Ser Pro Glu Ile Lys |     |     |     |
|                                                                 | 245 | 250 | 255 |
| Ser Glu Glu Pro Glu Ala Ser Lys Glu Asp Arg Gln Asn Thr Ala Ser |     |     |     |
|                                                                 | 260 | 265 | 270 |
| Val Asp Ala Ser Thr Thr Leu Ser Thr Glu Lys Ile Gln Ala Ile Gly |     |     |     |
|                                                                 | 275 | 280 | 285 |
| Ser Glu Ala Glu Val Asn Pro Ser Lys Arg Arg Thr Thr Ala Val Pro |     |     |     |
|                                                                 | 290 | 295 | 300 |
| Ser Ser Pro Lys Arg Lys Lys Val Leu Lys Ser Arg Ile Asp Asp Arg |     |     |     |
|                                                                 | 305 | 310 | 315 |
| Gly Arg Glu Val Thr Glu Val Val Trp Glu Glu Thr Glu Thr Asn Ala |     |     |     |
|                                                                 | 325 | 330 | 335 |
| Lys Lys Lys Glu Asp Thr Asn Thr Ser Lys Lys Leu Asp Asp Gly Lys |     |     |     |
|                                                                 | 340 | 345 | 350 |
| Thr Ala Asn Ala Val Asn Arg Ala Val Ala Gln Lys Lys Ser Pro Ala |     |     |     |
|                                                                 | 355 | 360 | 365 |
| Ile Gly Asn Thr Ala Ala Thr Asn Ala Gly Gly Lys Ala Gly Ser Lys |     |     |     |
|                                                                 | 370 | 375 | 380 |
| Lys Gly Gly Asn Val Lys Asp Pro Lys Gln Gly Asn Ile Met Ser Phe |     |     |     |
|                                                                 | 385 | 390 | 395 |
| Phe Lys Lys Val                                                 |     |     | 400 |

(2) INFORMATION FOR SEQ ID NO:942:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 779 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..779

(D) OTHER INFORMATION: / Ceres Seq. ID 1499232

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:942:

|             |            |            |             |             |            |     |
|-------------|------------|------------|-------------|-------------|------------|-----|
| atttctgttc  | atttcacott | tactaaaaag | agaactcaca  | tcaagaanaac | agtccatcat | 60  |
| tcacatgato  | tagatgagca | tcattactaa | ttatcttgta  | acgaatgato  | actaatgttt | 120 |
| ttgactatct  | tatgcagctc | tagtggcact | cctaccacag  | gaacaccaac  | tagtgggaca | 180 |
| ccaaccagt   | ggaccccgac | taccggaact | ccgaccaccg  | gaacccccac  | caotggaact | 240 |
| ccaaccagt   | ggactccaac | tagtggcttc | ccaaataccg  | ggactccgaa  | caacgggact | 300 |
| aaactatgga  | tgccaaattc | caacggggat | ccaacttcac  | cgctcatctc  | gggtgtcccg | 360 |
| gggactactc  | ttggacgcac | tggtagcggg | ggactaggcg  | atccaaatgc  | tgagagaga  | 420 |
| ctgtctgttc  | gaactaacac | attgtctctc | ttattaaccg  | gtgtagcagc  | aatgcttgtc | 480 |
| atatgagggc  | tttagtgctc | caacgggtta | tgggttgta   | tggtgttgct  | gagagatcat | 540 |
| atcttgccta  | cggtctatgg | ttgatagagc | catctttttt  | tcactcgtct  | ttctagagtt | 600 |
| tggaacttag  | ttggccgaga | gacataatgc | tggttagtagc | tagtattttg  | ggttatgtac | 660 |
| aaactttaact | aagagcttta | ctttttagaa | tcgggaggat  | gagatgctct  | ttgtttctct | 720 |
| atattctttt  | taatcctttt | actttgatct | ttcatctttt  | aatacgtacc  | atcattgtc  |     |

(2) INFORMATION FOR SEQ ID NO:943:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..123  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499233  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:943:  
Met Phe Leu Thr Ile Leu Cys Ser Ser Gly Thr Pro Thr Thr Gly  
1 5 10 15  
Thr Pro Thr Ser Gly Thr Pro Thr Ser Gly Thr Pro Thr Thr Gly Thr  
20 25 30  
Pro Thr Thr Gly Thr Pro Thr Thr Gly Thr Pro Thr Ser Gly Thr Pro  
35 40 45  
Thr Ser Gly Phe Pro Asn Thr Gly Thr Pro Asn Thr Gly Thr Asn Thr  
50 55 60  
Gly Met Pro Asn Ser Asn Gly Met Pro Thr Ser Ser Ser Ser Val  
65 70 75 80  
Phe Pro Gly Thr Thr Leu Gly Pro Thr Gly Ser Gly Gly Leu Gly Asp  
85 90 95  
Pro Asn Ala Gly Glu Lys Leu Ser Val Arg Thr Asn Thr Leu Val Phe  
100 105 110  
Leu Leu Thr Gly Val Ala Ala Met Leu Val Ile  
115 120

(2) INFORMATION FOR SEQ ID NO:944:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1412 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..1412

(D) OTHER INFORMATION: / Ceres Seq. ID 1499242

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:944:

|            |            |             |            |            |             |      |
|------------|------------|-------------|------------|------------|-------------|------|
| actccgagcg | tttctttct  | cacaagccaa  | tggcgcaatt | tactaatcc  | atcaattatc  | 60   |
| tctttctgt  | tctctctta  | ttattgtat   | cgttccactg | cttatgttt  | ctgttttcat  | 120  |
| tggttgacg  | ttgttcaaac | tccaccgacg  | accaacagat | tcaaacacat | caccacccga  | 180  |
| aatgggttg  | tcctccagcg | cacaaagtca  | tcaccgtctc | acttaacggc | cacgctcagt  | 240  |
| tctgctccg  | ccaagacgct | gtggattcca  | taccaaaagv | caataacaa  | agcatcacaa  | 300  |
| tcaagattg  | tcccggattt | tacagagaga  | aagtgggtgt | tccagctaca | aaacccgtaca | 360  |
| taaacgttc  | aaggagctcg | tagggatgtg  | accgctatag | agtggcacga | ccgtgcgtcc  | 420  |
| gaccttggt  | ctaaccgtca | acagttacgt  | acctatcaaa | ccgcttcgt  | caccgtctac  | 480  |
| gctaattatt | acccgctag  | aaacattagc  | ttcacggtac | tctattcaat | tctaacgcaa  | 540  |
| ttatatata  | agggaaactt | tcacaaaaat  | gcgagtcctt | ctttatttta | ttttaaattg  | 600  |
| tgaagaatac | tgcgcccgtt | ccattgccgg  | ggatgcaagg | gtggcgaagg | gtggcggtta  | 660  |
| ggatctccgg | cgacaaagct | ttcttttccg  | gctgcgggtt | ttacgggtga | caagacacct  | 720  |
| tatgcagaca | tgtctgccgt | cattacttca  | aggagtgtta | cattgaaggc | tctatcgact  | 780  |
| ttatcttttg | taatggcccg | tccatgtata  | aagattgtga | gttgattcgc | atagcgtcaa  | 840  |
| gattcgggtg | gatagcgcg  | catggtagga  | catgcccggg | agagaaaacg | ggtttcgcgt  | 900  |
| tctgtgggtg | tccggtaaca | ggtaggggtc  | cattgtacgt | gggcccggcc | atgggaccaa  | 960  |
| tactcaegta | tctgtttacg | ctacacttac  | tttgatgctc | tcgtcgctca | cggtgggttg  | 1020 |
| gacgattggg | accacaaatc | caacaaaagc  | aagacggcat | ttttcggagt | gtacaattgc  | 1080 |
| tatgggccag | gagcagcagc | gacgagagcg  | gtgtcttggt | ctagagcttt | ggacatagaa  | 1140 |
| tccggccatc | caattatcgc | ttaagagcttc | gttaatggga | gacattggat | gcctcctgca  | 1200 |
| gatgcttaac | caacttcaaa | ccttggccgg  | gtttcttttc | ctaatctctc | gggttctccc  | 1260 |
| agtcccaagt | cctaaaagct | tactatattt  | ttatcattgt | ttttattctt | ttattgttta  | 1320 |
| ttttttccaa | ttttattata | cattgtgtga  | tagtacaaca | aagtattgct | tctttctcat  | 1380 |
| ctgtatccat | ttcagttaaa | tgttttgagc  | tt         |            |             |      |

(2) INFORMATION FOR SEQ ID NO:945:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..126
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:945:

Ser Glu Arg Phe Leu Ser His Lys Pro Met Ala Gln Phe Thr Asn Ser  
1 5 10 15  
Ile Asn Tyr Leu Phe Ser Val Ser Leu Leu Phe Val Ser Phe His  
20 25 30  
Cys Leu Cys Phe Arg Phe Ser Leu Val Ala Ala Cys Ser Asn Ser Thr  
35 40 45  
Asp Asp Gln Gln Ile Gln His His His Arg Lys Trp Val Gly Pro  
50 55 60  
Ser Gly His Lys Val Ile Thr Val Ser Leu Asn Gly His Ala Gln Phe  
65 70 75 80  
Arg Ser Val Gln Asp Ala Val Asp Ser Ile Pro Lys Xaa Asn Asn Lys  
85 90 95  
Ser Ile Thr Ile Lys Ile Ala Pro Gly Phe Tyr Arg Glu Lys Val Val  
100 105 110  
Val Pro Ala Thr Lys Pro Tyr Ile Asn Val Gln Arg Ser Trp  
115 120 125

(2) INFORMATION FOR SEQ ID NO:946:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499244

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:946:

Met Pro Gly Arg Glu Asn Gly Phe Arg Val Arg Gly Leu Ser Gly Asn  
1 5 10 15  
Arg Tyr Gly Ser Ile Val Arg Gly Pro Gly His Gly Thr Asn Thr His  
20 25 30  
Val Ser Phe Thr Pro Thr Leu Thr Leu Met Leu Ser Ser Leu Thr Val  
35 40 45  
Val Gly Thr Ile Gly Thr Thr Asn Pro Thr Lys Ala Arg Arg His Phe  
50 55 60  
Ser Glu Cys Thr Ile Ala Met Gly Gln Glu Gln Arg Arg Glu Ala  
65 70 75 80  
Cys Leu Gly Leu Glu Leu Trp Thr Met Asn Arg Pro Ile His Leu Ser  
85 90 95  
Leu Arg Ala Ser Leu Met Gly Asp Ile Gly Ser Leu Leu Glu Met Leu  
100 105 110  
Asn Gln Leu Gln Thr Leu Ala Gly Phe Leu Phe Leu Ile Pro Arg Phe  
115 120 125  
Leu Pro Val Pro Ser Pro Lys Ser Leu Leu Tyr Phe Tyr His Ser Phe  
130 135 140  
Ile Ser Phe Ile Val Tyr Phe Phe Gln Phe Ile Tyr Thr Leu Cys Asp  
145 150 155 160  
Ser Thr Thr Lys Tyr Cys Phe Phe Phe Ile Cys Ile His Phe Ser

165 170 175

(2) INFORMATION FOR SEQ ID NO:947:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 134 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..134  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499245  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:947:  
Met Leu Ser Ser Leu Thr Val Val Gly Thr Ile Gly Thr Thr Asn Pro  
1 5 10 15  
Thr Lys Ala Arg Arg His Phe Ser Gly Cys Thr Ile Ala Met Gly Gln  
20 25 30  
Glu Gln Gln Arg Arg Glu Ala Cys Leu Gly Leu Glu Leu Trp Thr Met  
35 40 45  
Asn Arg Pro Ile His Leu Ser Leu Arg Ala Ser Leu Met Gly Asp Ile  
50 55 60  
Gly Ser Leu Leu Glu Met Leu Asn Gln Leu Gln Thr Leu Ala Gly Phe  
65 70 75 80  
Leu Phe Leu Ile Pro Arg Phe Leu Pro Val Pro Ser Pro Lys Ser Leu  
85 90 95  
Leu Tyr Phe Tyr His Ser Phe Ile Ser Phe Ile Val Tyr Phe Phe Gln  
100 105 110  
Phe Ile Tyr Thr Leu Cys Asp Ser Thr Thr Lys Tyr Cys Phe Phe Phe  
115 120 125  
Ile Cys Ile His Phe Ser  
130

(2) INFORMATION FOR SEQ ID NO:948:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1894 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1894  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499250  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:948:  
aacaccgtga cagctcctta gatctctcct cggttacttc ctttttaatt tccatgggtc 60  
tctaaaaatc tctctctctt tctctctctt ttacttgat tggttacgac tctgtctgaa 120  
gattatggac ggcgcggatg gaaccggttc cgtaagcctt ggtcgcggat tctgaacgga 180  
gacggatggt gcggtttcgt cgccagtgac acgtcagaaa gctgctgcag ctaagcaatt 240  
catcgagaat cattataaga attacttgca agccttgac gaacgaatgg agagacgcag 300  
ggagtctcag aggaagaatgc aagaagctca gttacctgtt gaggaacaag acgagatgat 360  
gaggaatctg gctcgtcgtg aaactgagta tatgagactt cagagacgta aaattgggat 420  
tgatgatttt gagcttttga ccgttatttg caaagggtcc ttgtgtgagg ttagattatg 480  
tcgtttgaga tctacatctg aagtttatgc catgaagaaa ttgaaaaaaa ctgagatgct 540  
tagccgtgga caggtagagc atgtcaggct cgagaggaaac ttacttgcag aagttgacag 600  
cggttaacat gtaaaagctt ttactctctt tcaagattct gaagtgttgt atcttatcat 660  
ggagattatta cctggggggt acatcatgac actactcatg agagaagaca ttctttctga 720  
agatgttgcc cgtttttata ttgctgagag actactcatg atccattcaa ttcatcaaca 780  
caactatggt cacagggaca tcaaacctga taatttgata ctgacaaaaa gtgggcattt 840  
gaagctttca gattttgggt tatgtaagcc acttgatgac aagtattctt cattgtcttt 900  
agaagacgat gaaattgttg ctacggattc agagaaccag tcagaaaaat cacagcgtga 960  
caaagcacc tggcaaatgc ctaagagaca gttactgcag tggaaacgca atcgccgtgc 1020  
attggcttat tcaaccgttg gaactcttga ttacatggct ccagaagtac tctaaagaa 1080



|            |            |            |            |             |             |      |
|------------|------------|------------|------------|-------------|-------------|------|
| aggatatgga | atggaatgtg | attggtgtgc | tctcggcgca | attttgtatg  | agatgttagt  | 1140 |
| tgggtatccc | ccattctgtt | ctgatgacc  | ccgtataaca | tgccggaaga  | taattaattg  | 1200 |
| gagggtatgc | ttgaagttcc | ctgaacaacc | aaaaatatca | gatgaagcca  | gagacttgat  | 1260 |
| ttgtcgggtg | ctttgtgatg | ttgattcaag | gttgggaacc | agaggtgtgt  | aggagataaa  | 1320 |
| gtcgcatcca | tggttcaaa  | gcaccccatg | ggacaaactg | tatgacatgg  | aggcagctta  | 1380 |
| tagaccattt | gtcgatggag | aactagacac | acaaaatttt | gagaagtttc  | ctgaagtgtga | 1440 |
| aggatcacca | tccgaagcac | cacaagttgg | tccttgga   | aagatgttga  | cgctcaagga  | 1500 |
| caccaacttc | ataggattta | catttaagaa | gtcagacatc | acaagatcaa  | tggaagtttc  | 1560 |
| aggtgcagac | atgaaatcaa | atggatcagg | ggaagccccc | tcgttgatat  | cattgttagg  | 1620 |
| tcgatcaaat | atggaagaag | gtgaaggtgg | tgagttaaac | cacaagacat  | agggaataa   | 1680 |
| caaatattat | tgattttttt | tccgcttgca | gtttgtttga | tcatttgcca  | gaggcaattg  | 1740 |
| agagggcgtg | gtagtttttt | aaccacatca | cttatgatgg | gggttcataaa | aacttctatt  | 1800 |
| tccttttttt | ttctttgta  | atatttgttt | ttttttcaat | ctaaaaaaga  | aactgtaaa   | 1860 |
| catggaagaa | taatttctgg | aactttttac | cccc       |             |             |      |

(2) INFORMATION FOR SEQ ID NO:949:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..515
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:949:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Gly | Ala | Asp | Gly | Thr | Val | Arg | Val | Lys | Pro | Gly | Arg | Gly | Phe |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Thr | Glu | Thr | Asp | Val | Ala | Val | Ser | Ser | Pro | Val | Thr | Arg | Gln | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Ala | Ala | Ala | Lys | Gln | Phe | Ile | Glu | Asn | His | Tyr | Lys | Asn | Tyr | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Gly | Leu | His | Glu | Arg | Met | Glu | Arg | Arg | Arg | Glu | Phe | Gln | Arg | Lys |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Val | Gln | Glu | Ala | Gln | Leu | Pro | Val | Glu | Glu | Gln | Asp | Glu | Met | Met | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Asn | Leu | Ala | Arg | Arg | Glu | Thr | Glu | Tyr | Met | Arg | Leu | Gln | Arg | Arg | Lys |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Ile | Gly | Ile | Asp | Asp | Phe | Glu | Leu | Leu | Thr | Val | Ile | Gly | Lys | Gly | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Gly | Glu | Val | Arg | Leu | Cys | Arg | Leu | Arg | Ser | Thr | Ser | Glu | Val | Tyr |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Met | Lys | Lys | Leu | Lys | Lys | Thr | Glu | Met | Leu | Ser | Arg | Gly | Gln | Val |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Glu | His | Val | Arg | Ser | Glu | Arg | Asn | Leu | Leu | Ala | Glu | Val | Asp | Ser | Arg |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Tyr | Ile | Val | Lys | Leu | Phe | Tyr | Ser | Phe | Gln | Asp | Ser | Glu | Cys | Leu | Tyr |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Leu | Ile | Met | Glu | Tyr | Leu | Pro | Gly | Gly | Asp | Ile | Met | Thr | Leu | Leu | Met |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Arg | Glu | Asp | Ile | Leu | Ser | Glu | Asp | Val | Ala | Arg | Phe | Tyr | Ile | Ala | Glu |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ser | Ile | Leu | Ala | Ile | His | Ser | Ile | His | Gln | His | Asn | Tyr | Val | His | Arg |
|     |     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Asp | Ile | Lys | Pro | Asp | Asn | Leu | Ile | Leu | Asp | Lys | Ser | Gly | His | Leu | Lys |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Leu | Ser | Asp | Phe | Gly | Leu | Cys | Lys | Pro | Leu | Asp | Asp | Lys | Tyr | Ser | Ser |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     | 255 |     |     |
| Leu | Leu | Leu | Glu | Asp | Asp | Glu | Met | Leu | Ser | Gln | Asp | Ser | Glu | Asn | Gln |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Ser | Gly | Lys | Ser | Asp | Ala | Asp | Lys | Ala | Pro | Trp | Gln | Met | Pro | Lys | Glu |

|                             |                                     |     |  |  |  |
|-----------------------------|-------------------------------------|-----|--|--|--|
| 275                         | 280                                 | 285 |  |  |  |
| Gln Leu Leu Gln Trp Lys Arg | Asn Arg Arg Ala Leu Ala Tyr Ser Thr |     |  |  |  |
| 290                         | 295                                 | 300 |  |  |  |
| Val Gly Thr Leu Asp Tyr Met | Ala Pro Glu Val Leu Leu Lys Lys Gly |     |  |  |  |
| 305                         | 310                                 | 315 |  |  |  |
| Tyr Gly Met Glu Cys Asp Trp | Trp Ser Leu Gly Ala Ile Leu Tyr Glu |     |  |  |  |
|                             | 320                                 | 325 |  |  |  |
| Met Leu Val Gly Tyr Pro Pro | Phe Cys Ser Asp Asp Pro Arg Ile Thr |     |  |  |  |
|                             | 330                                 | 335 |  |  |  |
| Cys Arg Lys Ile Ile Asn Trp | Arg Val Cys Leu Lys Phe Pro Glu Gln |     |  |  |  |
|                             | 340                                 | 345 |  |  |  |
| Pro Lys Ile Ser Asp Glu Ala | Arg Asp Leu Ile Cys Arg Leu Leu Cys |     |  |  |  |
|                             | 350                                 | 355 |  |  |  |
| Asp Val Asp Ser Arg Leu Gly | Thr Arg Gly Val Glu Glu Ile Lys Ser |     |  |  |  |
|                             | 360                                 | 365 |  |  |  |
| His Pro Trp Phe Lys Gly Thr | Pro Trp Asp Lys Leu Tyr Asp Met Glu |     |  |  |  |
|                             | 370                                 | 375 |  |  |  |
| Ala Ala Tyr Arg Pro Ile Val | Asp Gly Glu Leu Asp Thr Gln Asn Phe |     |  |  |  |
|                             | 380                                 | 385 |  |  |  |
| Glu Lys Phe Pro Glu Val Glu | Gly Ser Pro Ser Glu Ala Pro Gln Val |     |  |  |  |
|                             | 390                                 | 395 |  |  |  |
| Gly Pro Trp Arg Lys Met Leu | Thr Ser Lys Asp Thr Asn Phe Ile Gly |     |  |  |  |
|                             | 400                                 | 405 |  |  |  |
| Phe Thr Phe Lys Lys Ser Asp | Ile Thr Arg Ser Met Glu Ser Ser Gly |     |  |  |  |
|                             | 410                                 | 415 |  |  |  |
| Ala Asp Met Lys Ser Asn Gly | Ser Gly Glu Ala Pro Ser Leu Ile Ser |     |  |  |  |
|                             | 420                                 | 425 |  |  |  |
| Leu Leu Gly Arg Ile Asn Met | Glu Glu Gly Glu Gly Glu Leu Asn     |     |  |  |  |
|                             | 430                                 | 435 |  |  |  |
| His Lys Thr                 | 510                                 |     |  |  |  |
| 515                         |                                     |     |  |  |  |

(2) INFORMATION FOR SEQ ID NO:950:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 461 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..461

(D) OTHER INFORMATION: / Ceres Seq. ID 1499252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:950:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| Met Glu Arg Arg Arg Glu Phe Gln Arg Lys Val Gln Glu Ala Gln Leu |     |
| 1                                                               | 5   |
| Pro Val Glu Glu Gln Asp Glu Met Met Arg Asn Leu Ala Arg Arg Glu |     |
| 20                                                              | 25  |
| Thr Glu Tyr Met Arg Leu Gln Arg Arg Lys Ile Gly Ile Asp Asp Phe |     |
| 35                                                              | 40  |
| Glu Leu Thr Val Ile Gly Lys Gly Ala Phe Gly Glu Val Arg Leu     |     |
| 50                                                              | 55  |
| Cys Arg Leu Arg Ser Thr Ser Glu Val Tyr Ala Met Lys Lys Leu Lys |     |
| 65                                                              | 70  |
| Lys Thr Glu Met Leu Ser Arg Gly Gln Val Glu His Val Arg Ser Glu |     |
|                                                                 | 85  |
| Arg Asn Leu Leu Ala Glu Val Asp Ser Arg Tyr Ile Val Lys Leu Phe |     |
|                                                                 | 100 |
| Tyr Ser Phe Gln Asp Ser Glu Cys Leu Tyr Leu Ile Met Glu Tyr Leu |     |
|                                                                 | 115 |
| Pro Gly Gly Asp Ile Met Thr Leu Leu Met Arg Glu Asp Ile Leu Ser |     |
| 130                                                             | 135 |

Glu Asp Val Ala Arg Phe Tyr Ile Ala Glu Ser Ile Leu Ala Ile His  
145 150 155 160  
Ser Ile His Gln His Asn Tyr Val His Arg Asp Ile Lys Pro Asp Asn  
165 175  
Leu Ile Leu Asp Lys Ser Gly His Leu Lys Leu Ser Asp Phe Gly Leu  
180 185 190  
Cys Lys Pro Leu Asp Asp Lys Tyr Ser Ser Leu Leu Leu Glu Asp Asp  
195 200 205  
Glu Met Leu Ser Gln Asp Ser Glu Asn Gln Ser Gly Lys Ser Asp Ala  
210 215 220  
Asp Lys Ala Pro Trp Gln Met Pro Lys Glu Gln Leu Leu Gln Trp Lys  
225 230 235 240  
Arg Asn Arg Arg Ala Leu Ala Tyr Ser Thr Val Gly Thr Leu Asp Tyr  
245 250 255  
Met Ala Pro Glu Val Leu Leu Lys Lys Gly Tyr Gly Met Glu Cys Asp  
260 265 270  
Trp Trp Ser Leu Gly Ala Ile Leu Tyr Glu Met Leu Val Gly Tyr Pro  
275 280 285  
Pro Phe Cys Ser Asp Asp Pro Arg Ile Thr Cys Arg Lys Ile Ile Asn  
290 295 300  
Trp Arg Val Cys Leu Lys Phe Pro Glu Gln Pro Lys Ile Ser Asp Glu  
305 310 315 320  
Ala Arg Asp Leu Ile Cys Arg Leu Leu Cys Asp Val Asp Ser Arg Leu  
325 330 335  
Gly Thr Arg Gly Val Glu Glu Ile Lys Ser His Pro Trp Phe Lys Gly  
340 345 350  
Thr Pro Trp Asp Lys Leu Tyr Asp Met Glu Ala Ala Tyr Arg Pro Ile  
355 360 365  
Val Asp Gly Glu Leu Asp Thr Gln Asn Phe Glu Lys Phe Pro Glu Val  
370 375 380  
Glu Gly Ser Pro Ser Glu Ala Pro Gln Val Gly Pro Trp Arg Lys Met  
385 390 395 400  
Leu Thr Ser Lys Asp Thr Asn Phe Ile Gly Phe Thr Phe Lys Lys Ser  
405 410 415  
Asp Ile Thr Arg Ser Met Glu Ser Ser Gly Ala Asp Met Lys Ser Asn  
420 425 430  
Gly Ser Gly Glu Ala Pro Ser Leu Ile Ser Leu Leu Gly Arg Ile Asn  
435 440 445  
Met Glu Glu Gly Glu Gly Gly Glu Leu Asn His Lys Thr  
450 455 460

(2) INFORMATION FOR SEQ ID NO:951:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 438 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..438

(D) OTHER INFORMATION: / Ceres Seq. ID 1499253

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:951:

Met Met Arg Asn Leu Ala Arg Arg Glu Thr Glu Tyr Met Arg Leu Gln  
1 5 10 15  
Arg Arg Lys Ile Gly Ile Asp Asp Phe Glu Leu Leu Thr Val Ile Gly  
20 25 30  
Lys Gly Ala Phe Gly Glu Val Arg Leu Cys Arg Leu Arg Ser Thr Ser  
35 40 45  
Glu Val Tyr Ala Met Lys Lys Leu Lys Lys Thr Glu Met Leu Ser Arg  
50 55 60  
Gly Gln Val Glu His Val Arg Ser Glu Arg Asn Leu Leu Ala Glu Val

|                 |                         |                         |                 |
|-----------------|-------------------------|-------------------------|-----------------|
| 65              | 70                      | 75                      | 80              |
| Asp Ser Arg Tyr | Ile Val Lys Leu Phe     | Tyr Ser Phe Gln Asp Ser | Glu             |
|                 | 85                      | 90                      | 95              |
| Cys Leu Tyr Leu | Ile Met Glu Tyr Leu     | Pro Gly Gly Asp Ile     | Met Thr         |
|                 | 100                     | 105                     | 110             |
| Leu Leu Met Arg | Glu Asp Ile Leu Ser     | Glu Asp Val Ala Arg     | Phe Tyr         |
|                 | 115                     | 120                     | 125             |
| Ile Ala Glu Ser | Ile Leu Ala Ile His     | Ser Ile His Gln His     | Asn Tyr         |
|                 | 130                     | 135                     | 140             |
| Val His Arg Asp | Ile Lys Pro Asp Asn Leu | Ile Leu Asp Lys Ser     | Gly             |
|                 | 145                     | 150                     | 155             |
| His Leu Lys Leu | Ser Asp Phe Gly Leu     | Cys Lys Pro Leu Asp     | Asp Lys         |
|                 | 165                     | 170                     | 175             |
| Tyr Ser Ser Leu | Leu Leu Glu Asp Asp     | Glu Met Leu Ser         | Gln Asp Ser     |
|                 | 180                     | 185                     | 190             |
| Glu Asn Gln Ser | Gly Lys Ser Asp Ala     | Asp Lys Ala Pro         | Trp Gln Met     |
|                 | 195                     | 200                     | 205             |
| Pro Lys Glu Gln | Leu Leu Gln Trp         | Lys Arg Asn Arg         | Arg Ala Leu Ala |
|                 | 210                     | 215                     | 220             |
| Tyr Ser Thr Val | Gly Thr Leu Asp Tyr     | Met Ala Pro Glu         | Val Leu Leu     |
|                 | 225                     | 230                     | 235             |
| Lys Lys Gly Tyr | Gly Met Glu Cys Asp     | Trp Trp Ser Leu         | Gly Ala Ile     |
|                 | 245                     | 250                     | 255             |
| Leu Tyr Glu Met | Leu Val Gly Tyr Pro     | Pro Phe Cys Ser         | Asp Asp Pro     |
|                 | 260                     | 265                     | 270             |
| Arg Ile Thr Cys | Arg Lys Ile Ile Asn     | Trp Arg Val Cys         | Leu Lys Phe     |
|                 | 275                     | 280                     | 285             |
| Pro Glu Gln Pro | Lys Ile Ser Asp Glu     | Ala Arg Asp Leu         | Ile Cys Arg     |
|                 | 290                     | 295                     | 300             |
| Leu Leu Cys Asp | Val Asp Ser Arg Leu     | Gly Thr Arg Gly         | Val Glu Glu     |
|                 | 305                     | 310                     | 315             |
| Ile Lys Ser His | Pro Trp Phe Lys Gly     | Thr Pro Trp Asp         | Lys Leu Tyr     |
|                 | 325                     | 330                     | 335             |
| Asp Met Glu Ala | Ala Tyr Arg Pro Ile     | Val Asp Gly Glu         | Leu Asp Thr     |
|                 | 340                     | 345                     | 350             |
| Gln Asn Phe Glu | Lys Phe Pro Glu Val     | Glu Gly Ser Pro         | Ser Glu Ala     |
|                 | 355                     | 360                     | 365             |
| Pro Gln Val Gly | Pro Trp Arg Lys         | Met Leu Thr Ser         | Lys Asp Thr Asn |
|                 | 370                     | 375                     | 380             |
| Phe Ile Gly Phe | Thr Phe Lys Lys Ser     | Asp Ile Thr Arg         | Ser Met Glu     |
|                 | 385                     | 390                     | 395             |
| Ser Ser Gly Ala | Asp Met Lys Ser Asn     | Gly Ser Gly Glu         | Ala Pro Ser     |
|                 | 405                     | 410                     | 415             |
| Leu Ile Ser Leu | Leu Gly Arg Ile Asn     | Met Glu Glu Gly         | Glu Gly Gly     |
|                 | 420                     | 425                     | 430             |
| Glu Leu Asn His | Lys Thr                 |                         |                 |
|                 | 435                     |                         |                 |

(2) INFORMATION FOR SEQ ID NO:952:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1760 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1760
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499254

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:952:

aagcttttga agctttctcaa caatggcggc tattctctcc cacaacaacc ttcttaccat  
caaccacaaa aactccataa ccggttcttc ttcccttaat accaatttct cagaaatcaa

60  
120

|             |             |             |            |             |             |      |
|-------------|-------------|-------------|------------|-------------|-------------|------|
| ttttccgcc   | aaattccgag  | tagctacgag  | agctttgtcc | agaaccgacg  | agtcgtcttt  | 180  |
| atccgccgtg  | attttccgcc  | tcgagcgaga  | aagcggggaa | agacaaggtt  | tattaatcga  | 240  |
| aaaaaccgaa  | gaagaaagaa  | gactaaagaga | cacgtggcgt | aagatccaa   | gagaagacga  | 300  |
| ttgggcccgg  | ttaattggatc | caatggatcc  | aattcttaga | tcggagctaa  | tcggttacgg  | 420  |
| cgaatggct   | caagctgtgt  | acgacgttt   | cgatttcgat | ccgccttcca  | aatactcggg  | 480  |
| caoctccag   | ttcacgcgac  | tcgagttctt  | cgattctctc | ggaatgatcg  | attccggtta  | 540  |
| cgaggtggcg  | cgttacctct  | acgcgacgct  | gaacatcaat | ctcccgaa    | cttcttcgaa  | 600  |
| atcgcggtgg  | tctaaagtct  | ggagcaaaaa  | cgtaattgg  | atgggatacg  | tcgccgtttc  | 660  |
| agacgacgaa  | acgtctcgta  | accgactcgg  | ccgcgtgat  | atcgcgattg  | cggtggagagg | 720  |
| aaccgttaac  | aaacttgaat  | ggatcgcgga  | tctaaaggat | tatttataaac | cggttaaccga | 780  |
| aaacaagctc  | cgatccccgc  | accggccggt  | taagtcgaa  | tcgggattct  | tgaatctcta  | 840  |
| cactgacada  | gacacaacct  | gcaaatctcg  | gagattctca | gcgcgtgaac  | agattttaac  | 900  |
| ggaggtgaaa  | cggttagtgg  | aagaacacgg  | cgacgacgat | gattccgatt  | taagcatcac  | 960  |
| cgtagcgagg  | cacagtctcg  | cgccgcggtt  | agcgatatta | agcgcgtagc  | atatacgcca  | 1020 |
| gatgagattg  | aatcggaagta | agaaagggaa  | agtattccg  | gtgacggtgt  | tgacatacgg  | 1080 |
| aggacgcgaga | gttgggaacg  | ttaggtttag  | ggagaggatg | gaggaaggatg | gagtgaaagt  | 1140 |
| gatgagagta  | gtgaatgttc  | acgacgtgtg  | tcccaagtcg | ccgggattgt  | tttgaacga   | 1200 |
| gagtagacct  | cacgcgctga  | tgaagatagc  | ggaggggttg | ccgtggtgtt  | atagccacgt  | 1260 |
| ggggaggagg  | ctggcggttg  | atcatcagaa  | ctgcgcgttt | cttaaaccct  | ccgttgatgt  | 1320 |
| ttctactgct  | cataaatttg  | aagctatgct  | tcatttactt | gacgggtatc  | atggaaaagg  | 1380 |
| agagagattt  | gtgctgtctga | gtgggagaga  | ccatgcgcta | gtgaacaaag  | cgtcggaact  | 1440 |
| tttgaagagg  | catttacaag  | ttccaccggt  | ttggcgtaaa | gacgcgaata  | aagcaattgt  | 1500 |
| tcggaacagt  | gaaggtcggt  | ggattcaagc  | cgagcgtctc | cgtttgagg   | atcatcatc   | 1560 |
| tcttgataac  | caccaccatc  | tctctcagat  | ccgtcttgat | catccttggt  | aatcacacgc  | 1620 |
| acatatatat  | aatatacaca  | ttttccctaa  | tttgaagt   | acgcatccat  | cttttgaaaa  | 1680 |
| taaaatgtca  | caatactctc  | acttgcagcg  | tttggtcaac | gtacgttccc  | tattaataaa  | 1740 |
| actttattacg | ttttacgagc  |             |            |             |             |      |

(2) INFORMATION FOR SEQ ID NO:953:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..529
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:953:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Ile | Pro | Ser | His | Asn | Asn | Leu | Leu | Thr | Ile | Asn | His | Lys |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Ser | Ile | Thr | Gly | Ser | Ser | Ser | Leu | Asn | Thr | Asn | Phe | Ser | Glu | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Asn | Phe | Pro | Ala | Lys | Phe | Arg | Val | Ala | Thr | Arg | Ala | Leu | Ser | Arg | Thr |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Glu | Ser | Ser | Leu | Ser | Ala | Val | Ile | Ser | Arg | Leu | Glu | Arg | Glu | Arg |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| Arg | Glu | Arg | Gln | Gly | Leu | Leu | Ile | Glu | Glu | Ala | Glu | Gly | Ala | Gly | Glu |
|     |     |     | 65  |     |     |     | 70  |     |     |     |     | 75  |     | 80  |     |
| Leu | Trp | Met | Thr | Ala | Glu | Asp | Ile | Arg | Arg | Arg | Asp | Lys | Lys | Thr | Glu |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |     |
| Glu | Glu | Arg | Arg | Leu | Arg | Asp | Thr | Trp | Arg | Lys | Ile | Gln | Gly | Glu | Asp |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Asp | Trp | Ala | Gly | Leu | Met | Asp | Pro | Met | Asp | Pro | Ile | Leu | Arg | Ser | Glu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Ile | Arg | Tyr | Gly | Glu | Met | Ala | Gln | Ala | Cys | Tyr | Asp | Ala | Phe | Asp |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Phe | Asp | Pro | Ala | Ser | Lys | Tyr | Cys | Gly | Thr | Ser | Arg | Phe | Thr | Arg | Leu |
|     |     |     | 145 |     |     |     | 150 |     |     |     | 155 |     |     |     | 160 |
| Glu | Phe | Phe | Asp | Ser | Leu | Gly | Met | Ile | Asp | Ser | Gly | Tyr | Glu | Val | Ala |

Met Thr Ala Glu Asp Ile Arg Arg Arg Asp Lys Lys Thr Glu Glu Glu  
1 5 10 15

Arg Arg Leu Arg Asp Thr Trp Arg Lys Ile Gln Gly Glu Asp Asp Trp  
20 25 30  
Ala Gly Leu Met Asp Pro Met Asp Pro Ile Leu Arg Ser Glu Leu Ile  
35 40 45  
Arg Tyr Gly Glu Met Ala Gln Ala Cys Tyr Asp Ala Phe Asp Phe Asp  
50 55 60  
Pro Ala Ser Lys Tyr Cys Gly Thr Ser Arg Phe Thr Arg Leu Glu Phe  
65 70 75 80  
Phe Asp Ser Leu Gly Met Ile Asp Ser Gly Tyr Glu Val Ala Arg Tyr  
85 90 95  
Leu Tyr Ala Thr Ser Asn Ile Asn Leu Pro Asn Phe Phe Ser Lys Ser  
100 105 110  
Arg Trp Ser Lys Val Trp Ser Lys Asn Ala Asn Trp Met Gly Tyr Val  
115 120 125  
Ala Val Ser Asp Asp Glu Thr Ser Arg Asn Arg Leu Gly Arg Arg Asp  
130 135 140  
Ile Ala Ile Ala Trp Arg Gly Thr Val Thr Lys Leu Glu Trp Ile Ala  
145 150 155 160  
Asp Leu Lys Asp Tyr Leu Lys Pro Val Thr Glu Asn Lys Ile Arg Cys  
165 170 175  
Pro Asp Pro Ala Val Lys Val Glu Ser Gly Phe Leu Asp Leu Tyr Thr  
180 185 190  
Asp Lys Asp Thr Thr Cys Lys Phe Ala Arg Phe Ser Ala Arg Glu Gln  
195 200 205  
Ile Leu Thr Glu Val Lys Arg Leu Val Glu Glu His Gly Asp Asp Asp  
210 215 220  
Asp Ser Asp Leu Ser Ile Thr Val Thr Gly His Ser Leu Gly Gly Ala  
225 230 235 240  
Leu Ala Ile Leu Ser Ala Tyr Asp Ile Ala Glu Met Arg Leu Asn Arg  
245 250 255  
Ser Lys Lys Gly Lys Val Ile Pro Val Thr Val Leu Thr Tyr Gly Gly  
260 265 270  
Pro Arg Val Gly Asn Val Arg Phe Arg Glu Arg Met Glu Glu Leu Gly  
275 280 285  
Val Lys Val Met Arg Val Val Asn Val His Asp Val Val Pro Lys Ser  
290 295 300  
Pro Gly Leu Phe Leu Asn Glu Ser Arg Pro His Ala Leu Met Lys Ile  
305 310 315 320  
Ala Glu Gly Leu Pro Trp Cys Tyr Ser His Val Gly Glu Glu Leu Ala  
325 330 335  
Leu Asp His Gln Asn Ser Pro Phe Leu Lys Pro Ser Val Asp Val Ser  
340 345 350  
Thr Ala His Asn Leu Glu Ala Met Leu His Leu Leu Asp Gly Tyr His  
355 360 365  
Gly Lys Gly Glu Arg Phe Val Leu Ser Ser Gly Arg Asp His Ala Leu  
370 375 380  
Val Asn Lys Ala Ser Asp Phe Leu Lys Glu His Leu Gln Ile Pro Pro  
385 390 395 400  
Phe Trp Arg Gln Asp Ala Asn Lys Gly Met Val Arg Asn Ser Glu Gly  
405 410 415  
Arg Trp Ile Gln Ala Glu Arg Leu Arg Phe Glu Asp His His Ser Pro  
420 425 430  
Asp Ile His His His Leu Ser Gln Leu Arg Leu Asp His Pro Cys  
435 440 445

(2) INFORMATION FOR SEQ ID NO:955:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 412 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..412

(D) OTHER INFORMATION: / Ceres Seq. ID 1499257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:955:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Asp | Pro | Met | Asp | Pro | Ile | Leu | Arg | Ser | Glu | Leu | Ile | Arg | Tyr | Gly |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Glu | Met | Ala | Gln | Ala | Cys | Tyr | Asp | Ala | Phe | Asp | Phe | Asp | Pro | Ala | Ser |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |  |
| Lys | Tyr | Cys | Gly | Thr | Ser | Arg | Phe | Thr | Arg | Leu | Glu | Phe | Phe | Asp | Ser |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |
| Leu | Gly | Met | Ile | Asp | Ser | Gly | Tyr | Glu | Val | Ala | Arg | Tyr | Leu | Tyr | Ala |  |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Thr | Ser | Asn | Ile | Asn | Leu | Pro | Asn | Phe | Phe | Ser | Lys | Ser | Arg | Trp | Ser |  |
|     |     | 65  |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Lys | Val | Trp | Ser | Lys | Asn | Ala | Asn | Trp | Met | Gly | Tyr | Val | Ala | Val | Ser |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Asp | Asp | Glu | Thr | Ser | Arg | Asn | Arg | Leu | Gly | Arg | Arg | Asp | Ile | Ala | Ile |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ala | Trp | Arg | Gly | Thr | Val | Thr | Lys | Leu | Glu | Trp | Ile | Ala | Asp | Leu | Lys |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |     |     |     |  |
| Asp | Tyr | Leu | Lys | Pro | Val | Thr | Glu | Asn | Lys | Ile | Arg | Cys | Pro | Asp | Pro |  |
|     |     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |  |
| Ala | Val | Lys | Val | Glu | Ser | Gly | Phe | Leu | Asp | Leu | Tyr | Thr | Asp | Lys | Asp |  |
|     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |  |
| Thr | Thr | Cys | Lys | Phe | Ala | Arg | Phe | Ser | Ala | Arg | Glu | Gln | Ile | Leu | Thr |  |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     | 175 |     |     |  |
| Glu | Val | Lys | Arg | Leu | Val | Glu | Glu | His | Gly | Asp | Asp | Asp | Asp | Ser | Asp |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Leu | Ser | Ile | Thr | Val | Thr | Gly | His | Ser | Leu | Gly | Gly | Ala | Leu | Ala | Ile |  |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |  |
| Leu | Ser | Ala | Tyr | Asp | Ile | Ala | Glu | Met | Arg | Leu | Asn | Arg | Ser | Lys | Lys |  |
|     |     | 210 |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |  |
| Gly | Lys | Val | Ile | Pro | Val | Thr | Val | Leu | Thr | Tyr | Gly | Gly | Pro | Arg | Val |  |
|     |     | 225 |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |     |  |
| Gly | Asn | Val | Arg | Phe | Arg | Glu | Arg | Met | Glu | Glu | Leu | Gly | Val | Lys | Val |  |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |  |
| Met | Arg | Val | Val | Asn | Val | His | Asp | Val | Val | Pro | Lys | Ser | Pro | Gly | Leu |  |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |     |  |
| Phe | Leu | Asn | Glu | Ser | Arg | Pro | His | Ala | Leu | Met | Lys | Ile | Ala | Glu | Gly |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |
| Leu | Pro | Trp | Cys | Tyr | Ser | His | Val | Gly | Glu | Glu | Leu | Ala | Leu | Asp | His |  |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |
| Gln | Asn | Ser | Pro | Phe | Leu | Lys | Pro | Ser | Val | Asp | Val | Ser | Thr | Ala | His |  |
|     |     | 305 |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |  |
| Asn | Leu | Glu | Ala | Met | Leu | His | Leu | Leu | Asp | Gly | Tyr | His | Gly | Lys | Gly |  |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |     |  |
| Glu | Arg | Phe | Val | Leu | Ser | Ser | Gly | Arg | Asp | His | Ala | Leu | Val | Asn | Lys |  |
|     |     |     | 340 |     |     |     | 345 |     |     |     |     |     | 350 |     |     |  |
| Ala | Ser | Asp | Phe | Leu | Lys | Glu | His | Leu | Gln | Ile | Pro | Pro | Phe | Thr | Arg |  |
|     |     | 355 |     |     |     | 360 |     |     |     |     | 365 |     |     |     |     |  |
| Gln | Asp | Ala | Asn | Lys | Gly | Met | Val | Arg | Asn | Ser | Glu | Gly | Arg | Trp | Ile |  |
|     |     | 370 |     |     | 375 |     |     |     |     |     | 380 |     |     |     |     |  |
| Gln | Ala | Glu | Arg | Leu | Arg | Phe | Glu | Asp | His | His | Ser | Pro | Asp | Ile | His |  |
|     |     | 385 |     |     | 390 |     |     |     | 395 |     |     |     |     | 400 |     |  |
| His | His | Leu | Ser | Gln | Leu | Arg | Leu | Asp | His | Pro | Cys |     |     |     |     |  |
|     |     |     | 405 |     |     |     | 410 |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:956:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1361 base pairs

(B) TYPE: nucleic acid



(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..1361  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499258  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:956:

|             |             |            |            |            |             |      |
|-------------|-------------|------------|------------|------------|-------------|------|
| ggattagggg  | gactcgcaact | cttctctctc | ttctttgtac | ccagaaagaa | agtgagctcc  | 60   |
| aacaatggct  | gcttgcgcta  | ctcactcctc | tctcatgcta | gcatacgccg | cgcgatccac  | 120  |
| tcgtttccag  | gaccttacc   | ctactccatc | tcttttctct | tttgccagct | ccagacccaa  | 180  |
| ccaattgagc  | gtcccgcttc  | ttctccttgg | gggttccagg | gaccggagat | gtgctgtcat  | 240  |
| tgacagagct  | tccaaccaca  | agttttattg | ctccgcctgg | gcgctgagg  | ctgacctoga  | 300  |
| cacggaggag  | gacctggagc  | agaccgccac | cgccgtcctt | gatccgcccc | agcctaagaa  | 360  |
| agggaaaagcc | gctttgggtc  | tcaagagaga | tagaacaagg | tctaagaggt | ttttggaat   | 420  |
| ccaaaagctc  | agggaaacca  | aaaaggagta | tgatgtcaac | actgctatgt | ctttgcttaa  | 480  |
| acaaactgcc  | aacacaaggt  | ttgttgagtc | tgttgaagcc | catttccgtc | tcaacatcga  | 540  |
| tcctaagtac  | aatgaccagc  | agctgcgtgc | aacggtgagc | ctgcctaagg | gaactggcca  | 600  |
| gactgttata  | gtcgtgttgc  | ttgcacaagg | tgagaaggtt | gatgaagcca | aaagtgcagg  | 660  |
| ggcagatatt  | gtgggcagtg  | atgatttaat | cgaacagatt | aaaggaggct | tcattggagtt | 720  |
| tgacaagctg  | attgcatccc  | cggatatgat | ggccaaggtt | gctggcctgg | gaaagattct  | 780  |
| tggaccacgg  | gggctcatgc  | caaatcccaa | ggctgtgaca | gtcacagcga | acattcccca  | 840  |
| ggctattgaa  | gagttcaaga  | aggggaaaag | tgaattcaga | gcagacaaaa | ctgggattgt  | 900  |
| tcacattcca  | tttgggaaag  | ttaattttac | agaggaagac | cttctcataa | acttctctgc  | 960  |
| agcagtgaaa  | tcggtggaga  | caaaacaagc | aaagggagct | aaaggaggtg | actggaaag   | 1020 |
| cgctcacata  | gtctcgtcaa  | tggggccttc | catcaagttg | aacataagag | agatgataga  | 1080 |
| cttcaagcct  | cccaactgca  | actaatcgac | aacgcatttt | gtaaatgggg | tccttttggg  | 1140 |
| agacgggcaa  | tgcacagtga  | gacagagaag | agaaacacca | agcttagtct | gttagtaaat  | 1200 |
| ttttacagcc  | tcaactgctt  | gtatcacatt | gatggccatt | tactcttgt  | cgttatttat  | 1260 |
| ttactattgc  | ctattaaaat  | ttggcaaggg | gctgtacatg | tcaggacgca | gaactcttta  | 1320 |
| gtactctcta  | aaagaaaaa   | ccctacattg | atctttaggc | t          |             |      |

(2) INFORMATION FOR SEQ ID NO:957:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 346 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..346  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499259  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:957:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Cys | Ala | Thr | His | Ser | Ser | Leu | Met | Leu | Ala | Tyr | Ala | Ala |
| 1   |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ala | Ser | Thr | Arg | Ser | Gln | Asp | Leu | Thr | Pro | Thr | Pro | Ser | Leu | Phe | Ser |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Ala | Ser | Ser | Arg | Pro | Asn | His | Leu | Ser | Val | Pro | Leu | Leu | Leu | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Gly | Ser | Arg | Asp | Arg | Arg | Cys | Ala | Ala | Ile | Asp | Arg | Ala | Ser | Asn |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| His | Lys | Phe | Ile | Val | Ser | Ala | Val | Ala | Ala | Glu | Ala | Asp | Leu | Asp | Thr |
|     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Glu | Glu | Asp | Ser | Glu | Gln | Thr | Ala | Thr | Ala | Val | Leu | Asp | Pro | Pro | Lys |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Pro | Lys | Lys | Gly | Lys | Ala | Ala | Leu | Val | Leu | Lys | Arg | Asp | Arg | Thr | Arg |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Lys | Arg | Phe | Leu | Glu | Ile | Gln | Lys | Leu | Arg | Glu | Thr | Lys | Lys | Glu |
|     |     |     |     | 115 |     |     | 120 |     |     |     | 125 |     |     |     |     |
| Tyr | Asp | Val | Asn | Thr | Ala | Ile | Ser | Leu | Leu | Lys | Gln | Thr | Ala | Asn | Thr |
|     |     |     |     | 130 |     |     | 135 |     |     |     |     |     | 140 |     |     |

Arg Phe Val Glu Ser Val Glu Ala His Phe Arg Leu Asn Ile Asp Pro  
145 150 155 160  
Lys Tyr Asn Asp Gln Gln Leu Arg Ala Thr Val Ser Leu Pro Lys Gly  
165 170 175  
Thr Gly Gln Thr Val Ile Val Ala Val Leu Ala Gln Gly Glu Lys Val  
180 185 190  
Asp Glu Ala Lys Ser Ala Gly Ala Asp Ile Val Gly Ser Asp Asp Leu  
195 200 205  
Ile Glu Gln Ile Lys Gly Gly Phe Met Glu Phe Asp Lys Leu Ile Ala  
210 215 220  
Ser Pro Asp Met Met Val Lys Val Ala Gly Leu Gly Lys Ile Leu Gly  
225 230 235 240  
Pro Arg Gly Leu Met Pro Asn Pro Lys Ala Gly Thr Val Thr Ala Asn  
245 250 255  
Ile Pro Gln Ala Ile Glu Glu Phe Lys Lys Gly Lys Val Glu Phe Arg  
260 265 270  
Ala Asp Lys Thr Gly Ile Val His Ile Pro Phe Gly Lys Val Asn Phe  
275 280 285  
Thr Glu Glu Asp Leu Leu Ile Asn Phe Leu Ala Ala Val Lys Ser Val  
290 295 300  
Glu Thr Asn Lys Pro Lys Gly Ala Lys Gly Val Tyr Trp Lys Ser Ala  
305 310 315 320  
His Ile Cys Ser Ser Met Gly Pro Ser Ile Lys Leu Asn Ile Arg Glu  
325 330 335  
Met Ile Asp Phe Lys Pro Pro Thr Ala Asn  
340 345  
(2) INFORMATION FOR SEQ ID NO:958:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 336 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..336  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499260  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:958:  
Met Leu Ala Tyr Ala Ala Ala Ser Thr Arg Ser Gln Asp Leu Thr Pro  
1 5 10 15  
Thr Pro Ser Leu Phe Ser Phe Ala Ser Ser Arg Pro Asn His Leu Ser  
20 25 30  
Val Pro Leu Leu Leu Gly Gly Ser Arg Asp Arg Arg Cys Ala Ala  
35 40 45  
Ile Asp Arg Ala Ser Asn His Lys Phe Ile Val Ser Ala Val Ala Ala  
50 55 60  
Glu Ala Asp Leu Asp Thr Glu Glu Asp Leu Glu Gln Thr Ala Thr Ala  
65 70 75 80  
Val Leu Asp Pro Pro Lys Pro Lys Lys Gly Lys Ala Ala Leu Val Leu  
85 90 95  
Lys Arg Asp Arg Thr Arg Ser Lys Arg Phe Leu Glu Ile Gln Lys Leu  
100 105 110  
Arg Glu Thr Lys Lys Glu Tyr Asp Val Asn Thr Ala Ile Ser Leu Leu  
115 120 125  
Lys Gln Thr Ala Asn Thr Arg Phe Val Glu Ser Val Glu Ala His Phe  
130 135 140  
Arg Leu Asn Ile Asp Pro Lys Tyr Asn Asp Gln Gln Leu Arg Ala Thr  
145 150 155 160  
Val Ser Leu Pro Lys Gly Thr Gly Gln Thr Val Ile Val Ala Val Leu  
165 170 175  
Ala Gln Gly Glu Lys Val Asp Glu Ala Lys Ser Ala Gly Ala Asp Ile

(2) INFORMATION FOR SEQ ID NO:959:

(A) LENGTH: 1307 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..1307

SEQUENCE DESCRIPTION: SEQ ID NO:959:

| (X1) SEQUENCE DESCRIPTION |             |             |             |             |             |      |
|---------------------------|-------------|-------------|-------------|-------------|-------------|------|
| aattttcacgcg              | ctctttctct  | tttgcgtctct | tgagaaagttt | caaagctaat  | tcagctttctg | 60   |
| agaaattatgca              | acaattggaga | aacttcggcg  | ctctactggt  | acagactctag | ctctcgtaac  | 120  |
| ggcgataaac                | tcaaccacgc  | ctccactatc  | agccatactct | gaacaaagct  | tcagcaacaa  | 180  |
| acaccagaag                | gagttgcgag  | caaagcttcgc | atcactctact | aactcaattt  | ttctcacgga  | 240  |
| atctcaattc                | ttctctctct  | ctctcgctct  | ttcttaacca  | ccatctcgcg  | tcgataaac   | 300  |
| tacagagcat                | cgctctcttc  | aagcgaactt  | tatctctgag  | tacagtagaac | tcaacgtaca  | 360  |
| ttacagagctt               | gtctcttaac  | gtctctaagt  | cttaatgacg  | gaacttgact  | ctcttcgtca  | 420  |
| cgaaaacagat               | tctctccgct  | ttgaaatact  | agatctactc  | aaacttattc  | atatctctac  | 480  |
| ttctactctc                | ttctccgctg  | ctctctcggc  | ggcgatactc  | aaccgctaat  | tcgcgtacca  | 540  |
| gatctccgat                | tctctgcctg  | cgaaagagaa  | caatcaagag  | agaaactagt  | tcgctaaag   | 600  |
| ctactccgtc                | agatctcaag  | gatatctcaa  | gaacaaacct  | gattttaag   | cttcagatgt  | 660  |
| ccaaacaggt                | caactcagct  | ctaaactcgt  | gttgtcttct  | caaaagtggt  | tgtagtagca  | 720  |
| aacccaagaag               | gagagagagc  | ctactagaat  | tgaggtagta  | cgtaacggga  | gtgtagaac   | 780  |
| ggagctttgt                | acaaaatggc  | aagagactgg  | agcttgtgtt  | tacggcgata  | attgccaat   | 840  |
| cgctcacgga                | atcgacgacg  | tacgtctcgt  | tacttagcat  | caacgctaca  | aaactgaggt  | 900  |
| tttcagaaat                | attgtcaacc  | gagctattgt  | tccttacggt  | caacgtgtgc  | atttcgcga   | 960  |
| ctcacttact                | gattcagaga  | ggatgatgat  | gatgatgatt  | acctcgtgat  | ctggagaaga  | 1020 |
| agaagaaagc                | taattgaaa   | agagaaaata  | tatagtctgt  | tgtacagatt  | tcagagtaga  | 1080 |
| tacctataa                 | attatcgtac  | ttttctggat  | atttgtcata  | ggaataagga  | agagaaagaa  | 1140 |
| tttaataaat                | gtttgatagg  | attatagagg  | tataatttag  | gttgaagaa   | tggttggttc  | 1200 |
| tcggataaag                | ctggagagac  | ctgaaagaga  | atttagattt  | aacaaagata  | tgggaattgt  | 1260 |
| cttgataaag                | ctttttgact  | ttgtccagaa  | cttatcgact  | ttctctcc    |             |      |

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(D) TORCHES: THREE

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..311

(D) OTHER INFORMATION: / Ceres Seq. ID 1499262

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:960:

Met Glu Lys Leu Ala Ala Ser Thr Val Thr Asp Leu Ala Cys Val Thr  
1 5 10 15  
Ala Ile Asn Ser Pro Pro Pro Pro Leu Ser Pro Ile Ser Glu Gln Ser  
20 25 30  
Phe Ser Asn Lys His Gln Glu Glu Phe Ala Ala Ser Phe Ala Ser Leu  
35 40 45  
Tyr Asn Ser Ile Phe Ser Pro Glu Ser Gln Phe Ser Pro Ser Pro Pro  
50 55 60  
Ser Ser Ser Ser Pro Pro Ser Arg Val Asp Thr Thr Thr Glu His Arg  
65 70 75 80  
Leu Leu Gln Ala Lys Leu Ile Leu Glu Tyr Asp Glu Leu Asn Asp His  
85 90 95  
Tyr Glu Leu Cys Leu Asn Arg Leu Gln Ser Leu Met Thr Glu Leu Asp  
100 105 110  
Ser Leu Arg His Glu Asn Asp Ser Leu Arg Phe Glu Asn Ser Asp Leu  
115 120 125  
Leu Lys Leu Ile His Ile Ser Thr Ser Ser Ser Ser Val Ser Pro  
130 135 140  
Pro Ala Pro Ile His Asn Arg Gln Phe Arg His Gln Ile Ser Asp Ser  
145 150 155 160  
Arg Ser Ala Lys Arg Asn Asn Gln Glu Arg Asn Ser Leu Pro Lys Ser  
165 170 175  
Ile Ser Val Arg Ser Gln Gly Tyr Leu Lys Ile Asn His Gly Phe Glu  
180 185 190  
Ala Ser Asp Arg Gln Thr Ser Gln Leu Ser Ser Asn Ser Val Leu Ser  
195 200 205  
Ser Gln Lys Val Cys Val Val Gln Thr Lys Gly Glu Arg Glu Ala Leu  
210 215 220  
Glu Leu Glu Val Tyr Arg Gln Gly Met Met Lys Thr Glu Leu Cys Asn  
225 230 235 240  
Lys Trp Gln Glu Thr Gly Ala Cys Cys Tyr Gly Asp Asn Cys Gln Phe  
245 250 255  
Ala His Gly Ile Asp Glu Leu Arg Pro Val Ile Arg His Pro Arg Tyr  
260 265 270  
Lys Thr Glu Val Cys Arg Met Ile Val Thr Gly Ala Met Cys Pro Tyr  
275 280 285  
Gly His Arg Cys His Phe Arg His Ser Leu Thr Asp Gln Glu Arg Met  
290 295 300  
Met Met Met Met Leu Thr Arg  
305 310

(2) INFORMATION FOR SEQ ID NO:961:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..204

(D) OTHER INFORMATION: / Ceres Seq. ID 1499263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:961:

Met Thr Glu Leu Asp Ser Leu Arg His Glu Asn Asp Ser Leu Arg Phe  
1 5 10  
Glu Asn Ser Asp Leu Leu Lys Leu Ile His Ile Ser Thr Ser Ser Ser

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| 20  |     |     |     |     |     |     |     |     |     | 25  |     |     |     |     | 30  |     |  |  |  |  |
| Ser | Ser | Val | Ser | Pro | Pro | Ala | Pro | Ile | His | Asn | Arg | Gln | Phe | Arg | His |     |  |  |  |  |
| 35  |     |     |     |     |     |     |     |     |     | 40  |     |     |     |     | 45  |     |  |  |  |  |
| Gln | Ile | Ser | Asp | Ser | Arg | Ser | Ala | Lys | Arg | Asn | Asn | Gln | Glu | Arg | Asn |     |  |  |  |  |
| 50  |     |     |     |     |     |     |     |     |     | 55  |     |     |     |     | 60  |     |  |  |  |  |
| Ser | Leu | Pro | Lys | Ser | Ile | Ser | Val | Arg | Ser | Gln | Gly | Tyr | Leu | Lys | Ile |     |  |  |  |  |
| 65  | 70  |     |     |     |     |     |     |     |     |     | 75  |     |     |     |     | 80  |  |  |  |  |
| Asn | His | Gly | Phe | Glu | Ala | Ser | Asp | Arg | Gln | Thr | Ser | Gln | Leu | Ser | Ser |     |  |  |  |  |
| 85  |     |     |     |     |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |  |  |
| Asn | Ser | Val | Leu | Ser | Ser | Gln | Lys | Val | Cys | Val | Val | Gln | Thr | Lys | Gly |     |  |  |  |  |
| 100 |     |     |     |     |     |     |     |     |     | 105 |     |     |     |     | 110 |     |  |  |  |  |
| Glu | Arg | Glu | Ala | Leu | Glu | Leu | Glu | Val | Tyr | Arg | Gln | Gly | Met | Met | Lys |     |  |  |  |  |
| 115 |     |     |     |     |     |     |     |     |     | 120 |     |     |     |     | 125 |     |  |  |  |  |
| Thr | Glu | Leu | Cys | Asn | Lys | Trp | Gln | Glu | Thr | Gly | Ala | Cys | Cys | Tyr | Gly |     |  |  |  |  |
| 130 |     |     |     |     |     |     |     |     |     | 135 |     |     |     |     | 140 |     |  |  |  |  |
| Asp | Asn | Cys | Gln | Phe | Ala | His | Gly | Ile | Asp | Glu | Leu | Arg | Pro | Val | Ile |     |  |  |  |  |
| 145 | 150 |     |     |     |     |     |     |     |     |     | 155 |     |     |     |     | 160 |  |  |  |  |
| Arg | His | Pro | Arg | Tyr | Lys | Thr | Glu | Val | Cys | Arg | Met | Ile | Val | Thr | Gly |     |  |  |  |  |
| 165 |     |     |     |     |     |     |     |     |     | 170 |     |     |     |     | 175 |     |  |  |  |  |
| Ala | Met | Cys | Pro | Tyr | Gly | His | Arg | Cys | His | Phe | Arg | His | Ser | Leu | Thr |     |  |  |  |  |
| 180 |     |     |     |     |     |     |     |     |     | 185 |     |     |     |     | 190 |     |  |  |  |  |
| Asp | Gln | Glu | Arg | Met | Met | Met | Met | Met | Leu | Thr | Arg |     |     |     |     |     |  |  |  |  |
| 195 |     |     |     |     |     |     |     |     |     | 200 |     |     |     |     |     |     |  |  |  |  |

(2) INFORMATION FOR SEQ ID NO:962:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1372 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1

(D) OTHER INFORMATION: / Ceres Seq. ID 1499264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:962:

| (A1)        |             |             |              |             |             |      |
|-------------|-------------|-------------|--------------|-------------|-------------|------|
| aaaaatagct  | tctcttccatt | ggcccccctac | ccagagatagat | attctttatat | actactcagaa | 60   |
| atctctcaatt | tctgcgaacct | tgttatctctc | ctctgatgga   | gtctctcaggt | ccccccactaa | 120  |
| gtcacattcat | gtgtggtaaat | gttggaaaaat | ctgtatgaaga  | gagaaataatt | gtggcgagta  | 180  |
| aagtcctgttg | agaagacacaa | tgtggggtttt | cagattcttaa  | gaatgctctc  | gtgggagcttc | 240  |
| cgaaagccgtc | tgtctctcttg | cggagagcttt | cgctgcgcgt   | cgctgctgtgt | ctagtgttcaa | 300  |
| tgaattgttga | agttgttgttg | gggataataag | ccaatgattgt  | agctatataa  | acagatgcag  | 360  |
| ctcaatttgc  | ctctcgaagt  | gtgcctcttg  | ctatctccct   | ctttctcattg | tggcgctgctg | 420  |
| gttgggaagc  | gacctctcag  | caggaattacg | ggttcttcac   | tgtgatagat  | tgtgggtgtct | 480  |
| tgttatctcat | cgactcattt  | gggttgtctca | cgggtattct   | ggtttatgaa  | gcgattatca  | 540  |
| gaattgtttaa | agagacccagt | gaggtttaatg | tactctccat   | gtttcttggt  | gctgcctttg  | 600  |
| gtctagtgttg | gaacatcata  | aggctgtgtc  | tgtcagggca   | tgatcatgg   | cacagtcatg  | 660  |
| gcacatggcca | tggcccacgct | catgacatcc  | acacatagat   | ccatgggggtg | actgttaacca | 720  |
| ctcatcagct  | ctatcacagat | catgacatgt  | ccatagatca   | tggctcatgga | gaggacacag  | 780  |
| atactgtctca | tggggatgtt  | actgagcaact | tgttgagacaa  | atcgaaagat  | gaactcgcag  | 840  |
| caaaaagagaa | agaaagaagaa | aacatcaatc  | tccaaggaagc  | tatatcgcat  | cttctgtggg  | 900  |
| attctccatca | gagtgcttgt  | gttatgattg  | gaggagacat   | catttggttac | aatcccaacta | 960  |
| ggaagatagtg | ggatctgtatc | tgcacactgt  | ctctttcgg    | tattgtctca  | ggagcagaaga | 1020 |
| tcaacatgat  | tgcgaacatt  | ctagaagatt  | tgttggaagag  | tacaccccaga | gagatttgacg | 1080 |
| ccacaacatct | cgaaaacattt | tgtctgaaa   | tggaaagagc   | ggtgtcgtgt  | cttagactctt | 1140 |
| acatatgggc  | tatcacagtg  | ggaaaagctg  | tattggctgt   | ccatgtcaat  | atgacagacc  | 1200 |
| agacagatgc  | agatatgggt  | ctcaaacagc  | taattgatta   | catcgcgag   | catgacaaca  | 1260 |
| tttgtcatgt  | cacgtacaaa  | atcagaaact  | aaaagcttaag  | taagatctga  | tgaagggttt  | 1320 |
| tgtgtatcagc | attcttcatta | acagataaac  | ctaataaagt   | ttctacattt  |             |      |

(2) INFORMATION FOR SEQ ID NO:963:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..398  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1499265  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:963:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Ser | Ser | Ser | Pro | His | His | Ser | His | Ile | Val | Glu | Val | Asn | Val |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Gly | Lys | Ser | Asp | Glu | Glu | Arg | Ile | Ile | Val | Ala | Ser | Lys | Val | Cys | Gly |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Glu | Ala | Pro | Cys | Gly | Phe | Ser | Asp | Ser | Lys | Asn | Ala | Ser | Gly | Asp | Ala |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| His | Glu | Arg | Ser | Ala | Ser | Met | Arg | Lys | Leu | Cys | Ile | Ala | Val | Val | Leu |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Cys | Leu | Val | Phe | Met | Ser | Val | Glu | Val | Val | Gly | Gly | Ile | Lys | Ala | Asn |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | Leu | Ala | Ile | Leu | Thr | Asp | Ala | Ala | His | Leu | Leu | Ser | Asp | Val | Ala |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Ala | Phe | Ala | Ile | Ser | Leu | Phe | Ser | Leu | Trp | Ala | Ala | Gly | Trp | Glu | Ala |
|     |     |     | 100 |     |     |     |     |     | 105 |     |     |     | 110 |     |     |
| Thr | Pro | Arg | Gln | Thr | Tyr | Gly | Phe | Phe | Arg | Ile | Glu | Ile | Leu | Gly | Ala |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Val | Ser | Ile | Gln | Leu | Ile | Trp | Leu | Leu | Thr | Gly | Ile | Leu | Val | Tyr |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Glu | Ala | Ile | Ile | Arg | Ile | Val | Thr | Glu | Thr | Ser | Glu | Val | Asn | Gly | Phe |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Met | Phe | Leu | Val | Ala | Ala | Phe | Gly | Leu | Val | Val | Asn | Ile | Ile | Met |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ala | Val | Leu | Leu | Gly | His | Asp | His | Gly | His | Ser | His | Gly | His | Gly | His |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | His | Gly | His | Asp | His | His | Asn | His | Ser | His | Gly | Val | Thr | Val | Thr |
|     |     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |
| Thr | His | His | His | His | His | Asp | His | Glu | His | Gly | His | Ser | His | Gly | His |
|     |     |     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |
| Gly | Glu | Asp | Lys | His | His | Ala | His | Gly | Asp | Val | Thr | Glu | Gln | Leu | Leu |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     | 240 |
| Asp | Lys | Ser | Lys | Thr | Gln | Val | Ala | Ala | Lys | Glu | Lys | Arg | Lys | Arg | Asn |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ile | Asn | Leu | Gln | Gly | Ala | Tyr | Leu | His | Val | Leu | Gly | Asp | Ser | Ile | Gln |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ser | Val | Gly | Val | Met | Ile | Gly | Gly | Ala | Ile | Ile | Trp | Tyr | Asn | Pro | Glu |
|     |     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |
| Trp | Lys | Ile | Val | Asp | Leu | Ile | Cys | Thr | Leu | Ala | Phe | Ser | Val | Ile | Val |
|     |     |     | 290 |     |     |     | 295 |     |     |     | 300 |     |     |     |     |
| Leu | Gly | Thr | Thr | Ile | Asn | Met | Ile | Arg | Asn | Ile | Leu | Glu | Val | Leu | Met |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     |     | 320 |
| Glu | Ser | Thr | Pro | Arg | Glu | Ile | Asp | Ala | Thr | Lys | Leu | Glu | Lys | Gly | Leu |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Leu | Glu | Met | Glu | Glu | Val | Val | Ala | Val | His | Glu | Leu | His | Ile | Trp | Ala |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Ile | Thr | Val | Gly | Lys | Val | Leu | Leu | Ala | Cys | His | Val | Asn | Ile | Arg | Pro |
|     |     |     | 355 |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Glu | Ala | Asp | Ala | Asp | Met | Val | Leu | Asn | Lys | Val | Ile | Asp | Tyr | Ile | Arg |
|     |     |     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |
| Arg | Glu | Tyr | Asn | Ile | Ser | His | Val | Thr | Ile | Gln | Ile | Glu | Arg |     |     |
| 385 |     |     |     | 390 |     |     |     |     |     | 395 |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:964:  
(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 344 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..344  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499266  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:964:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Lys | Leu | Cys | Ile | Ala | Val | Val | Leu | Cys | Leu | Val | Phe | Met | Ser |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Val | Glu | Val | Val | Gly | Gly | Ile | Lys | Ala | Asn | Ser | Leu | Ala | Ile | Leu | Thr |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Asp | Ala | Ala | His | Leu | Leu | Ser | Asp | Val | Ala | Ala | Phe | Ala | Ile | Ser | Leu |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Phe | Ser | Leu | Trp | Ala | Ala | Gly | Trp | Glu | Ala | Thr | Pro | Arg | Gln | Thr | Tyr |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Gly | Phe | Phe | Arg | Ile | Glu | Ile | Leu | Gly | Ala | Leu | Val | Ser | Ile | Gln | Leu |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |     |
| Ile | Trp | Leu | Leu | Thr | Gly | Ile | Leu | Val | Tyr | Glu | Ala | Ile | Ile | Arg | Ile |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Val | Thr | Glu | Thr | Ser | Glu | Val | Asn | Gly | Phe | Leu | Met | Phe | Leu | Val | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Phe | Gly | Leu | Val | Val | Asn | Ile | Ile | Met | Ala | Val | Leu | Leu | Gly | His |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Asp | His | Gly | His | Ser | His | Gly | His | Gly | His | Gly | His | Gly | His | Asp | His |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| His | Asn | His | Ser | His | Gly | Val | Thr | Val | Thr | Thr | His | His | His | His | His |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     | 160 |
| Asp | His | Glu | His | Gly | His | Ser | His | Gly | His | Gly | Glu | Asp | Lys | His | His |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Ala | His | Gly | Asp | Val | Thr | Glu | Gln | Leu | Leu | Asp | Lys | Ser | Lys | Thr | Gln |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Val | Ala | Ala | Lys | Glu | Lys | Arg | Lys | Arg | Asn | Ile | Asn | Leu | Gln | Gly | Ala |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Tyr | Leu | His | Val | Leu | Gly | Asp | Ser | Ile | Gln | Ser | Val | Gly | Val | Met | Ile |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Gly | Gly | Ala | Ile | Ile | Trp | Tyr | Asn | Pro | Glu | Trp | Lys | Ile | Val | Asp | Leu |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     | 240 |     |
| Ile | Cys | Thr | Leu | Ala | Phe | Ser | Val | Ile | Val | Leu | Gly | Thr | Thr | Ile | Asn |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     | 255 |     |     |
| Met | Ile | Arg | Asn | Ile | Leu | Glu | Val | Leu | Met | Glu | Ser | Thr | Pro | Arg | Glu |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ile | Asp | Ala | Thr | Lys | Leu | Glu | Lys | Gly | Leu | Leu | Glu | Met | Glu | Glu | Val |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Val | Ala | Val | His | Glu | Leu | His | Ile | Trp | Ala | Ile | Thr | Val | Gly | Lys | Val |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Leu | Leu | Ala | Cys | His | Val | Asn | Ile | Arg | Pro | Glu | Ala | Asp | Ala | Asp | Met |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     | 320 |     |
| Val | Leu | Asn | Lys | Val | Ile | Asp | Tyr | Ile | Arg | Arg | Glu | Tyr | Asn | Ile | Ser |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |     |
| His | Val | Thr | Ile | Gln | Ile | Glu | Arg |     |     |     |     |     |     |     |     |
|     |     | 340 |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:965:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 330 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..330

(D) OTHER INFORMATION: / Ceres Seq. ID 1499267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:965:

Met Ser Val Glu Val Val Gly Gly Ile Lys Ala Asn Ser Leu Ala Ile  
1 5 10 15  
Leu Thr Asp Ala Ala His Leu Leu Ser Asp Val Ala Ala Phe Ala Ile  
20 25 30  
Ser Leu Phe Ser Leu Trp Ala Ala Gly Trp Glu Ala Thr Pro Arg Gln  
35 40 45  
Thr Tyr Gly Phe Phe Arg Ile Glu Ile Leu Gly Ala Leu Val Ser Ile  
50 55 60  
Gln Leu Ile Trp Leu Leu Thr Gly Ile Leu Val Tyr Glu Ala Ile Ile  
65 70 75 80  
Arg Ile Val Thr Glu Thr Ser Glu Val Asn Gly Phe Leu Met Phe Leu  
85 90 95  
Val Ala Ala Phe Gly Leu Val Val Asn Ile Ile Met Ala Val Leu Leu  
100 105 110  
Gly His Asp His Gly His Ser His Gly His Gly His Gly His  
115 120 125  
Asp His His Asn His Ser His Gly Val Thr Val Thr Thr His His His  
130 135 140  
His His Asp His Glu His Gly His Ser His Gly His Gly Glu Asp Lys  
145 150 155 160  
His His Ala His Gly Asp Val Thr Glu Gln Leu Leu Asp Lys Ser Lys  
165 170 175  
Thr Gln Val Ala Ala Lys Glu Lys Arg Lys Arg Asn Ile Asn Leu Gln  
180 185 190  
Gly Ala Tyr Leu His Val Leu Gly Asp Ser Ile Gln Ser Val Gly Val  
195 200 205  
Met Ile Gly Gly Ala Ile Ile Trp Tyr Asn Pro Glu Trp Lys Ile Val  
210 215 220  
Asp Leu Ile Cys Thr Leu Ala Phe Ser Val Ile Val Leu Gly Thr Thr  
225 230 235 240  
Ile Asn Met Ile Arg Asn Ile Leu Glu Val Leu Met Glu Ser Thr Pro  
245 250 255  
Arg Glu Ile Asp Ala Thr Lys Leu Glu Lys Gly Leu Leu Glu Met Glu  
260 265 270  
Glu Val Val Ala Val His Glu Leu His Ile Trp Ala Ile Thr Val Gly  
275 280 285  
Lys Val Leu Leu Ala Cys His Val Asn Ile Arg Pro Glu Ala Asp Ala  
290 295 300  
Asp Met Val Leu Asn Lys Val Ile Asp Tyr Ile Arg Arg Glu Tyr Asn  
305 310 315 320  
Ile Ser His Val Thr Ile Gln Ile Glu Arg  
325 330

(2) INFORMATION FOR SEQ ID NO:966:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 945 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..945

(D) OTHER INFORMATION: / Ceres Seq. ID 1499310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:966:

accaaaccac caccctgcctc aactaatcgg gtcagatcag gtcacgggga agggccgccat  
ggacgacgag gagcacgagg tttaaggcca ggagatccct gaggacggcg atatggacgg

60

120



|             |            |            |             |             |            |     |
|-------------|------------|------------|-------------|-------------|------------|-----|
| cgcgtgacgtt | gatatggccg | cgcgcgggga | cgacgcggcg  | aacttcagga  | gcttgacgag | 180 |
| atgaagcgca  | astganagga | gatggaggag | gaggccgcgc  | ccctccgcga  | tatgcaggcc | 240 |
| aaggtcgcca  | aggagatgca | aggaggtgac | cctagtatat  | ctacagctga  | rgcgaaggag | 300 |
| cagggtgatg  | cccggtctgt | gtatgttgga | aatgttgatt  | atgcttgca   | cccagaagaa | 360 |
| gtgcagcagc  | atttccaagc | ttgtggaact | gtcaacacggg | tgacaactctt | gactgacaag | 420 |
| tttgggcagc  | caaaagggtt | tgcttatgtt | gaatttctgg  | aacaagaagc  | tgctcaggaa | 480 |
| gctctgaact  | tgaatgaatc | ggaattgcat | ggtcgacaga  | ttaagggtgc  | gccgaagagg | 540 |
| actaatgtcc  | ctgggatgaa | gcagcgtcca | ccacgcgggt  | ataatcccta  | ccatgggtac | 600 |
| ccttatagat  | catatggagc | accgtacttc | ccccatcacg  | gttatgggag  | ggctcctaga | 660 |
| ttccgcgcgc  | ctatgcgcta | cagaccttac | ttctgaagta  | cgtgcggggg  | aataatgttc | 720 |
| aatgcacaa   | cagccatggt | tagtggctag | tctcggaat   | aattaaacct  | actgctgtat | 780 |
| cggtttgcgt  | gttcaatagt | tgacatcggt | gcggttcaat  | gctcccttac  | cagctgcctt | 840 |
| tcttgacctc  | tggtctcgca | taagcgacat | gtagacacag  | gacgtagggt  | tacaattgtt | 900 |
| tgcatattct  | gtcattcttg | attctgatga | ccctatacac  | cactc       |            |     |

(2) INFORMATION FOR SEQ ID NO:967:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..164
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:967:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Glu | Glu | Ala | Ala | Ala | Leu | Arg | Asp | Met | Gln | Ala | Lys | Val | Ala |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Lys | Glu | Met | Gln | Gly | Gly | Asp | Pro | Ser | Ile | Ser | Thr | Ala | Xaa | Ala | Lys |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Glu | Gln | Val | Asp | Ala | Arg | Ser | Val | Tyr | Val | Gly | Asn | Val | Asp | Tyr | Ala |
|     |     |     | 35  |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Cys | Thr | Pro | Glu | Glu | Val | Gln | Gln | His | Phe | Gln | Ala | Cys | Gly | Thr | Val |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Asn | Arg | Val | Thr | Ile | Leu | Thr | Asp | Lys | Phe | Gly | Gln | Pro | Lys | Gly | Phe |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |
| Ala | Tyr | Val | Glu | Phe | Leu | Glu | Gln | Glu | Ala | Val | Gln | Glu | Ala | Leu | Asn |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Asn | Glu | Ser | Glu | Leu | His | Gly | Arg | Gln | Ile | Lys | Val | Ala | Pro | Lys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Thr | Asn | Val | Pro | Gly | Met | Lys | Gln | Arg | Pro | Pro | Arg | Gly | Tyr | Asn |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Tyr | His | Gly | Tyr | Pro | Tyr | Arg | Ser | Tyr | Gly | Ala | Pro | Tyr | Phe | Pro |
|     |     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Pro | Tyr | Gly | Tyr | Gly | Arg | Ala | Pro | Arg | Phe | Arg | Arg | Pro | Met | Arg | Tyr |
|     |     |     | 145 |     |     | 150 |     |     | 155 |     |     |     |     | 160 |     |
| Arg | Pro | Tyr | Phe |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:968:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:968:

Met Gln Ala Lys Val Ala Lys Glu Met Gln Gly Gly Asp Pro Ser Ile

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| 1                                                               | 5   | 10  | 15  |
| Ser Thr Ala Xaa Ala Lys Glu Gln Val Asp Ala Arg Ser Val Tyr Val |     |     |     |
|                                                                 | 20  | 25  | 30  |
| Gly Asn Val Asp Tyr Ala Cys Thr Pro Glu Glu Val Gln Gln His Phe |     |     |     |
|                                                                 | 35  | 40  | 45  |
| Gln Ala Cys Gly Thr Val Asn Arg Val Thr Ile Leu Thr Asp Lys Phe |     |     |     |
|                                                                 | 50  | 55  | 60  |
| Gly Gln Pro Lys Gly Phe Ala Tyr Val Glu Phe Leu Glu Gln Glu Ala |     |     |     |
|                                                                 | 65  | 70  | 75  |
| Val Gln Glu Ala Leu Asn Leu Asn Glu Ser Glu Leu His Gly Arg Gln |     |     |     |
|                                                                 | 85  | 90  | 95  |
| Ile Lys Val Ala Pro Lys Arg Thr Asn Val Pro Gly Met Lys Gln Arg |     |     |     |
|                                                                 | 100 | 105 | 110 |
| Pro Pro Arg Gly Tyr Asn Pro Tyr His Gly Tyr Pro Tyr Arg Ser Tyr |     |     |     |
|                                                                 | 115 | 120 | 125 |
| Gly Ala Pro Tyr Phe Pro Pro Tyr Gly Tyr Gly Arg Ala Pro Arg Phe |     |     |     |
|                                                                 | 130 | 135 | 140 |
| Arg Arg Pro Met Arg Tyr Arg Pro Tyr Phe                         |     |     |     |
| 145                                                             | 150 |     |     |

(2) INFORMATION FOR SEQ ID NO:969:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1499313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:969:

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| Met Gln Gly Gly Asp Pro Ser Ile Ser Thr Ala Xaa Ala Lys Glu Gln |     |     |     |
| 1                                                               | 5   | 10  | 15  |
| Val Asp Ala Arg Ser Val Tyr Val Gly Asn Val Asp Tyr Ala Cys Thr |     |     |     |
|                                                                 | 20  | 25  | 30  |
| Pro Glu Glu Val Gln Gln His Phe Gln Ala Cys Gly Thr Val Asn Arg |     |     |     |
|                                                                 | 35  | 40  | 45  |
| Val Thr Ile Leu Thr Asp Lys Phe Gly Gln Pro Lys Gly Phe Ala Tyr |     |     |     |
|                                                                 | 50  | 55  | 60  |
| Val Glu Phe Leu Glu Gln Glu Ala Val Gln Glu Ala Leu Asn Leu Asn |     |     |     |
|                                                                 | 65  | 70  | 75  |
| Glu Ser Glu Leu His Gly Arg Gln Ile Lys Val Ala Pro Lys Arg Thr |     |     |     |
|                                                                 | 85  | 90  | 95  |
| Asn Val Pro Gly Met Lys Gln Arg Pro Pro Arg Gly Tyr Asn Pro Tyr |     |     |     |
|                                                                 | 100 | 105 | 110 |
| His Gly Tyr Pro Tyr Arg Ser Tyr Gly Ala Pro Tyr Phe Pro Pro Tyr |     |     |     |
|                                                                 | 115 | 120 | 125 |
| Gly Tyr Gly Arg Ala Pro Arg Phe Arg Arg Pro Met Arg Tyr Arg Pro |     |     |     |
|                                                                 | 130 | 135 | 140 |
| Tyr Phe                                                         |     |     |     |
| 145                                                             |     |     |     |

(2) INFORMATION FOR SEQ ID NO:970:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 917 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..917

(D) OTHER INFORMATION: / Ceres Seq. ID 1499314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:970:

|             |             |            |            |            |             |     |
|-------------|-------------|------------|------------|------------|-------------|-----|
| atgggggttrg | cctagtgtgtg | cccgttgagc | actagcagcc | tccttgaaac | ctccagatct  | 60  |
| gtgcctccaa  | ggccccggtt  | cctcgccaac | aagtcccatc | tgamggacct | tgttccctgt  | 120 |
| rccegcscac  | gtggcctcct  | ctgcagccgt | ccagatggac | accgcgcgcg | ccctgcaact  | 180 |
| gaaagcctgc  | gcccgcgagc  | ccgcggagaa | gtgtctgtct | gccgtcgagc | ccgaggggtcc | 240 |
| tatctgttgt  | gtgccagact  | tcaaatgatg | gggaaagaag | agtgatgarc | togaacctgt  | 300 |
| cgatrcctgc  | gatgaagatg  | atgatggtgg | tgacgatggg | gacgaggatg | gtgactttgg  | 360 |
| ggagggaggt  | gaagaggagc  | tctcagaagg | ggagggtatg | gacaacccaa | agggcaatga  | 420 |
| gaccaagawg  | camagagggtg | atcctgagga | aaatggtgag | gaagatgagg | aagaaccaga  | 480 |
| agatcaggag  | ggtggcggcg  | acgacgatga | tgacgacgat | gacgatgatg | agaacggggg  | 540 |
| tgacgaggag  | gacgacaagt  | gggatgacga | tgaggagggt | gtagatgaag | aagacgatga  | 600 |
| ccaggacgag  | gatgaggagc  | aagatgatga | tgaagactcg | ctccagcccc | caaagaagag  | 660 |
| gaagaagtga  | agatcttctg  | ccgctttagt | taccgtgcgc | tgagtcttgc | ctggcttttc  | 720 |
| gtcatatcct  | cgcatttcaa  | ctttcccata | gagagttaa  | aaggatccac | acgttcagca  | 780 |
| gcacgtgtgg  | gctttgtagga | gctttatgat | ttgaggcaat | tagggacaac | tcttatgtca  | 840 |
| ttgttgcttg  | cttctgttga  | gtcgaacaga | gttttcgcta | acataattcg | acttgagtga  | 900 |
| tgaaagcctc  | cagattg     |            |            |            |             |     |

(2) INFORMATION FOR SEQ ID NO:971:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..171

(D) OTHER INFORMATION: / Ceres Seq. ID 1499315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:971:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Thr | Ala | Ala | Pro | Leu | Gln | Leu | Lys | Ala | Cys | Ala | Gly | Asp | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Glu | Lys | Leu | Leu | Leu | Ala | Val | Ala | Ala | Glu | Gly | Pro | Ile | Cys | Xaa |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |
| Val | Pro | Asp | Phe | Lys | Met | Arg | Gly | Lys | Lys | Ser | Asp | Xaa | Leu | Glu | Pro |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |
| Val | Asp | Xaa | Gly | Asp | Glu | Asp | Asp | Asp | Gly | Gly | Asp | Asp | Gly | Asp | Glu |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Asp | Gly | Asp | Phe | Gly | Glu | Glu | Gly | Glu | Glu | Asp | Val | Ser | Glu | Gly | Glu |
|     |     |     | 65  |     |     |     | 70  |     |     | 75  |     |     |     | 80  |     |
| Gly | Tyr | Asp | Asn | Pro | Lys | Gly | Asn | Glu | Thr | Lys | Xaa | Xaa | Arg | Gly | Asp |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |     |
| Pro | Glu | Glu | Asn | Gly | Glu | Glu | Asp | Glu | Glu | Pro | Glu | Asp | Gln | Glu |     |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Gly | Gly | Gly | Asp | Asp | Asp | Asp | Asp | Asp | Asp | Asp | Asp | Asp | Glu | Asn | Gly |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Asp | Glu | Asp | Asp | Asp | Asn | Gly | Asp | Asp | Asp | Asp | Glu | Glu | Gly | Val |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| Glu | Glu | Asp | Asp | Asp | Gln | Asp | Glu | Asp | Glu | Glu | Glu | Asp | Asp | Asp | Glu |
|     |     |     | 145 |     |     |     | 150 |     |     |     | 155 |     |     |     | 160 |
| Asp | Ser | Leu | Gln | Pro | Pro | Lys | Lys | Arg | Lys | Lys |     |     |     |     |     |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:972:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1499316

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:972:

Met Arg Gly Lys Lys Ser Asp Xaa Leu Glu Pro Val Asp Xaa Gly Asp  
1 5 10 15  
Glu Asp Asp Asp Gly Gly Asp Asp Gly Asp Glu Asp Gly Asp Phe Gly  
20 25 30  
Glu Glu Gly Glu Glu Asp Val Ser Glu Gly Glu Gly Tyr Asp Asn Pro  
35 40 45  
Lys Gly Asn Glu Thr Lys Xaa Xaa Arg Gly Asp Pro Glu Glu Asn Gly  
50 55 60  
Glu Glu Asp Glu Glu Glu Pro Glu Asp Gln Glu Gly Gly Asp Asp  
65 70 75 80  
Asp Asp Asp Asp Asp Asp Asp Glu Asn Gly Asp Asp Glu Asp Asp  
85 90 95  
Asp Asn Gly Asp Asp Asp Glu Glu Gly Val Asp Glu Glu Asp Asp Asp  
100 105 110  
Gln Asp Glu Asp Glu Glu Glu Asp Asp Glu Asp Ser Leu Gln Pro  
115 120 125  
Pro Lys Lys Arg Lys Lys  
130

(2) INFORMATION FOR SEQ ID NO:973:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1499317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:973:

Met Xaa Ser Asn Leu Ser Xaa Leu Ala Met Lys Met Met Val Val  
1 5 10 15  
Thr Met Gly Thr Arg Met Val Thr Leu Gly Arg Arg Val Lys Arg Thr  
20 25 30  
Ser Gln Lys Gly Arg Asp Met Thr Thr Gln Arg Ala Met Arg Pro Arg  
35 40 45  
Xaa Xaa Glu Val Ile Leu Arg Lys Met Val Arg Lys Met Arg Lys Asn  
50 55 60  
Gln Lys Ile Arg Arg Val Ala Ala Thr Thr Met Met Thr Thr Met Thr  
65 70 75 80  
Met Met Arg Thr Gly Met Thr Arg Thr Thr Thr Met Gly Met Thr Met  
85 90 95  
Arg Arg Val

(2) INFORMATION FOR SEQ ID NO:974:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 948 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..948

(D) OTHER INFORMATION: / Ceres Seq. ID 1499344

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:974:

ctygcgtcc cctctcgvt cctcgcgatc cttctttact gcccgagagt tctgactagc  
cacatccagt caagcagtaa aggcgcacca tggaggcgcc gccggagaat aaggaggccg

60

120

|             |            |             |             |             |             |     |
|-------------|------------|-------------|-------------|-------------|-------------|-----|
| agcaggagga  | gcagcagcta | ccgcacgcgc  | agaagataa   | cgcgccccgc  | gccgcccagg  | 180 |
| aagacgaagc  | ggattcggag | gagaccgagc  | gccgcaaccg  | cgacctcaag  | tccggccttc  | 240 |
| acccoccttag | gcacaaactc | gtgctctggt  | acactgcgcg  | gacgcctgga  | gcgaggctgc  | 300 |
| agtcgtacga  | ggacaaactc | aagaagatca  | tcgatttcag  | cacagtcgaa  | tcgtctcggg  | 360 |
| tttctactgt  | ccaccttgcg | cgcccttctt  | ccctgcgcag  | ccccactgac  | cttcatctct  | 420 |
| tcaaggatgg  | catccgtccc | ctctgggagg  | atcctgcгаа  | ccagaatggt  | ggcaagtgga  | 480 |
| taattagatt  | caaaaaagca | gtttcaggtc  | gattttggga  | ggatttggtg  | ctagtggtag  | 540 |
| taggcgacca  | gottgagtat | agcgatgatg  | tctgtggtgt  | tgtgcttagt  | gtccggtttca | 600 |
| atgaagacat  | tctgagcgtc | tggaaacgga  | acgcatcaga  | ccatcaggct  | gtgatggcat  | 660 |
| tgagggattc  | tatcaagagg | cacctcaagc  | tgccgcacag  | ctatctgatg  | gagtacaaaac | 720 |
| cccatgatst  | tcgcggcgtg | acaactcgtc  | ctacaggaaac | acatggctga  | gaggatagat  | 780 |
| aaacctcatg  | atactcggca | gcttcaactgc | gacggttctg  | aagcaaaagag | actcttttat  | 840 |
| gtaccaagaa  | cgcagactat | tatgcaatgt  | agtactacta  | ctactactac  | tcaaaagccc  | 900 |
| ctacaatgtg  | acgcgcaaca | atttactat   | ctaattgttt  | ttttttgc    |             |     |

(2) INFORMATION FOR SEQ ID NO:975:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..160
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:975:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Xaa | Arg | Xaa | Pro | Pro | Xaa | Leu | Leu | Ala | Ile | Leu | Leu | Tyr | Cys | Pro | Arg |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Val | Leu | Thr | Ser | His | Ile | Gln | Ser | Ser | Ser | Lys | Gly | Ala | Pro | Trp | Arg |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Arg | Arg | Arg | Arg | Ile | Arg | Arg | Pro | Ser | Arg | Arg | Ser | Ser | Ser | Tyr | Arg |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Thr | Arg | Arg | Arg | Ile | Thr | Arg | Pro | Pro | Pro | Pro | Arg | Lys | Thr | Lys | Arg |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |  |
| Ile | Arg | Arg | Arg | Pro | Ser | Ala | Ala | Thr | Ala | Thr | Ser | Ser | Pro | Ala | Phe |  |
|     |     |     | 65  |     |     |     | 70  |     |     |     | 75  |     |     | 80  |     |  |
| Thr | Pro | Leu | Gly | Thr | Asn | Ser | Cys | Ser | Gly | Thr | Leu | Ala | Gly | Arg | Leu |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |     |  |
| Glu | Arg | Gly | Arg | Ser | Arg | Thr | Arg | Thr | Thr | Ser | Arg | Arg | Ser | Ser | Ile |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ser | Ala | Gln | Ser | Asn | Arg | Ser | Gly | Phe | Ala | Thr | Ala | Thr | Leu | Arg | Ala |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Leu | Leu | Pro | Cys | Arg | Ala | Pro | Leu | Thr | Phe | Ile | Ser | Ser | Arg | Met | Ala |  |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |  |
| Ser | Val | Pro | Ser | Gly | Arg | Ile | Leu | Gln | Thr | Arg | Met | Val | Ala | Ser | Gly |  |
|     |     |     | 145 |     |     |     | 150 |     |     |     | 155 |     |     |     | 160 |  |

(2) INFORMATION FOR SEQ ID NO:976:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..226
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499346

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:976:

Met Glu Ala Ala Ala Glu Asn Lys Glu Ala Glu Gln Glu Gln Gln

|             |                                 |                             |                 |
|-------------|---------------------------------|-----------------------------|-----------------|
| 1           | 5                               | 10                          | 15              |
| Leu Pro His | Ala Gln Lys Asp Asn Ala         | Pro Ala Ala Ala             | Glu Glu Asp     |
|             | 20                              | 25                          | 30              |
| Glu Ala Asp | Ser Glu Glu Thr                 | Glu Arg Arg Asn Arg         | Asp Leu Lys Ser |
|             | 35                              | 40                          | 45              |
| Gly Leu His | Pro Leu Arg His Lys Leu Val     | Leu Trp Tyr Thr Arg Arg     |                 |
|             | 50                              | 55                          | 60              |
| Thr Pro Gly | Ala Arg Ser Gln Ser Tyr         | Glu Asp Asn Ile Lys Lys Ile |                 |
|             | 65                              | 70                          | 75              |
| Ile Asp Phe | Ser Thr Val Glu Ser Phe         | Trp Val Cys Tyr Cys His Leu |                 |
|             | 85                              | 90                          | 95              |
| Ala Arg Pro | Ser Ser Leu Pro Ser Pro         | Thr Asp Leu His Leu Phe Lys |                 |
|             | 100                             | 105                         | 110             |
| Asp Gly Ile | Arg Pro Leu Trp Glu Asp         | Pro Ala Asn Gln Asn Gly Gly |                 |
|             | 115                             | 120                         | 125             |
| Lys Trp Ile | Ile Arg Phe Lys Lys Ala Val     | Ser Gly Arg Phe Trp Glu     |                 |
|             | 130                             | 135                         | 140             |
| Asp Leu Val | Leu Val Val Val Gly Asp         | Gln Leu Glu Tyr Ser Asp Asp |                 |
|             | 145                             | 150                         | 155             |
| Val Cys Gly | Val Val Leu Ser Val Arg         | Phe Asn Glu Asp Ile Leu Ser |                 |
|             | 165                             | 170                         | 175             |
| Val Trp Asn | Arg Asn Ala Ser Asp His         | Gln Ala Val Met Ala Leu Arg |                 |
|             | 180                             | 185                         | 190             |
| Asp Ser Ile | Lys Arg His Leu Lys Leu         | Pro His Ser Tyr Leu Met Glu |                 |
|             | 195                             | 200                         | 205             |
| Tyr Lys Pro | His Asp Xaa Arg Gly Val Thr Thr | Arg Pro Thr Gly Thr         |                 |
|             | 210                             | 215                         | 220             |
| His Gly     |                                 |                             |                 |
| 225         |                                 |                             |                 |

(2) INFORMATION FOR SEQ ID NO:977:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..537
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499353

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:977:

|             |             |            |             |            |            |     |
|-------------|-------------|------------|-------------|------------|------------|-----|
| aaaaaacacca | cacaacacaa  | cacaataata | cagcaaaggga | ggctagcaga | agtgcaggat | 60  |
| taataagcta  | agctagttaga | aattaagcaa | agcataggca  | cagccatggc | tacctcctct | 120 |
| ggttcttgcc  | ttattattagc | ctgtgwggtg | gtggtggttg  | cggcgccgct | gtcggcctca | 180 |
| acggcgctcg  | cacagctgtc  | gtcgacgttc | tacgacacgt  | cgtgccccag | cgcgatgtcc | 240 |
| accatcacga  | gcggcgtaga  | ctccgcctgt | gcgcasagcc  | tcgtgtgggg | gcgtcgctgc | 300 |
| tccggctcca  | cttcacagac  | tgtctgtctc | aaggctgcga  | cgcgtccatt | ctgctgaacg | 360 |
| acacgtccgg  | ggagcagacc  | cagccgcgca | acctaactct  | gaacccgagg | gccttcgacg | 420 |
| tcgtcaacag  | catcaaggcg  | caggtggagg | cggcggtccc  | ggcgctgcgc | tcctgcgcgc | 480 |
| acatcctcgc  | cgtcgcgcc   | cgcgacgagt | tgctgcgctc  | ggcggggcct | cgtgggac   |     |

(2) INFORMATION FOR SEQ ID NO:978:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..83
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:978:  
Met Ala Thr Ser Ser Gly Ser Cys Leu Ile Ile Ser Leu Xaa Val Val  
1 5 10 15  
Val Val Ala Ala Ala Leu Ser Ala Ser Thr Ala Ser Ala Gln Leu Ser  
20 25 30  
Ser Thr Phe Tyr Asp Thr Ser Cys Pro Ser Ala Met Ser Thr Ile Ser  
35 40 45  
Ser Gly Val Asn Ser Ala Val Ala Xaa Arg Leu Val Trp Gly Arg Arg  
50 55 60  
Cys Ser Gly Ser Thr Ser Thr Thr Ala Ser Ser Lys Ala Ala Thr Arg  
65 70 75 80  
Pro Phe Cys

(2) INFORMATION FOR SEQ ID NO:979:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..460

(D) OTHER INFORMATION: / Ceres Seq. ID 1499362

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:979:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| accacatagca gccagtcgcc cgcacgactc ttcccggt acccacaccg cgcgagatct   | 60  |
| ccgatccccg cccaaatccc acgacgocgg cggsgccatg ggcggcaagg acctgacgga  | 120 |
| ggaccagatc cctcogatgc gggaggcctt ctgctgttcc gacacggacg gggacggccg  | 180 |
| catcgcgccc tcggagctgg cgcctctcat cgcctccctc ggcgggaacc ccacgcagggc | 240 |
| gcastccggg acatcgcgcc gcaggagaag ctacccgcac ccttcgactt cccgcgtttt  | 300 |
| ctcgactcca tgcgcgccca cctcaagccc gagcccttcg accgchcgct ccgcgamgcc  | 360 |
| ttcmcgctcc tcgacaagga cggctccggc accgtcggcc tmgcmrasct ccgccacgtc  | 420 |
| ctcaactcca tcggcgagaa gctcgaggcc cacgagttcg                        |     |

(2) INFORMATION FOR SEQ ID NO:980:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1499363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:980:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Thr His Ser Ser Gln Ser Pro Ala Arg Leu Phe Pro Gly Tyr Pro His |  |
| 1 5 10 15                                                       |  |
| Arg Ala Arg Ser Pro Ile Pro Ala Gln Ile Pro Arg Arg Arg Arg Xaa |  |
| 20 25 30                                                        |  |
| His Gly Arg Gln Gly Pro Asp Gly Gly Pro Asp Arg Leu Asp Ala Gly |  |
| 35 40 45                                                        |  |
| Gly Leu Leu Ala Val Arg His Gly Arg Gly Arg Pro His Arg Ala Leu |  |
| 50 55 60                                                        |  |
| Gly Ala Gly Arg Pro His Ala Leu Pro Arg Arg Glu Pro His Ala Gly |  |
| 65 70 75 80                                                     |  |
| Ala Xaa Arg Asp Ile Ala Ala Gln Glu Lys Leu Thr Ala Pro Phe Asp |  |
| 85 90 95                                                        |  |
| Phe Pro Arg Phe Leu Asp Leu Met Arg Ala His Leu Lys Pro Glu Pro |  |
| 100 105 110                                                     |  |
| Phe Asp Arg Xaa Leu Arg Xaa Ala Phe Xaa Val Leu Asp Lys Asp Gly |  |
| 115 120 125                                                     |  |

Ser Gly Thr Val Ala Xaa Xaa Xaa Leu Arg His Val Leu Thr Ser Ile  
130 135 140  
Gly Glu Lys Leu Glu Ala His Glu Phe  
145 150

(2) INFORMATION FOR SEQ ID NO:981:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1499364

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:981:

Pro Ile Ala Ala Ser Arg Pro His Asp Ser Phe Pro Ala Thr His Thr  
1 5 10 15  
Ala Arg Asp Leu Arg Ser Pro Pro Lys Ser His Asp Ala Gly Xaa Ala  
20 25 30  
Met Gly Gly Lys Asp Leu Thr Glu Asp Gln Ile Ala Ser Met Arg Glu  
35 40 45  
Ala Phe Ser Leu Phe Asp Thr Asp Gly Asp Gly Arg Ile Ala Pro Ser  
50 55 60  
Glu Leu Gly Val Leu Met Arg Ser Leu Gly Gly Asn Pro Thr Gln Ala  
65 70 75 80  
Xaa Ser Gly Thr Ser Arg Arg Arg Arg Ser Ser Pro His Pro Ser Thr  
85 90 95  
Ser Arg Ala Phe Ser Thr Ser Cys Ala Pro Thr Ser Ser Pro Ser Pro  
100 105 110  
Ser Thr Xaa Arg Ser Ala Xaa Pro Xaa Ala Ser Ser Thr Arg Thr Ala  
115 120 125  
Pro Ala Pro Ser Pro Xaa Xaa Xaa Ser Ala Thr Ser Ser Pro Pro Ser  
130 135 140  
Ala Arg Ser Ser Arg Pro Thr Ser Ser  
145 150

(2) INFORMATION FOR SEQ ID NO:982:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..121

(D) OTHER INFORMATION: / Ceres Seq. ID 1499365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:982:

Met Gly Gly Lys Asp Leu Thr Glu Asp Gln Ile Ala Ser Met Arg Glu  
1 5 10 15  
Ala Phe Ser Leu Phe Asp Thr Asp Gly Asp Gly Arg Ile Ala Pro Ser  
20 25 30  
Glu Leu Gly Val Leu Met Arg Ser Leu Gly Gly Asn Pro Thr Gln Ala  
35 40 45  
Xaa Ser Gly Thr Ser Arg Arg Arg Arg Ser Ser Pro His Pro Ser Thr  
50 55 60  
Ser Arg Ala Phe Ser Thr Ser Cys Ala Pro Thr Ser Ser Pro Ser Pro  
65 70 75 80  
Ser Thr Xaa Arg Ser Ala Xaa Pro Xaa Ala Ser Ser Thr Arg Thr Ala  
85 90 95  
Pro Ala Pro Ser Pro Xaa Xaa Xaa Ser Ala Thr Ser Ser Pro Pro Ser



100 105 110  
Ala Arg Ser Ser Arg Pro Thr Ser Ser  
115 120

(2) INFORMATION FOR SEQ ID NO:983:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 736 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:  
(A) NAME/KEY: -  
(B) LOCATION: 1..736  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499370  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:983:

|             |            |             |             |             |             |     |
|-------------|------------|-------------|-------------|-------------|-------------|-----|
| gcattcgtac  | aaccgcagcc | gagacggtg   | accaacgctg  | ccacgattcc  | gtccacacgc  | 60  |
| cgacgcggcg  | ggctcctggc | cgacgagcac  | tcccctccga  | acgccgcgtt  | ggccggcccc  | 120 |
| gccccacgag  | gccacgatgc | agtagcacgc  | ttcacaccat  | ctgtctgtct  | caagtgtcac  | 180 |
| ggcgctccgtc | attcgattca | accccccaac  | ccccatgggc  | ctggccgtat  | aaatcaaccg  | 240 |
| ccggtgaagt  | ctagtcgtct | ctgcgctcgg  | tccaccacct  | cagctccgcc  | gcttgccccc  | 300 |
| ttttgctctc  | tccctcccg  | ctctcggtt   | cttctacacg  | ctaccgtctc  | acagccgtaa  | 360 |
| acgccccctcc | cggatccgc  | tagttcgcca  | ccgcccgcgc  | cccgccccgc  | gttcgcctca  | 420 |
| tcattggcgc  | ctcgtcgacc | gcccaactcc  | gtccatgact  | tcacgtcaa   | ggatggaggt  | 480 |
| ggcgcccggt  | gaggcgccg  | tggcggtatac | gggtggcgggc | gccgtgatgg  | aggcgcgctac | 540 |
| ggcggtggcg  | gtggaggcta | cggcggtggt  | cggtggaggct | acggcgccgg  | tgggggatac  | 600 |
| gggtggtgcaa | acccgcggcg | cggctacggc  | aacaacgacg  | ggaaactggag | gaactgagcg  | 660 |
| gtgggggtccg | ctgaggccta | gttatcttgt  | tcgcttctgc  | taccgtgttc  | accctagtct  | 720 |

agagggggtt tatctt

(2) INFORMATION FOR SEQ ID NO:984:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 119 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..119  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499371  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:984:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Phe | Val | Gln | Pro | Gln | Pro | Arg | Arg | Leu | Thr | Asn | Ala | Ala | Thr | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Ser | Thr | Arg | Arg | Arg | Gly | Gly | Leu | Ala | Asp | Glu | His | Ser | Pro |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Asn | Ala | Ala | Leu | Ala | Gly | Pro | Ala | Pro | Arg | Gly | His | Asp | Ala | Val |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Ala | Ala | Phe | Thr | Pro | Ser | Val | Cys | Leu | Lys | Cys | His | Gly | Val | Arg | His |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |
| Ser | Ile | Gln | Pro | Pro | Thr | Pro | His | Gly | Pro | Gly | Arg | Ile | Asn | Gln | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Pro | Val | Lys | Ser | Ser | Arg | Leu | Val | Ala | Arg | Ser | Thr | Thr | Ser | Ala | Pro |
|     |     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |
| Pro | Leu | Ala | Arg | Phe | Cys | Ser | Leu | Pro | Pro | Gly | Ser | Arg | Leu | Leu | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| His | Ala | Thr | Val | Ser | Gln | Pro |     |     |     |     |     |     |     |     |     |

115

(2) INFORMATION FOR SEQ ID NO:985:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 94 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..94  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1499372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:985:  
Met Thr Ser Ser Ser Arg Met Glu Val Ala Ala Val Glu Ala Ala Val  
1                    5                    10                    15  
Ala Asp Thr Val Ala Gly Ala Val Met Glu Ala Ala Thr Ala Val Ala  
                    20                    25                    30  
Val Glu Ala Thr Ala Val Val Val Glu Ala Thr Ala Ala Val Gly Asp  
                    35                    40                    45  
Thr Val Val Gln Thr Ala Ala Ala Thr Ala Thr Thr Thr Gly Thr  
                    50                    55                    60  
Gly Gly Thr Glu Arg Trp Gly Pro Leu Arg Pro Ser Tyr Leu Val Arg  
65                    70                    75                    80  
Phe Cys Tyr Arg Val His Pro Ser Leu Glu Gly Val Tyr Leu  
                    85                    90

- (2) INFORMATION FOR SEQ ID NO:986:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 88 amino acids  
        (B) TYPE: amino acid  
        (C) STRANDEDNESS:  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
    (ix) FEATURE:  
        (A) NAME/KEY: peptide  
        (B) LOCATION: 1..88  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1499373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:986:  
Met Glu Val Ala Ala Val Glu Ala Ala Val Ala Asp Thr Val Ala Gly  
1                    5                    10                    15  
Ala Val Met Glu Ala Ala Thr Ala Val Ala Val Glu Ala Thr Ala Val  
                    20                    25                    30  
Val Val Glu Ala Thr Ala Ala Val Gly Asp Thr Val Val Gln Thr Ala  
                    35                    40                    45  
Ala Ala Ala Thr Ala Thr Thr Thr Gly Thr Gly Gly Thr Glu Arg Trp  
                    50                    55                    60  
Gly Pro Leu Arg Pro Ser Tyr Leu Val Arg Phe Cys Tyr Arg Val His  
65                    70                    75                    80  
Pro Ser Leu Glu Gly Val Tyr Leu  
                    85

- (2) INFORMATION FOR SEQ ID NO:987:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 914 base pairs  
        (B) TYPE: nucleic acid  
        (C) STRANDEDNESS: single  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: DNA (genomic)  
    (ix) FEATURE:  
        (A) NAME/KEY: -  
        (B) LOCATION: 1..914  
        (D) OTHER INFORMATION: / Ceres Seq. ID 1499380

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:987:  
gnacccttcg gcgcaccgc caccgcaaca gcacgcacct aggcccggtc cgtgtcgtcg 60  
tcgtagtctg tcccttccgc cgcgcgccca gcagcagcgg attccccctg agagatccgg 120  
cccttgccgc ggtgcgcgga gagagcgcca tggggctctg ggactcgctc ctcaactggc 180  
tccgagcttt gtttttcaag caagaaatgg agctctccct cgttgggttg cagaatgctg 240  
ggaagacgtc gctggtcaat gctgttgcta caggtggcta cagcgaggac atgattccaa 300  
cggtaggctt caatatgcgg aaggtcacca agggaaatgt caccgattaag ctitgggata 360

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| ttgttggtgga | gcgagatgc  | cgcactatgt | gggagcgcta | ttgccgtgga | gtttctgcta | 420 |
| ttctatatgt  | tgtggacgtc | gctgacgcag | atagtgtccc | aatcgcgaaa | agtgagttgc | 480 |
| atgatctgtc  | gacgaacacg | tccttggctg | ggattccctt | gcttgcctt  | ggcaacaaaa | 540 |
| ttgacaagtc  | agaagcgctt | tcgaaagcag | ccttggttga | tcaacttga  | ctggaattga | 600 |
| taaaggacgc  | tgagggtttg | tgctacatga | tctcctgtaa | ggattctgtg | aacatagacg | 660 |
| tcgtcatcga  | ctggcttata | aagcactcta | gaacagcgaa | gtaggctttc | tggtgttttg | 720 |
| tatcgcttga  | tgacaggtgt | tttatctttt | gtgaatctga | gcctgggttc | ttggtcccca | 780 |
| tgttaaaagc  | ggccaccttg | taatttatga | cccttttggt | gtcacagacg | aactgcatgg | 840 |
| tatctagact  | agaaacatgt | cttccctttg | taaactcctt | gaacctttga | ttattcttat | 900 |
| tggtgaatgcc | gtcc       |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:988:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..233

(D) OTHER INFORMATION: / Ceres Seq. ID 1499381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:988:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Pro | Ala | Pro | His | Pro | His | Gly | Asn | Ser | Ile | Asp | Leu | Gly | Pro | Val |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Pro | Cys | Arg | Phe | Val | Val | Arg | Pro | Leu | Pro | Arg | Ala | Pro | Ser | Ser | Ser |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Gly | Phe | Pro | Ser | Arg | Asp | Pro | Ala | Leu | Gly | Ala | Val | Ala | Gly | Glu | Ser |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Gly | Met | Gly | Leu | Trp | Asp | Ser | Leu | Leu | Asn | Trp | Leu | Arg | Ser | Leu | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Lys | Gln | Glu | Met | Glu | Leu | Ser | Leu | Val | Gly | Leu | Gln | Asn | Ala | Gly |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Lys | Thr | Ser | Leu | Val | Asn | Ala | Val | Ala | Thr | Gly | Gly | Tyr | Ser | Glu | Asp |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Met | Ile | Pro | Thr | Val | Gly | Phe | Asn | Met | Arg | Lys | Val | Thr | Lys | Gly | Asn |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Val | Thr | Ile | Lys | Leu | Trp | Asp | Leu | Gly | Gly | Gln | Arg | Arg | Phe | Arg | Thr |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Met | Trp | Glu | Arg | Tyr | Cys | Arg | Gly | Val | Ser | Ala | Ile | Leu | Tyr | Val | Val |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Asp | Ala | Ala | Asp | Arg | Asp | Ser | Val | Pro | Ile | Ala | Lys | Ser | Glu | Leu | His |
|     | 145 |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Asp | Leu | Leu | Thr | Lys | Gln | Ser | Leu | Ala | Gly | Ile | Pro | Leu | Leu | Val | Leu |
|     |     | 165 |     |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Gly | Asn | Lys | Ile | Asp | Lys | Ser | Glu | Ala | Leu | Ser | Lys | Gln | Ala | Leu | Val |
|     | 180 |     |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Asp | Gln | Leu | Gly | Leu | Glu | Leu | Ile | Lys | Asp | Arg | Glu | Val | Cys | Cys | Tyr |
|     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| Met | Ile | Ser | Cys | Lys | Asp | Ser | Val | Asn | Ile | Asp | Val | Val | Ile | Asp | Trp |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Leu | Ile | Lys | His | Ser | Arg | Thr | Ala | Lys |     |     |     |     |     |     |     |
|     | 225 |     |     |     | 230 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:989:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..184

(D) OTHER INFORMATION: / Ceres Seq. ID 1499382

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:989:

Met Gly Leu Trp Asp Ser Leu Leu Asn Trp Leu Arg Ser Leu Phe  
1 5 10 15  
Lys Gln Glu Met Glu Leu Ser Leu Val Gly Leu Gln Asn Ala Gly Lys  
20 25 30  
Thr Ser Leu Val Asn Ala Val Ala Thr Gly Gly Tyr Ser Glu Asp Met  
35 40 45  
Ile Pro Thr Val Gly Phe Asn Met Arg Lys Val Thr Lys Gly Asn Val  
50 55 60  
Thr Ile Lys Leu Trp Asp Leu Gly Gly Gln Arg Arg Phe Arg Thr Met  
65 70 75 80  
Trp Glu Arg Tyr Cys Arg Gly Val Ser Ala Ile Leu Tyr Val Val Asp  
85 90 95  
Ala Ala Asp Arg Asp Ser Val Pro Ile Ala Lys Ser Glu Leu His Asp  
100 105 110  
Leu Leu Thr Lys Gln Ser Leu Ala Gly Ile Pro Leu Leu Val Leu Gly  
115 120 125  
Asn Lys Ile Asp Lys Ser Glu Ala Leu Ser Lys Gln Ala Leu Val Asp  
130 135 140  
Gln Leu Gly Leu Glu Leu Ile Lys Asp Arg Glu Val Cys Cys Tyr Met  
145 150 155 160  
Ile Ser Cys Lys Asp Ser Val Asn Ile Asp Val Val Ile Asp Trp Leu  
165 170 175  
Ile Lys His Ser Arg Thr Ala Lys  
180

(2) INFORMATION FOR SEQ ID NO:990:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 165 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..165

(D) OTHER INFORMATION: / Ceres Seq. ID 1499383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:990:

Met Glu Leu Ser Leu Val Gly Leu Gln Asn Ala Gly Lys Thr Ser Leu  
1 5 10 15  
Val Asn Ala Val Ala Thr Gly Gly Tyr Ser Glu Asp Met Ile Pro Thr  
20 25 30  
Val Gly Phe Asn Met Arg Lys Val Thr Lys Gly Asn Val Thr Ile Lys  
35 40 45  
Leu Trp Asp Leu Gly Gly Gln Arg Arg Phe Arg Thr Met Trp Glu Arg  
50 55 60  
Tyr Cys Arg Gly Val Ser Ala Ile Leu Tyr Val Val Asp Ala Ala Asp  
65 70 75 80  
Arg Asp Ser Val Pro Ile Ala Lys Ser Glu Leu His Asp Leu Leu Thr  
85 90 95  
Lys Gln Ser Leu Ala Gly Ile Pro Leu Leu Val Leu Gly Asn Lys Ile  
100 105 110  
Asp Lys Ser Glu Ala Leu Ser Lys Gln Ala Leu Val Asp Gln Leu Gly  
115 120 125  
Leu Glu Leu Ile Lys Asp Arg Glu Val Cys Cys Tyr Met Ile Ser Cys  
130 135 140  
Lys Asp Ser Val Asn Ile Asp Val Val Ile Asp Trp Leu Ile Lys His  
145 150 155 160  
Ser Arg Thr Ala Lys  
165

(2) INFORMATION FOR SEQ ID NO:991:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..536
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:991:

|             |            |            |            |            |            |     |
|-------------|------------|------------|------------|------------|------------|-----|
| acacagcgag  | ccaatcgccg | taatcatgaa | ggtcctcatc | gttctcgccg | cgtagcgttg | 60  |
| cgccgcccctg | gctggcatcc | cctccgagtc | tgagatccag | gctcattggg | agagcttcaa | 120 |
| ggctaccac   | ggcaagacct | acgccaatgc | cgtagaggag | gctacaggg  | ccaaggtgtt | 180 |
| caaggaanaac | gccaatcagg | tcgccaagca | caatgaccgt | ttcgccagcg | gsanggtcac | 240 |
| cttcaaggtc  | ggctacaacc | agtacgctga | catgcacacc | cacgaggtca | ccgagaagat | 300 |
| gaacgggttc  | cgcatggaga | tgaagaaacc | ctccgctaac | gtgcacgagg | gcaacgactc | 360 |
| ctggccctgg  | agcaagaagg | tcgactggag | atccaagggc | tacgtcaccc | ccatcaagga | 420 |
| ccaggagacg  | tgcgggtcct | gctggtcttt | ctctgccact | ggttccctcg | agggtcacgt | 480 |
| cttcaagata  | ccgcaagct  | ggctccctc  | tctgacgaga | acctggctga | ctgctc     |     |

(2) INFORMATION FOR SEQ ID NO:992:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..178
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499385

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:992:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Ser | Glu | Pro | Ile | Ala | Val | Ile | Met | Lys | Val | Leu | Ile | Val | Leu | Ala |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Cys | Val | Ala | Ala | Ala | Leu | Ala | Gly | Ile | Pro | Ser | Glu | Ser | Glu | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Ala | His | Trp | Glu | Ser | Phe | Lys | Ala | Thr | His | Gly | Lys | Thr | Tyr | Ala |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Asn | Ala | Val | Glu | Glu | Ala | Tyr | Arg | Ala | Lys | Val | Phe | Lys | Glu | Asn | Ala |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ile | Arg | Ile | Ala | Lys | His | Asn | Asp | Arg | Phe | Ala | Ser | Xaa | Xaa | Val | Thr |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Phe | Lys | Val | Gly | Tyr | Asn | Gln | Tyr | Ala | Asp | Met | His | Thr | His | Glu | Val |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Glu | Lys | Met | Asn | Gly | Phe | Arg | Met | Glu | Met | Lys | Lys | Pro | Ser | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Val | His | Glu | Gly | Asn | Asp | Ser | Trp | Pro | Trp | Ser | Lys | Lys | Val | Asp |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Trp | Arg | Ser | Lys | Gly | Tyr | Val | Thr | Pro | Ile | Lys | Asp | Gln | Gly | Gln | Cys |
|     |     | 130 |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Gly | Ser | Cys | Trp | Ser | Phe | Ser | Ala | Thr | Gly | Ser | Leu | Glu | Gly | Gln | Leu |
|     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Phe | Lys | Ile | Pro | Ala | Ser | Trp | Ser | Pro | Ser | Leu | Ser | Arg | Thr | Trp | Ser |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Thr | Ala |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:993:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
(A) NAME/KEY: peptide  
(B) LOCATION: 1..170  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499386  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:993:  
Met Lys Val Leu Ile Val Leu Ala Ala Cys Val Ala Ala Leu Ala  
1 5 10 15  
Gly Ile Pro Ser Glu Ser Glu Ile Glu Ala His Trp Glu Ser Phe Lys  
20 25 30  
Ala Thr His Gly Lys Thr Tyr Ala Asn Ala Val Glu Glu Ala Tyr Arg  
35 40 45  
Ala Lys Val Phe Lys Glu Asn Ala Ile Arg Ile Ala Lys His Asn Asp  
50 55 60  
Arg Phe Ala Ser Xaa Xaa Val Thr Phe Lys Val Gly Tyr Asn Gln Tyr  
65 70 75 80  
Ala Asp Met His Thr His Glu Val Thr Glu Lys Met Asn Gly Phe Arg  
85 90 95  
Met Glu Met Lys Lys Pro Ser Ala Asn Val His Glu Gly Asn Asp Ser  
100 105 110  
Trp Pro Trp Ser Lys Lys Val Asp Trp Arg Ser Lys Gly Tyr Val Thr  
115 120 125  
Pro Ile Lys Asp Gln Gly Gln Cys Gly Ser Cys Trp Ser Phe Ser Ala  
130 135 140  
Thr Gly Ser Leu Glu Gly Gln Leu Phe Lys Ile Pro Ala Ser Trp Ser  
145 150 155 160  
Pro Ser Leu Ser Arg Thr Trp Ser Thr Ala  
165 170

(2) INFORMATION FOR SEQ ID NO:994:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..470

(D) OTHER INFORMATION: / Ceres Seq. ID 1499389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:994:

gaccttttct ttcccaaaagc cgagcagcga ccagcgaggg tgccactgcc accgcccgcgc 60  
ccccagtccc ccactcactc actagctagc ttgctagctg cgactacggt gctacgcgga 120  
gctagagtcc ggcgatccaca gcccgccagg ccggccatgg ccaccgcgcc cgctegtcgt 180  
ctagtctctgc acgtttctgct aggcgtgcga gcggccgctt gcgccgcggc ggcaggaggt 240  
agcagcaagg tgccggcgat gtacgtgttc ggcgactcca cgccggacgt gggcaccacac 300  
aactacttgc cggcgccggc cgaagtgcgc cgtgccaaact tccccacaa cggcgctgac 360  
ttccccasgg sgccgcmccac cggcaggttc agcaacgggt tcaacggcgt cgactctttg 420  
gccgtgaaca tggcgcttcaa gcgcasmccc gcgcgttctt cgcmtgtggcc

(2) INFORMATION FOR SEQ ID NO:995:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide  
(B) LOCATION: 1..156

(D) OTHER INFORMATION: / Ceres Seq. ID 1499390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:995:

Asp Pro Phe Phe Pro Lys Ala Glu Gln Arg Pro Ala Arg Val Pro Leu  
1 5 10 15  
Pro Pro Pro Ala Pro Gln Ser Pro Thr His Ser Leu Ala Ser Leu Leu  
20 25 30  
Ala Ala His Tyr Gly Leu Arg Arg Ala Arg Val Arg Arg Ser Gln Pro  
35 40 45  
Gly Arg Pro Ala Met Ala Thr Ala Pro Val Val Val Leu Val Leu His  
50 55 60  
Val Leu Leu Gly Ala Ala Ala Ala Cys Ala Ala Ala Gly Ser  
65 70 75 80  
Ser Ser Lys Val Pro Ala Met Tyr Val Phe Gly Asp Ser Thr Ala Asp  
85 90 95  
Val Gly Thr Asn Asn Tyr Leu Pro Gly Gly Ala Glu Val Pro Arg Ala  
100 105 110  
Asn Phe Pro His Asn Gly Val Asp Phe Pro Xaa Xaa Arg Xaa Thr Gly  
115 120 125  
Arg Phe Ser Asn Gly Phe Asn Gly Val Asp Phe Leu Ala Val Asn Met  
130 135 140  
Gly Phe Lys Arg Xaa Pro Arg Arg Ser Ser Xaa Trp  
145 150 155

(2) INFORMATION FOR SEQ ID NO:996:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1499391

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:996:

Met Ala Thr Ala Pro Val Val Val Leu Val Leu His Val Leu Leu Gly  
1 5 10 15  
Ala Ala Ala Ala Ala Cys Ala Ala Ala Gly Ser Ser Ser Lys Val  
20 25 30  
Pro Ala Met Tyr Val Phe Gly Asp Ser Thr Ala Asp Val Gly Thr Asn  
35 40 45  
Asn Tyr Leu Pro Gly Gly Ala Glu Val Pro Arg Ala Asn Phe Pro His  
50 55 60  
Asn Gly Val Asp Phe Pro Xaa Xaa Arg Xaa Thr Gly Arg Phe Ser Asn  
65 70 75 80  
Gly Phe Asn Gly Val Asp Phe Leu Ala Val Asn Met Gly Phe Lys Arg  
85 90 95  
Xaa Pro Arg Arg Ser Ser Xaa Trp  
100

(2) INFORMATION FOR SEQ ID NO:997:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..519

(D) OTHER INFORMATION: / Ceres Seq. ID 1499402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:997:

cagascagaa ascacccgca gcccccgcc ccacaagacg aggcaacaat ggcgctagaa  
gcagccaccg cccccgcgc acctctcgcc gcgtgcctcg tctgtctggt cctcgggggc

60  
120

ggcaccggcgc cgtcgtcggt gctgcgcggc gccggggcgc aggcgggcag gggagccgga 180  
tccaggatac gtcattgtat cggcatgggg ccccgccgtc cactaatcgt cgtcgttoga 240  
ggcgagcagc gacgctccgc cgccaacgac ggcgagtgcc acatgcctat gctctcgtgt 300  
gggcccgcga cgttattgag cgctactagt actagggaat gtgtacgtgt gatgtgtgtc 360  
actcagtgct gattgatcaa tgatgctcat ttccgagcag acccaggaat gctgagtgca 420  
gagagcagag cgtntgttct acaagtgcac cgaggaataa agtggacaga aatgttggct 480  
ggttcagctg ccttctgagt aataaaatgg acatcttcg

(2) INFORMATION FOR SEQ ID NO:998:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 165 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..165

(D) OTHER INFORMATION: / Ceres Seq. ID 1499403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:998:

Gln Xaa Arg Xaa Gln Pro Gln Pro Gln Pro Gln Asp Glu Ala Thr  
1 5 10 15  
Met Ala Leu Glu Ala Ala Thr Ala Pro Arg Ala Leu Leu Ala Cys  
20 25 30  
Leu Val Leu Leu Val Leu Gly Gly Thr Gly Pro Ser Ser Val Leu  
35 40 45  
Arg Gly Ala Gly Ala Gln Ala Gly Arg Gly Ala Gly Ser Arg Ile Arg  
50 55 60  
His Val Ser Gly Met Gly Pro Arg Arg Pro Leu Ile Val Val Val Arg  
65 70 75 80  
Gly Arg Arg Arg Arg Ser Ala Ala Asn Asp Gly Glu Cys His Met Pro  
85 90 95  
Met Leu Ser Cys Gly Pro Arg Thr Leu Leu Ser Ala Thr Ser Thr Arg  
100 105 110  
Glu Ser Val Arg Val Met Cys Val Thr Gln Cys Arg Leu Ile Asn Asp  
115 120 125  
Ala His Phe Arg Ala Asp Pro Gly Met Leu Ser Ala Glu Ser Arg Ala  
130 135 140  
Xaa Val Leu Gln Val His Arg Gly Ile Lys Trp Thr Glu Met Leu Ala  
145 150 155 160  
Gly Ser Arg Ala Phe  
165

(2) INFORMATION FOR SEQ ID NO:999:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1499404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:999:

Xaa Gln Lys Xaa Ala Ala Ala Pro Ala Pro Thr Arg Arg Gly Asn Asn  
1 5 10 15  
Gly Ala Arg Ser Ser His Arg Pro Pro Arg Thr Pro Arg Arg Val Pro  
20 25 30  
Arg Pro Ala Gly Pro Arg Arg Arg His Arg Pro Val Val Gly Ala Ala  
35 40 45  
Arg Arg Arg Gly Ala Gly Arg Gln Gly Ser Arg Ile Gln Asp Thr Ser  
50 55 60



Cys Ile Arg His Gly Ala Pro Pro Ser Thr Asn Arg Arg Arg Ser Arg  
65 70 75 80  
Ala Thr Thr Thr Leu Arg Arg Gln Arg Arg Arg Val Pro His Ala Tyr  
85 90 95  
Ala Leu Val Trp Ala Pro Tyr Val Ile Glu Arg Tyr  
100 105

(2) INFORMATION FOR SEQ ID NO:1000:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..149
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1000:

Met Ala Leu Glu Ala Ala Thr Ala Pro Arg Ala Leu Leu Ala Ala Cys  
1 5 10 15  
Leu Val Leu Leu Val Leu Gly Gly Gly Thr Gly Pro Ser Ser Val Leu  
20 25 30  
Arg Gly Ala Gly Ala Gln Ala Gly Arg Gly Ala Gly Ser Arg Ile Arg  
35 40 45  
His Val Ser Gly Met Gly Pro Arg Arg Pro Leu Ile Val Val Val Arg  
50 55 60  
Gly Arg Arg Arg Arg Ser Ala Ala Asn Asp Gly Glu Cys His Met Pro  
65 70 75 80  
Met Leu Ser Cys Gly Pro Arg Thr Leu Leu Ser Ala Thr Ser Thr Arg  
85 90 95  
Glu Ser Val Arg Val Met Cys Val Thr Gln Cys Arg Leu Ile Asn Asp  
100 105 110  
Ala His Phe Arg Ala Asp Pro Gly Met Leu Ser Ala Glu Ser Arg Ala  
115 120 125  
Xaa Val Leu Gln Val His Arg Gly Ile Lys Trp Thr Glu Met Leu Ala  
130 135 140  
Gly Ser Arg Ala Phe  
145

(2) INFORMATION FOR SEQ ID NO:1001:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1040 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1040
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1001:

gcattctect cgccgcgagggt tgccgagagac cgtacgggca ttctctcttag gtgcgggggt 60  
tctctctcgag tctcggaac gacgaaaacg aaaatacga gtCgagtcag cgatgaatcc 120  
cttcgcaaaa aaaccaactc cgccgagaggt gatcgcgasa gcaagcgga cctgacgaat 180  
gctacgcgag ggatcgagag ggacattgcg tcattacagc agggaggaga gaaactcgtt 240  
gtcgaaaatta aaaggacagc aaaaactggc aatgaggcag caacgaaaaat tctagcccggt 300  
cagctgatca ggttaaggca gcagatttct aatttgcaag gtgagccgag tcagattcgg 360  
gggattgcga cacatactca gccaatgcac gccaacactt cagtggtctac tggtttacaa 420  
agtgcgagca aagcaatggg agctttgaat aagcaaatgg aacctaccaa gcagatgaaa 480  
ataatgcaag aattccaaaa gcagtcagca caaatggata tgacaaaatga gatgatgtct 540  
gattcaatcg atgatgtctt agacgatgac caggccgagg aagaaaactga agaacttgct 600  
aatcagggttc tggatgagat tgggtgtagc attgcatcac agttgtcttc ggctcccaaa 660

ggaaaaattg ctgggaagaa ggttcagggt gatggaagtt cggagttgga ggaactagag 720  
aagagactgg ctgctctaaa aaatgcataa gatcagttta caaccctctc ctctatgcac 780  
atagcaagcc tgcggtgtac cttaattcca aatcttcatt cgacacgcaa agtcactgtg 840  
atattgtatg atcaaaagga agatgatgca aaccccccaag tttttgggag aatcagatgtt 900  
gctgctgttc gtacacactc acgcataaga tggggctgtg ctgccttatt agcgacatga 960  
ttcagagcaa gggattccat agtcttgtaa agaagtttga ttatttttac atgacagcct 1020  
ttgttttttg gtcgttcggt

(2) INFORMATION FOR SEQ ID NO:1002:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..249

(D) OTHER INFORMATION: / Ceres Seq. ID 1499407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1002:

Ala Phe Ser Ser Ala Arg Val Ala Glu Thr Arg Thr Gly Ile Leu Leu  
1 5 10 15  
Arg Cys Gly Gly Ser Ser Arg Val Ser Ala Thr Thr Lys Thr Lys Ile  
20 25 30  
Pro Ser Arg Val Ser Asp Glu Ser Leu Arg Gln Lys Thr Asn Ser Ala  
35 40 45  
Arg Gly Asp Ala Xaa Ser Lys Arg Asp Leu Thr Asn Ala Thr Arg Gly  
50 55 60  
Ile Glu Arg Asp Ile Ala Ser Leu Gln Gln Glu Glu Lys Lys Leu Val  
65 70 75 80  
Ala Glu Ile Lys Arg Thr Ala Lys Thr Gly Asn Glu Ala Ala Thr Lys  
85 90 95  
Ile Leu Ala Arg Gln Leu Ile Arg Leu Gln Gln Ile Ser Asn Leu  
100 105 110  
Gln Gly Ser Arg Ala Gln Ile Arg Gly Ile Ala Thr His Thr Gln Ala  
115 120 125  
Met His Ala Asn Thr Ser Val Ala Thr Gly Leu Gln Ser Ala Ser Lys  
130 135 140  
Ala Met Gly Ala Leu Asn Lys Gln Met Glu Pro Thr Lys Gln Met Lys  
145 150 155 160  
Ile Met Gln Glu Phe Gln Lys Gln Ser Ala Gln Met Asp Met Thr Asn  
165 170 175  
Glu Met Met Ser Asp Ser Ile Asp Asp Val Leu Asp Asp Asp Gln Ala  
180 185 190  
Glu Glu Glu Thr Glu Glu Leu Ala Asn Gln Val Leu Asp Glu Ile Gly  
195 200 205  
Val Asp Ile Ala Ser Gln Leu Ser Ser Ala Pro Lys Gly Lys Ile Ala  
210 215 220  
Gly Lys Lys Val Gln Val Asp Gly Ser Ser Glu Leu Glu Glu Leu Glu  
225 230 235 240  
Lys Arg Leu Ala Ala Leu Lys Asn Ala  
245

(2) INFORMATION FOR SEQ ID NO:1003:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 485 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..485

(D) OTHER INFORMATION: / Ceres Seq. ID 1499408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1003:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| attgctctct | ctcagagtc  | ccggcgcttc | agtggggggc | attcatggcg | gggcagtcgc | 60  |
| accgcgacct | ctccatcttc | tgcgccctcg | agtgaggagt | cgtggcgagg | gatgagattg | 120 |
| togaaatcgt | ccccaaacat | cgcatggagc | ccctcaacat | gatctgcggg | gatttcgggc | 180 |
| ctttcttccc | ccagattccc | accaaaggtg | ctctctgggt | cgctgtcgcg | ctcaagaagc | 240 |
| gtasaagtgc | accatccgca | ccccggactg | gatgactgtt | gaccgcttga | cacaggtatt | 300 |
| ggaagcgga  | agagagtcgc | cacgagaatt | ccagccatta | ccattccact | atattgaaat | 360 |
| ttctaagctt | ctgtttgatc | atgctcgtga | tgacatctca | gatgcatacc | tgggtgattg | 420 |
| ttaatgaatc | ttggtgcaga | tttgttagtt | gtgtctagta | agccctaata | aataaccacc | 480 |
| accac      |            |            |            |            |            |     |

(2) INFORMATION FOR SEQ ID NO:1004:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..53

(D) OTHER INFORMATION: / Ceres Seq. ID 1499409

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1004:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Ala | Leu | Ser | His | Glu | Ser | Arg | Arg | Ser | Ser | Gly | Gly | His | Ser | Trp |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Gly | Ser | Pro | Thr | Arg | Thr | Ser | Pro | Ser | Ser | Arg | Pro | Pro | Arg | Trp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Ser | Ser | Trp | Arg | Arg | Met | Arg | Leu | Ser | Lys | Ser | Ser | Pro | Thr | Ser | Ala |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Trp | Thr | Pro | Ser | Thr |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 50  |

(2) INFORMATION FOR SEQ ID NO:1005:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..90

(D) OTHER INFORMATION: / Ceres Seq. ID 1499410

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1005:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Ser | Leu | Ser | Arg | Val | Pro | Ala | Phe | Gln | Trp | Gly | Ala | Phe | Met | Ala |
| 1   |     |     |     |     | 5   |     |     |     |     |     |     |     |     | 15  |     |
| Gly | Gln | Ser | Asp | Pro | His | Leu | Ser | Ile | Phe | Ser | Pro | Ser | Glu | Val | Glu |
|     |     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |
| Phe | Val | Ala | Glu | Asp | Glu | Ile | Val | Glu | Ile | Val | Pro | Asn | Ile | Arg | Met |
|     |     |     |     |     | 35  |     |     | 40  |     |     |     | 45  |     |     |     |
| Asp | Ala | Leu | Asn | Met | Ile | Cys | Gly | Asp | Phe | Gly | Pro | Phe | Phe | Pro | Gln |
|     |     |     |     |     | 50  |     | 55  |     |     |     | 60  |     |     |     |     |
| Ile | Pro | Thr | Lys | Val | Pro | Leu | Trp | Leu | Ala | Val | Ala | Leu | Lys | Lys | Arg |
|     |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Xaa | Ser | Ala | Pro | Ser | Ala | Pro | Arg | Thr | Gly |     |     |     |     |     |     |
|     |     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1006:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide  
(ix) FEATURE:  
    (A) NAME/KEY: peptide  
    (B) LOCATION: 1..76  
    (D) OTHER INFORMATION: / Ceres Seq. ID 1499411  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1006:  
Met Ala Gly Gln Ser Asp Pro His Leu Ser Ile Phe Ser Pro Ser Glu  
1                  5                  10                  15  
Val Glu Phe Val Ala Glu Asp Glu Ile Val Glu Ile Val Pro Asn Ile  
                  20                  25                  30  
Arg Met Asp Ala Leu Asn Met Ile Cys Gly Asp Phe Gly Pro Phe Phe  
                  35                  40                  45  
Pro Gln Ile Pro Thr Lys Val Pro Leu Trp Leu Ala Val Ala Leu Lys  
                  50                  55                  60  
Lys Arg Xaa Ser Ala Pro Ser Ala Pro Arg Thr Gly  
65                  70                  75

(2) INFORMATION FOR SEQ ID NO:1007:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..468
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1007:

agcctctatc tcattccact cgcacattca cgtgcagctg tcggggagcag gcaatggcgc 60  
cggtactaaq cgaactcgcc gccgcgcgtc cagcccgctg cgctacctc gccgcgctcg 120  
gtgtggaagc aqaagagagc agagaggaga ggtgcgagct ggtgagatgg atcggttgga 180  
ggagcggaac attaagaara aggavaagga ggtatgganga ngcgcgcaag gaagangagc 240  
ggaargagga ggcggggggac aggaataccc aggagccgca gcaaggtcaa ggcctcarcc 300  
tmwvactcgm caacggcagc kacacgncag gtctgcaatg ttgccgatgt cgaacccttc 360  
agctaatccc acacagctta caattttcta tgggtgatca gtatgtgtgt atgactcggg 420  
tgccaccaga aaaggctcag gcaatcatgc ttatagctgc agctgcgg

(2) INFORMATION FOR SEQ ID NO:1008:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..155
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499413

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1008:

Ala Ser Ile Ser Phe His Ser Asp Ile His Val Gln Leu Ser Gly Ala  
1                  5                  10                  15  
Gly Asn Gly Ala Gly Ser Lys Arg Thr Arg Arg Arg Arg Ser Ser Pro  
                  20                  25                  30  
Trp Arg Leu Pro Arg Arg Arg Arg Cys Gly Lys Arg Lys Arg Glu Arg  
                  35                  40                  45  
Gly Glu Val Arg Ala Gly Glu Met Asp Arg Leu Glu Glu Arg Asn Ile  
                  50                  55                  60  
Lys Xaa Lys Xaa Lys Glu Asp Gly Xaa Xaa Ala Gln Gly Arg Xaa Ala  
65                  70                  75                  80  
Glu Xaa Gly Gly Gly Gly Gln Glu Tyr Pro Gly Ala Ala Ala Arg Ser  
                  85                  90                  95  
Arg Pro Xaa Pro Xaa Thr Xaa Gln Arg Gln Xaa Xaa Xaa Arg Ser Ala

100 105 110  
Met Leu Pro Met Ser Asn Pro Ser Ala Asn Pro Thr Gln Leu Thr Ile  
115 120 125  
Phe Tyr Gly Gly Ser Val Cys Val Tyr Asp Ser Gly Ala Thr Arg Lys  
130 135 140  
Gly Ser Gly Asn His Ala Tyr Ser Cys Ser Cys  
145 150 155

(2) INFORMATION FOR SEQ ID NO:1009:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..155

(D) OTHER INFORMATION: / Ceres Seq. ID 1499414

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1009:

Pro Leu Ser His Ser Thr Pro Thr Phe Thr Cys Ser Cys Arg Glu Gln  
1 5 10 15  
Ala Met Ala Pro Asp Leu Ser Glu Leu Ala Ala Ala Pro Ala Arg  
20 25 30  
Gly Ala Tyr Leu Ala Gly Val Gly Val Glu Arg Glu Arg Glu Arg Glu  
35 40 45  
Glu Arg Cys Glu Leu Val Arg Trp Ile Gly Trp Arg Ser Gly Thr Leu  
50 55 60  
Arg Xaa Arg Xaa Arg Arg Met Xaa Xaa Ala Arg Lys Glu Xaa Glu Arg  
65 70 75 80  
Xaa Glu Glu Ala Gly Asp Arg Asn Thr Gln Glu Pro Gln Gln Gly Gln  
85 90 95  
Gly Leu Xaa Xaa Leu Xaa Asn Gly Ser Xaa Xaa Xaa Gly Leu Gln  
100 105 110  
Cys Cys Arg Cys Arg Thr Leu Gln Leu Ile Pro His Ser Leu Gln Phe  
115 120 125  
Ser Met Val Asp Gln Tyr Val Cys Met Thr Arg Val Pro Pro Glu Lys  
130 135 140  
Ala Gln Ala Ile Met Leu Ile Ala Ala Ala Ala  
145 150 155

(2) INFORMATION FOR SEQ ID NO:1010:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1499415

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1010:

Met Ala Pro Asp Leu Ser Glu Leu Ala Ala Ala Pro Ala Arg Gly  
1 5 10 15  
Ala Tyr Leu Ala Gly Val Gly Val Glu Arg Glu Arg Glu Arg Glu  
20 25 30  
Arg Cys Glu Leu Val Arg Trp Ile Gly Trp Arg Ser Gly Thr Leu Arg  
35 40 45  
Xaa Arg Xaa Arg Arg Met Xaa Xaa Ala Arg Lys Glu Xaa Glu Arg Xaa  
50 55 60  
Glu Glu Ala Gly Asp Arg Asn Thr Gln Glu Pro Gln Gln Gly Gln Gly  
65 70 75 80

Leu Xaa Xaa Xaa Leu Xaa Asn Gly Ser Xaa Xaa Xaa Gly Leu Gln Cys  
85 90 95  
Cys Arg Cys Arg Thr Leu Gln Leu Ile Pro His Ser Leu Gln Phe Ser  
100 105 110  
Met Val Asp Gln Tyr Val Cys Met Thr Arg Val Pro Pro Glu Lys Ala  
115 120 125  
Gln Ala Ile Met Leu Ile Ala Ala Ala Ala  
130 135

(2) INFORMATION FOR SEQ ID NO:1011:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..392
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499416

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1011:

cgtgccacac atccatcccc gttagcctct tctctccct cctgccgggt ccttaataaaa 60  
gagcagcagc gcaagagggt gtagagcga gcgagaagaa ggcaatggcg gcggagagct 120  
tctgtttcac ctccgagttcc gtgaacgarg ggcaccacaga caagctgtgc gaccaggtgt 180  
cggaacgcgtt gctggagcgc tgctggcgcc aggaacccga cagcaagggt gcctgcgaga 240  
cctgcaccaa gacgaacatg gtgatggtgt tcggcgagat caccaccaag gcgagcgtgg 300  
actacgagaa gatcgtdcgc gacacctgcc gcgagatcgg gttcacctcc gacgacgtgg 360  
ggctgcagcg cgaccgtgac aargtgctgg tg

(2) INFORMATION FOR SEQ ID NO:1012:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..47
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499417

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1012:

Arg Ala Thr His Pro Ser Pro Phe Ala Ser Ser Pro Pro Ser Cys Arg  
1 5 10 15  
Val Leu Asn Lys Glu Gln Gln Arg Lys Arg Leu Val Glu Arg Ala Arg  
20 25 30  
Arg Arg Gln Trp Arg Arg Arg Ala Ser Cys Ser Pro Arg Ser Pro  
35 40 45

(2) INFORMATION FOR SEQ ID NO:1013:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..96
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499418

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1013:

Met Ala Ala Glu Ser Phe Leu Phe Thr Ser Glu Ser Val Asn Xaa Gly  
1 5 10 15  
His Pro Asp Lys Leu Cys Asp Gln Val Ser Asp Ala Val Leu Asp Ala  
20 25 30

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Leu | Ala | Gln | Asp | Pro | Asp | Ser | Lys | Val | Ala | Cys | Glu | Thr | Cys | Thr |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Thr | Asn | Met | Val | Met | Val | Phe | Gly | Glu | Ile | Thr | Thr | Lys | Ala | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Asp | Tyr | Glu | Lys | Ile | Xaa | Arg | Asp | Thr | Cys | Arg | Glu | Ile | Gly | Phe |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Thr | Ser | Asp | Asp | Val | Gly | Leu | Asp | Ala | Asp | Arg | Cys | Xaa | Val | Leu | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

(2) INFORMATION FOR SEQ ID NO:1014:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..486
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1014:

|             |            |            |            |             |             |     |
|-------------|------------|------------|------------|-------------|-------------|-----|
| gaacagggttt | acaggcgcg  | tccgcacgc  | atgccccaac | ccttttttga  | caagctcagc  | 60  |
| gtccaccact  | aaatggcgg  | ggagaccaaa | ccgcttcg   | ccatcggggt  | tgccggcgag  | 120 |
| atggagggtg  | aggcatacc  | ccgcctattc | ccagtggcct | tcttgaggag  | ccacctgggt  | 180 |
| gagtcggtcc  | gcatacgat  | ccgcgcgctg | aragaggccc | gcaccaccac  | cgctgcgcctc | 240 |
| ggcgccggtg  | cctccgcgc  | tggttccgct | ctcgtccgct | ttggcgacac  | cgccatgctc  | 300 |
| gcgtcggtca  | agctcgaggt | gatgtcgccc | tcggccgagt | acccagacga  | aggatccgtc  | 360 |
| tctgttgagt  | tccacatgcc | gcccatctgc | tccccgctgg | ttaggccagg  | ccgatctcgt  | 420 |
| gaggtggcac  | cagtcatctc | caaggccctt | gaagacgttt | tggtgatgatt | ccagaatgct  | 480 |
| aaattt      |            |            |            |             |             |     |

(2) INFORMATION FOR SEQ ID NO:1015:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..69
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1015:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Arg | Phe | Thr | Gly | Ala | Leu | Pro | His | Ala | Cys | Pro | Asn | Pro | Phe | Leu |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Thr | Ser | Ser | Ala | Ser | Thr | Thr | Lys | Trp | Arg | Arg | Arg | Pro | Asn | Arg | Leu |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Arg | Pro | Ser | Gly | Leu | Pro | Ala | Arg | Trp | Arg | Trp | Arg | His | Thr | Ala | Ala |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Tyr | Ser | Gln | Trp | Pro | Ser | Trp | Ser | Ala | Thr | Trp | Val | Ser | Pro | Ser | Ala |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Ser | Met | Pro | Ala | Ala |     |     |     |     |     |     |     |     |     |     |     |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1016:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..138
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1016:

Met Ala Ala Glu Thr Lys Pro Ala Ala Ala Ile Gly Val Ala Gly Glu  
1 5 10 15  
Met Glu Val Glu Ala Tyr Arg Arg Leu Phe Pro Val Ala Phe Leu Glu  
20 25 30  
Arg His Leu Gly Glu Ser Val Arg Ile Asp Ala Arg Arg Leu Xaa Glu  
35 40 45  
Ala Arg Thr Thr Thr Val Ala Leu Gly Ala Val Ser Ser Ala His Gly  
50 55 60  
Ser Ala Leu Val Arg Val Gly Asp Thr Ala Met Leu Ala Ser Val Lys  
65 70 75 80  
Leu Glu Val Met Ser Pro Ser Ala Glu Tyr Pro Asp Glu Gly Ser Val  
85 90 95  
Ser Val Glu Phe His Met Pro Pro Ile Cys Ser Pro Leu Val Arg Pro  
100 105 110  
Gly Arg Ser Ala Glu Val Ala Pro Val Ile Ser Lys Ala Leu Glu Asp  
115 120 125  
Val Leu Asp Glu Phe Gln Asn Ala Lys Phe  
130 135

(2) INFORMATION FOR SEQ ID NO:1017:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..122
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1017:

Met Glu Val Glu Ala Tyr Arg Arg Leu Phe Pro Val Ala Phe Leu Glu  
1 5 10 15  
Arg His Leu Gly Glu Ser Val Arg Ile Asp Ala Arg Arg Leu Xaa Glu  
20 25 30  
Ala Arg Thr Thr Thr Val Ala Leu Gly Ala Val Ser Ser Ala His Gly  
35 40 45  
Ser Ala Leu Val Arg Val Gly Asp Thr Ala Met Leu Ala Ser Val Lys  
50 55 60  
Leu Glu Val Met Ser Pro Ser Ala Glu Tyr Pro Asp Glu Gly Ser Val  
65 70 75 80  
Ser Val Glu Phe His Met Pro Pro Ile Cys Ser Pro Leu Val Arg Pro  
85 90 95  
Gly Arg Ser Ala Glu Val Ala Pro Val Ile Ser Lys Ala Leu Glu Asp  
100 105 110  
Val Leu Asp Glu Phe Gln Asn Ala Lys Phe  
115 120

(2) INFORMATION FOR SEQ ID NO:1018:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1617 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1617
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499446



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1018:

|             |             |            |            |             |             |      |
|-------------|-------------|------------|------------|-------------|-------------|------|
| aaactgaaag  | ttaggacctt  | tcatttccaa | ttctataaac | catttctcta  | cgattagaga  | 60   |
| agctgacatc  | aaaattgaaa  | cttggaattt | tttagatttg | ttcttcttct  | atggcaactg  | 120  |
| aagacgatgg  | tgaattgtca  | gctcgtttac | agaacacggt | ggatgcattg  | tcgtctttga  | 180  |
| tcacaaaaacg | tgccggttta  | gctagtaaca | accaatctca | cggattccgt  | ttgctctttc  | 240  |
| attatctcaa  | ggttcttgag  | cttgaagatg | cagtttcaca | aatgaaaatc  | attcatgttg  | 300  |
| cgggaactaa  | aggaagaggga | tcacatgtta | catttgcgga | gtctattctt  | cggtgtttacg | 360  |
| gtcttctgaac | tggttctctc  | acatctctct | acttaatcga | gtcccgagag  | agattccogtc | 420  |
| ttaacggcat  | tgagataaagc | caggagaaat | ttgtgaacta | cttttgggtg  | tcctttccata | 480  |
| agctcaaggga | gaaaaccagc  | aattgaggtg | atgttggtat | actagaagtt  | gttgatcgata | 540  |
| ggagattccga | tgcgactaact | gtgattcaga | aacctgtcgt | ctgtgggtatt | tcctctctgat | 600  |
| ggatgacca   | ttaggagatt  | cttgataaca | cacttgctga | aattgtcgca  | ggagaaacccg | 660  |
| gtatcttcaa  | gagtgaggatt | cctgctttta | cagtggtcca | acctgatgaa  | gcaatgcggtg | 720  |
| tactcaatga  | aaaagcttca  | aaattggagg | tgaattctca | ggtgtgggaa  | ccgttggact  | 780  |
| caagccagag  | actcgggctt  | caaggcgaa  | atcaatatct | aaacgctggt  | cttgcgtgtg  | 840  |
| cggtgtgctt  | tacatttctt  | aaagagattg | gtattgagga | caagaatggt  | ttggatcaga  | 900  |
| caaacggttc  | acccgaaaaa  | ttcatctctg | gattgtcaaa | tgcttatttg  | atgggacgag  | 960  |
| ctatgatagt  | gcctgattca  | gaactccctg | aagagattgt | gtattacctt  | gatggagctc  | 1020 |
| atagtcctga  | aagcatggaa  | gcttgcgcta | tatgggtttc | aaaaacagatc | aaacaaaaac  | 1080 |
| aagaaaagaa  | ccagaaaaag  | tcagagcaga | tactcttggt | caattgtatg  | tcgtttcgtg  | 1140 |
| accggagttt  | gcttctctcg  | cgattaaaga | gtaaatgcat | tgatcaagga  | gttgatttca  | 1200 |
| agagagccgt  | ttttgtgcc   | aacgtatcag | tgtacaacca | agtggtgatct | tcgacaaaacg | 1260 |
| ttggcacaac  | tgctcgagtc  | atgtcgtggc | agttcggctc | tcagagaggt  | tgggagaggtt | 1320 |
| tagctcgagg  | tgaagcaaaa  | tctaattcaa | aaagtgtatt | taaaggcaaa  | gaagaagaga  | 1380 |
| agagtttctg  | tttctctgta  | cttctctgtg | ctgttgagtc | gctccgggag  | aatgcctgcc  | 1440 |
| aaagtataaca | agttcgtttt  | caggtgttgg | taactggttc | attacatttg  | gtgggtgatc  | 1500 |
| tccttgagatt | tatacaagaa  | tgaatatgtt | ttcgccatgt | attcttgccc  | aatctttgcc  | 1560 |
| tgtaatgact  | atatatctca  | caacatgatt | tacaaaaaga | aaagaaaaga  | tatttcg     |      |

(2) INFORMATION FOR SEQ ID NO:1019:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..470
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1019:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Thr | Glu | Asp | Asp | Gly | Glu | Leu | Ser | Ala | Arg | Tyr | Gln | Asn | Thr |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Leu | Asp | Ala | Leu | Ser | Ser | Leu | Ile | Thr | Lys | Arg | Gly | Arg | Leu | Ala | Ser |
|     |     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Asn | Gln | Ser | His | Arg | Phe | Arg | Leu | Leu | Phe | His | Tyr | Leu | Lys | Val |
|     |     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |
| Leu | Glu | Leu | Glu | Asp | Ala | Val | Ser | Gln | Met | Lys | Ile | Ile | His | Val | Ala |
|     |     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |
| Gly | Thr | Lys | Gly | Lys | Gly | Ser | Thr | Cys | Thr | Phe | Ala | Glu | Ser | Ile | Leu |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |     |
| Arg | Cys | Tyr | Gly | Leu | Arg | Thr | Gly | Leu | Phe | Thr | Ser | Pro | His | Leu | Ile |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Asp | Val | Arg | Glu | Arg | Phe | Arg | Leu | Asn | Gly | Ile | Glu | Ile | Ser | Gln | Glu |
|     |     |     |     | 100 |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Phe | Val | Asn | Tyr | Phe | Trp | Cys | Ser | Phe | His | Lys | Leu | Lys | Glu | Lys |
|     |     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |
| Thr | Ser | Asn | Glu | Val | Asp | Val | Val | Ile | Leu | Glu | Val | Gly | Leu | Gly | Gly |
|     |     |     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |
| Arg | Phe | Asp | Ala | Thr | Asn | Val | Ile | Gln | Lys | Pro | Val | Val | Cys | Gly | Ile |
|     |     |     |     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |
| Ser | Ser | Leu | Gly | Tyr | Asp | His | Met | Glu | Ile | Leu | Gly | Tyr | Thr | Leu | Ala |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Ile | Ile | His | Val | Ala | Gly | Thr | Lys | Gly | Lys | Gly | Ser | Thr | Cys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Phe | Ala | Glu | Ser | Ile | Leu | Arg | Cys | Thr | Gly | Leu | Arg | Thr | Gly | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Thr | Ser | Pro | His | Leu | Ile | Asp | Val | Arg | Glu | Arg | Phe | Arg | Leu | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Ile | Glu | Ile | Ser | Gln | Glu | Lys | Phe | Val | Asn | Thr | Phe | Trp | Cys | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Phe | His | Lys | Leu | Lys | Glu | Lys | Thr | Ser | Asn | Glu | Val | Asp | Val | Val | Ile |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |

Leu Glu Val Gly Leu Gly Gly Arg Phe Asp Ala Thr Asn Val Ile Gln  
85 90 95  
Lys Pro Val Val Cys Gly Ile Ser Ser Leu Gly Tyr Asp His Met Glu  
100 105 110  
Ile Leu Gly Tyr Thr Leu Ala Glu Ile Ala Ala Glu Lys Ala Gly Ile  
115 120 125  
Phe Lys Ser Gly Val Pro Ala Phe Thr Val Ala Gln Pro Asp Glu Ala  
130 135 140  
Met Arg Val Leu Asn Glu Lys Ala Ser Lys Leu Glu Val Asn Leu Gln  
145 150 155 160  
Val Val Glu Pro Leu Asp Ser Ser Gln Arg Leu Gly Leu Gln Gly Glu  
165 170 175  
His Gln Tyr Leu Asn Ala Gly Leu Ala Val Ala Leu Cys Ser Thr Phe  
180 185 190  
Leu Lys Glu Ile Gly Ile Glu Asp Lys Asn Gly Leu Asp Gln Thr Asn  
195 200 205  
Gly Leu Pro Glu Lys Phe Ile Ser Gly Leu Ser Asn Ala Tyr Leu Met  
210 215 220  
Gly Arg Ala Met Ile Val Pro Asp Ser Glu Leu Pro Glu Glu Ile Val  
225 230 235 240  
Tyr Tyr Leu Asp Gly Ala His Ser Pro Glu Ser Met Glu Ala Cys Ala  
245 250 255  
Ile Trp Phe Ser Lys Gln Ile Lys Gln Asn Gln Glu Arg Asn Gln Lys  
260 265 270  
Arg Ser Glu Gln Ile Leu Leu Phe Asn Cys Met Ser Val Arg Asp Pro  
275 280 285  
Ser Leu Leu Leu Pro Arg Leu Arg Ser Lys Cys Ile Asp Gln Gly Val  
290 295 300  
Asp Phe Lys Arg Ala Val Phe Val Pro Asn Val Ser Val Tyr Asn Gln  
305 310 315 320  
Val Gly Ser Ser Thr Asn Val Gly Thr Arg Val Glu Ser Met Ser Trp  
325 330 335  
Gln Phe Gly Leu Gln Arg Ile Trp Glu Ser Leu Ala Arg Gly Glu Ala  
340 345 350  
Lys Ser Asn Ser Lys Ser Asp Ser Lys Gly Lys Glu Glu Glu Lys Ser  
355 360 365  
Phe Val Phe Ser Ser Leu Pro Val Ala Val Asp Trp Leu Arg Asp Asn  
370 375 380  
Ala Arg Gln Ser Lys Gln Val Arg Phe Gln Val Leu Val Thr Gly Ser  
385 390 395 400  
Leu His Leu Val Gly Asp Leu Leu Arg Phe Ile Lys Lys  
405 410

(2) INFORMATION FOR SEQ ID NO:1021:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..303
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499449

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1021:

Met Glu Ile Leu Gly Tyr Thr Leu Ala Glu Ile Ala Ala Glu Lys Ala  
1 5 10 15  
Gly Ile Phe Lys Ser Gly Val Pro Ala Phe Thr Val Ala Gln Pro Asp  
20 25 30  
Glu Ala Met Arg Val Leu Asn Glu Lys Ala Ser Lys Leu Glu Val Asn  
35 40 45  
Leu Gln Val Val Glu Pro Leu Asp Ser Ser Gln Arg Leu Gly Leu Gln

|     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 50  |     |     |     |     |     | 55  |     |     |     |     |     | 60  |
| Gly | Glu | His | Gln | Tyr | Leu | Asn | Ala | Gly | Leu | Ala | Val | Ala |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     | 80  |
| Thr | Phe | Leu | Lys | Glu | Ile | Gly | Ile | Glu | Asp | Lys | Asn | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     | 95  |
| Thr | Asn | Gly | Leu | Pro | Glu | Lys | Phe | Ile | Ser | Gly | Leu | Ser |
|     |     |     |     | 100 |     |     |     |     | 105 |     |     | 110 |
| Leu | Met | Gly | Arg | Ala | Met | Ile | Val | Pro | Asp | Ser | Glu | Leu |
|     |     |     |     | 115 |     |     |     |     | 120 |     |     | 125 |
| Ile | Val | Tyr | Tyr | Leu | Asp | Gly | Ala | His | Ser | Pro | Glu | Ser |
|     |     |     |     | 130 |     |     |     |     | 135 |     |     | 140 |
| Cys | Ala | Ile | Trp | Phe | Ser | Lys | Gln | Ile | Lys | Gln | Asn | Gln |
|     |     |     |     | 145 |     |     |     |     | 150 |     |     | 155 |
| Gln | Lys | Arg | Ser | Glu | Gln | Ile | Leu | Leu | Phe | Asn | Cys | Met |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     | 175 |
| Asp | Pro | Ser | Leu | Leu | Leu | Pro | Arg | Leu | Arg | Ser | Lys | Cys |
|     |     |     |     | 180 |     |     |     |     | 185 |     |     | 190 |
| Gly | Val | Asp | Phe | Lys | Arg | Ala | Val | Phe | Val | Pro | Asn | Val |
|     |     |     |     | 195 |     |     |     |     | 200 |     |     | 205 |
| Asn | Gln | Val | Gly | Ser | Ser | Thr | Asn | Val | Gly | Thr | Arg | Val |
|     |     |     |     | 210 |     |     |     |     | 215 |     |     | 220 |
| Ser | Trp | Gln | Phe | Gly | Leu | Gln | Arg | Ile | Trp | Glu | Ser | Leu |
|     |     |     |     | 225 |     |     |     |     | 230 |     |     | 235 |
| Glu | Ala | Lys | Ser | Asn | Ser | Lys | Ser | Asp | Ser | Lys | Gly | Lys |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     | 255 |
| Lys | Ser | Phe | Val | Phe | Ser | Ser | Leu | Pro | Val | Ala | Val | Asp |
|     |     |     |     | 260 |     |     |     |     | 265 |     |     | 270 |
| Asp | Asn | Ala | Arg | Gln | Ser | Lys | Gln | Val | Arg | Phe | Gln | Val |
|     |     |     |     | 275 |     |     |     |     | 280 |     |     | 285 |
| Gly | Ser | Leu | His | Leu | Val | Gly | Asp | Leu | Leu | Arg | Phe | Ile |
|     |     |     |     | 290 |     |     |     |     | 295 |     |     | 300 |

(2) INFORMATION FOR SEQ ID NO:1022:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1755 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1755
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1022:

|             |              |            |             |             |             |      |
|-------------|--------------|------------|-------------|-------------|-------------|------|
| atctcacaca  | ccgaagaagtta | ttttcgaaac | cactaacgaa  | tcttcacacag | caaaaaactt  | 60   |
| tcgtgttccct | ctgtaatttc   | tcagtatata | tagataccaa  | atcgagcagt  | gaaaaaaatg  | 120  |
| ctatggcgag  | tttatatcgg   | cgatctcttc | cttctcctcc  | ggccattgac  | ttttcttcog  | 180  |
| ccgaagaagn  | ctaattctca   | atgaagcgct | tcagaaagga  | actatggaag  | gatttttccag | 240  |
| gttgatttcg  | tattttcaga   | cacaatccga | acctgcgtat  | tgtgtgtttg  | ctagtctctc  | 300  |
| agtggtgttg  | aatgctcttt   | ctatcgatcc | tggacgtaaa  | tggaaaaggc  | cttgagggtg  | 360  |
| gtttatgaaa  | tcaatgttgg   | attgctgcga | acctctggaa  | gtagtgaagg  | aaaaaggcat  | 420  |
| ttcaatttga  | aaagtgtctc   | gtttgggtca | ttgttcagga  | gcacaaagtg  | aggctttccg  | 480  |
| tacaaatcga  | agcaccattg   | atgattttcc | gcamaattgt  | cgtagaatgc  | acgagtctcg  | 540  |
| agaattgcga  | tatgatctca   | acatatcaca | gaggtgtatt  | taagcagact  | gggactggct  | 600  |
| acttttcacc  | tattgtgtgc   | tataatgctg | agagagatat  | ggctttgatt  | cttgatgttg  | 660  |
| ctcgtttcaa  | gtatccccct   | cactgggttc | ctcttaaaact | tctttgggaa  | gccatggaca  | 720  |
| gtattgatca  | gtcaacaggg   | aaacgtagag | ggttcatgct  | catatctgaa  | ccacacagag  | 780  |
| aaaccggatt  | gctctatact   | ctgagctcga | aggatgaaag  | ctggatcgaa  | atagccaagt  | 840  |
| atttgaagga  | agatgttctc   | cgtcttgtaa | gttcacagca  | gtgatattct  | gtggagaaaa  | 900  |
| tcataatcagt | ttgtttcaga   | tcacttccat | caaatctcaa  | ccaattctca  | agatgggtgg  | 960  |
| ctgagatccg  | aattacagag   | gactcaaac  | aaaatctcag  | cgcagaggag  | aagtctaggc  | 1020 |
| tgaacaataa  | gcaattgtgt   | ctgaaggga  | tgcaagaaac  | tgaactgttc  | aaacacatca  | 1080 |

|             |             |            |            |             |             |      |
|-------------|-------------|------------|------------|-------------|-------------|------|
| ataagttctt  | atccacagtg  | ggttatgaag | acagtcgtac | ttatgctgct  | gcaaaggctt  | 1140 |
| gttgccaagg  | agctgaaatc  | ttatccggaa | gctcatcaaa | agagttttgt  | tgtcgggaaa  | 1200 |
| cttgcgtgaa  | atgcatcaaa  | ggctcgtgat | actctgaagg | cacagtggtg  | actggagttg  | 1260 |
| tggtgcgtga  | tgggaatgaa  | caaaagggtg | atctgttagt | gccatcgacg  | caaaactgag  | 1320 |
| gtgaatgtgg  | tcctgaagca  | acttatccag | caggaaacga | tgtgttcact  | gcactttcat  | 1380 |
| tggctttacc  | tccacagaca  | tggtcaggga | tcaaagacca | agctcttatg  | catgaaatga  | 1440 |
| agcagctcat  | ttccatggct  | tccttcccaa | ctttgcttca | agaagaggta  | ttgcaatctt  | 1500 |
| gaecggcaact | tcagctgcta  | aaacgatgcc | aagagaaaca | ggaagaggat  | gatctcgctg  | 1560 |
| ctctcgctta  | ttagtctcatt | gtcccaaatc | cactctcttc | cccatgttga  | tccacagttc  | 1620 |
| tcaacacttg  | attgttagaa  | agtctcttta | ttgtctgtac | gattcaaaact | ctatttgcaa  | 1680 |
| tgagagatat  | ttgtaaacat  | attcattcta | tgaattgtta | atcacaataa  | gtaaaagaatc | 1740 |
| ttagaatcat  | atttc       |            |            |             |             |      |

(2) INFORMATION FOR SEQ ID NO:1023:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..357
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499451

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1023:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Phe | Arg | Xaa | Xaa | Val | Val | Lys | Cys | Thr | Ser | Ser | Glu | Asn | Cys |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     | 15  |     |
| His | Met | Ile | Ser | Thr | Tyr | His | Arg | Gly | Val | Phe | Lys | Gln | Thr | Gly | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | His | Phe | Ser | Pro | Ile | Gly | Gly | Tyr | Asn | Ala | Glu | Arg | Asp | Met | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Ile | Leu | Asp | Val | Ala | Arg | Phe | Lys | Tyr | Pro | Pro | His | Trp | Val | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Lys | Leu | Leu | Trp | Glu | Ala | Met | Asp | Ser | Ile | Asp | Gln | Ser | Thr | Gly |
| 65  |     |     |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| Lys | Arg | Arg | Gly | Phe | Met | Leu | Ile | Ser | Arg | Pro | His | Arg | Glu | Pro | Gly |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Leu | Tyr | Thr | Leu | Ser | Cys | Lys | Asp | Glu | Ser | Trp | Ile | Glu | Ile | Ala |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Tyr | Leu | Lys | Glu | Asp | Val | Pro | Arg | Leu | Val | Ser | Ser | Gln | His | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Ser | Val | Glu | Lys | Ile | Ile | Ser | Val | Val | Phe | Lys | Ser | Leu | Pro | Ser |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asn | Phe | Asn | Gln | Phe | Ile | Arg | Trp | Val | Ala | Glu | Ile | Arg | Ile | Thr | Glu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Asp | Ser | Asn | Gln | Asn | Leu | Ser | Ala | Glu | Glu | Lys | Ser | Arg | Leu | Lys | Leu |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Lys | Gln | Leu | Val | Leu | Lys | Glu | Val | His | Glu | Thr | Glu | Leu | Phe | Lys | His |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | Asn | Lys | Phe | Leu | Ser | Thr | Val | Gly | Tyr | Glu | Asp | Ser | Leu | Thr | Tyr |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ala | Ala | Ala | Lys | Ala | Cys | Cys | Gln | Gly | Ala | Glu | Ile | Leu | Ser | Gly | Ser |
|     |     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Ser | Ser | Lys | Glu | Phe | Cys | Cys | Arg | Glu | Thr | Cys | Val | Lys | Cys | Ile | Lys |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Gly | Pro | Asp | Asp | Ser | Glu | Gly | Thr | Val | Val | Thr | Gly | Val | Val | Val | Arg |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Asp | Gly | Asn | Glu | Gln | Lys | Val | Asp | Leu | Val | Pro | Ser | Thr | Gln | Thr |     |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Glu | Cys | Glu | Cys | Gly | Pro | Glu | Ala | Thr | Tyr | Pro | Ala | Gly | Asn | Asp | Val |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Phe | Thr | Ala | Leu | Leu | Leu | Ala | Leu | Pro | Pro | Gln | Thr | Trp | Ser | Gly | Ile |

290 295 300  
Lys Asp Gln Ala Leu Met His Glu Met Lys Gln Leu Ile Ser Met Ala  
305 310 315 320  
Ser Leu Pro Thr Leu Leu Gln Glu Glu Val Leu His Leu Arg Arg Gln  
325 330 335  
Leu Gln Leu Leu Lys Arg Cys Gln Glu Asn Lys Glu Glu Asp Asp Leu  
340 345 350  
Ala Ala Pro Ala Tyr  
355

(2) INFORMATION FOR SEQ ID NO:1024:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 340 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..340

(D) OTHER INFORMATION: / Ceres Seq. ID 1499452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1024:

Met Ile Ser Thr Tyr His Arg Gly Val Phe Lys Gln Thr Gly Thr Gly  
1 5 10 15  
His Phe Ser Pro Ile Gly Gly Tyr Asn Ala Glu Arg Asp Met Ala Leu  
20 25 30  
Ile Leu Asp Val Ala Arg Phe Lys Tyr Pro Pro His Trp Val Pro Leu  
35 40 45  
Lys Leu Leu Trp Glu Ala Met Asp Ser Ile Asp Gln Ser Thr Gly Lys  
50 55 60  
Arg Arg Gly Phe Met Leu Ile Ser Arg Pro His Arg Glu Pro Gly Leu  
65 70 75 80  
Leu Tyr Thr Leu Ser Cys Lys Asp Glu Ser Trp Ile Glu Ile Ala Lys  
85 90 95  
Tyr Leu Lys Glu Asp Val Pro Arg Leu Val Ser Ser Gln His Val Asp  
100 105 110  
Ser Val Glu Lys Ile Ile Ser Val Val Phe Lys Ser Leu Pro Ser Asn  
115 120 125  
Phe Asn Gln Phe Ile Arg Trp Val Ala Glu Ile Arg Ile Thr Glu Asp  
130 135 140  
Ser Asn Gln Asn Leu Ser Ala Glu Glu Lys Ser Arg Leu Lys Leu Lys  
145 150 155 160  
Gln Leu Val Leu Lys Glu Val His Glu Thr Glu Leu Phe Lys His Ile  
165 170 175  
Asn Lys Phe Leu Ser Thr Val Gly Tyr Glu Asp Ser Leu Thr Tyr Ala  
180 185 190  
Ala Ala Lys Ala Cys Cys Gln Gly Ala Glu Ile Leu Ser Gly Ser Ser  
195 200 205  
Ser Lys Glu Phe Cys Cys Arg Glu Thr Cys Val Lys Cys Ile Lys Gly  
210 215 220  
Pro Asp Asp Ser Glu Gly Thr Val Val Thr Gly Val Val Val Arg Asp  
225 230 235 240  
Gly Asn Glu Gln Lys Val Asp Leu Leu Val Pro Ser Thr Gln Thr Glu  
245 250 255  
Cys Glu Cys Gly Pro Glu Ala Thr Tyr Pro Ala Gly Asn Asp Val Phe  
260 265 270  
Thr Ala Leu Leu Leu Ala Leu Pro Gln Thr Trp Ser Gly Ile Lys  
275 280 285  
Asp Gln Ala Leu Met His Glu Met Lys Gln Leu Ile Ser Met Ala Ser  
290 295 300  
Leu Pro Thr Leu Leu Gln Glu Glu Val Leu His Leu Arg Arg Gln Leu  
305 310 315 320

Gln Leu Leu Lys Arg Cys Gln Glu Asn Lys Glu Glu Asp Asp Leu Ala  
325 330 335  
Ala Pro Ala Tyr  
340

(2) INFORMATION FOR SEQ ID NO:1025:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..311

(D) OTHER INFORMATION: / Ceres Seq. ID 1499453

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1025:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Leu | Ile | Leu | Asp | Val | Ala | Arg | Phe | Lys | Tyr | Pro | Pro | His | Trp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Pro | Leu | Lys | Leu | Leu | Trp | Glu | Ala | Met | Asp | Ser | Ile | Asp | Gln | Ser |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Thr | Gly | Lys | Arg | Arg | Gly | Phe | Met | Leu | Ile | Ser | Arg | Pro | His | Arg | Glu |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Pro | Gly | Leu | Leu | Tyr | Thr | Leu | Ser | Cys | Lys | Asp | Glu | Ser | Trp | Ile | Glu |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Ala | Lys | Tyr | Leu | Lys | Glu | Asp | Val | Pro | Arg | Leu | Val | Ser | Ser | Gln |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| His | Val | Asp | Ser | Ser | Val | Glu | Lys | Ile | Ile | Ser | Val | Val | Phe | Lys | Ser |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Ser | Asn | Phe | Asn | Gln | Phe | Ile | Arg | Trp | Val | Ala | Glu | Ile | Arg | Ile |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Thr | Glu | Asp | Ser | Asn | Gln | Asn | Leu | Ser | Ala | Glu | Glu | Lys | Ser | Arg | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Lys | Leu | Lys | Gln | Leu | Val | Leu | Lys | Glu | Val | His | Glu | Thr | Glu | Leu | Phe |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | His | Ile | Asn | Lys | Phe | Leu | Ser | Thr | Val | Gly | Tyr | Glu | Asp | Ser | Leu |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Thr | Tyr | Ala | Ala | Ala | Lys | Ala | Cys | Cys | Gln | Gly | Ala | Glu | Ile | Leu | Ser |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gly | Ser | Ser | Ser | Lys | Glu | Phe | Cys | Cys | Arg | Glu | Thr | Cys | Val | Lys | Cys |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Ile | Lys | Gly | Pro | Asp | Asp | Ser | Glu | Gly | Thr | Val | Val | Thr | Gly | Val | Val |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Val | Arg | Asp | Gly | Asn | Glu | Gln | Lys | Val | Asp | Leu | Leu | Val | Pro | Ser | Thr |
|     |     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |
| Gln | Thr | Glu | Cys | Glu | Cys | Gly | Pro | Glu | Ala | Thr | Tyr | Pro | Ala | Gly | Asn |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     | 240 |     |
| Asp | Val | Phe | Thr | Ala | Leu | Leu | Leu | Ala | Leu | Pro | Pro | Gln | Thr | Trp | Ser |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gly | Ile | Lys | Asp | Gln | Ala | Leu | Met | His | Glu | Met | Lys | Gln | Leu | Ile | Ser |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Met | Ala | Ser | Leu | Pro | Thr | Leu | Leu | Gln | Glu | Glu | Val | Leu | His | Leu | Arg |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Arg | Gln | Leu | Gln | Leu | Leu | Lys | Arg | Cys | Gln | Glu | Asn | Lys | Glu | Glu | Asp |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Asp | Leu | Ala | Ala | Pro | Ala | Tyr |     |     |     |     |     |     |     |     |     |
| 305 |     |     |     | 310 |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:1026:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1283 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)  
(ix) FEATURE:

(A) NAME/KEY: -  
(B) LOCATION: 1..1283  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499458

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1026:

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| gaaggaccag  | accgagagaga | agttgagctg  | tatgtggaag  | agatactgtc  | actgatgcag  | 60   |
| ttgggtgagg  | actataccga  | gttcatgggtg | tcaaaaatca  | agtctttgac  | gtcggtagat  | 120  |
| cctgaattgt  | tgccaacggc  | tacaaaggca  | tttagaaata  | agagttttag  | caaagcgatt  | 180  |
| caggatgtga  | cgagatatata | tgttatacta  | gaagggttct  | ttatggttga  | gaatgcagat  | 240  |
| aaagctatta  | ggatcgatga  | gcattgtacct | gacagcctta  | ccacttcaat  | gtggacaggt  | 300  |
| gtgtttctacg | tggttcagag  | ttgtctgagg  | agagcgattt  | caacttcaaa  | cataagttct  | 360  |
| gtgatttgctg | tggttgagcta | tgcttggtagc | ttgtttggcca | atgattacca  | tgaagctctta | 420  |
| caacagaaga  | ttagagagcc  | taaccttgggt | gctaggttgt  | tcttgggtgg  | tataggtaatg | 480  |
| gaaaacaccg  | gaactgagat  | tgcaactgct  | ttgaacaata  | tggacgtgag  | ctgcgagtagc | 540  |
| attctcaaac  | taaaacatga  | aatcgaggag  | caatgtactg  | aggtatttcc  | tgccaccagca | 600  |
| gatcgagaga  | ggataaaatc  | atgtctatcc  | gagctaggcg  | agttaaagcag | cacgttcaag  | 660  |
| cagttactca  | actcaggcat  | ggaacagcta  | gtagcaaccg  | taacaccaag  | aatccgtccg  | 720  |
| gtttcagaca  | ccgtggctac  | cataagctac  | gagttaacag  | aaaccgagta  | cgcagagaaat | 780  |
| gaggttaaacg | acccttgggt  | ccaaagactt  | ctccactcag  | tcgaaacaaa  | tgccgcgtgg  | 840  |
| ctcccaaccac | taatgacatc  | caacaactac  | gactcgtttc  | tgcatctcat  | aattgatttc  | 900  |
| atagttaaaga | gactcgaagt  | cataatgatg  | cagaaacggt  | ttanccagct  | tggtgggctt  | 960  |
| cagcttgatc  | gagacacaag  | gcttttgggt  | agccatttct  | cggtgatgac  | tcaaaagaaca | 1020 |
| gtgagagata  | agtttgctcg  | gttaacgcag  | atggcgacga  | tactgaactt  | ggaaaaaggtc | 1080 |
| tcagagatttt | tggacttttg  | gggagaaaaa  | tcaggaccga  | tgactttgag  | actcacacaa  | 1140 |
| gctgaggttta | gacgggtttt  | gggtctccgg  | ctgcagttca  | aaaccggaatc | aattgctgct  | 1200 |
| ctcaagttgt  | gatgttaact  | cttttcttta  | ttatgtcatc  | tacacaactc  | gaaccaattc  | 1260 |
| tttcgaaatc  | tgattggttc  | ccc         |             |             |             |      |

- (2) INFORMATION FOR SEQ ID NO:1027:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 403 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

(A) NAME/KEY: peptide  
(B) LOCATION: 1..403  
(D) OTHER INFORMATION: / Ceres Seq. ID 1499459

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1027:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Gly | Pro | Asp | Pro | Arg | Glu | Val | Glu | Leu | Tyr | Val | Glu | Glu | Ile | Leu |
| 1   |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |     |     |
| Ser | Leu | Met | Gln | Leu | Gly | Glu | Asp | Tyr | Thr | Glu | Phe | Met | Val | Ser | Lys |
|     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |     |
| Ile | Lys | Ser | Leu | Thr | Ser | Val | Asp | Pro | Glu | Leu | Leu | Pro | Thr | Ala | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Lys | Ala | Phe | Arg | Asn | Lys | Ser | Phe | Ser | Lys | Ala | Ile | Gln | Asp | Val | Thr |
|     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Arg | Tyr | Tyr | Val | Ile | Leu | Glu | Gly | Phe | Phe | Met | Val | Glu | Asn | Val | Arg |
|     |     | 65  |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |     |
| Lys | Ala | Ile | Arg | Ile | Asp | Glu | His | Val | Pro | Asp | Ser | Leu | Thr | Thr | Ser |
|     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |     |
| Met | Val | Asp | Asp | Val | Phe | Tyr | Val | Leu | Gln | Ser | Cys | Leu | Arg | Arg | Ala |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Ile | Ser | Thr | Ser | Asn | Ile | Ser | Ser | Val | Ile | Ala | Val | Leu | Ser | Tyr | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gly | Ser | Leu | Leu | Gly | Asn | Asp | Tyr | His | Glu | Ala | Leu | Gln | Gln | Lys | Ile |
|     |     | 130 |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Arg | Glu | Pro | Asn | Leu | Gly | Ala | Arg | Leu | Phe | Leu | Gly | Gly | Ile | Gly | Met |
|     |     | 145 |     |     | 150 |     |     |     | 155 |     |     |     |     |     |     |



Glu Asn Thr Gly Thr Glu Ile Ala Thr Ala Leu Asn Asn Met Asp Val  
165 170 175  
Ser Cys Glu Tyr Ile Leu Lys Leu Lys His Glu Ile Glu Glu Gln Cys  
180 185 190  
Thr Glu Val Phe Pro Ala Pro Ala Asp Arg Glu Arg Ile Lys Ser Cys  
195 200 205  
Leu Ser Glu Leu Gly Glu Leu Ser Ser Thr Phe Lys Gln Leu Leu Asn  
210 215 220  
Ser Gly Met Glu Gln Leu Val Ala Thr Val Thr Pro Arg Ile Arg Pro  
225 230 235  
Val Leu Asp Thr Val Ala Thr Ile Ser Tyr Glu Leu Thr Glu Thr Glu  
245 250 255  
Tyr Ala Glu Asn Glu Val Asn Asp Pro Trp Val Gln Arg Leu Leu His  
260 265 270  
Ser Val Glu Thr Asn Ala Ala Trp Leu Gln Pro Leu Met Thr Ser Asn  
275 280 285  
Asn Tyr Asp Ser Phe Leu His Leu Ile Ile Asp Phe Ile Val Lys Arg  
290 295 300  
Leu Glu Val Ile Met Met Gln Lys Arg Phe Xaa Gln Leu Gly Gly Leu  
305 310 315 320  
Gln Leu Asp Arg Asp Thr Arg Ala Leu Val Ser His Phe Ser Gly Met  
325 330 335  
Thr Gln Arg Thr Val Arg Asp Lys Phe Ala Arg Leu Thr Gln Met Ala  
340 345 350  
Thr Ile Leu Asn Leu Glu Lys Val Ser Glu Ile Leu Asp Phe Trp Gly  
355 360 365  
Glu Asn Ser Gly Pro Met Thr Trp Arg Leu Thr Pro Ala Glu Val Arg  
370 375 380  
Arg Val Leu Gly Leu Arg Val Glu Phe Lys Pro Glu Ser Ile Ala Ala  
385 390 395 400  
Leu Lys Leu

(2) INFORMATION FOR SEQ ID NO:1028:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..385

(D) OTHER INFORMATION: / Ceres Seq. ID 1499460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1028:

Met Gln Leu Gly Glu Asp Tyr Thr Glu Phe Met Val Ser Lys Ile Lys  
1 5 10 15  
Ser Leu Thr Ser Val Asp Pro Glu Leu Leu Pro Thr Ala Thr Lys Ala  
20 25 30  
Phe Arg Asn Lys Ser Phe Ser Lys Ala Ile Gln Asp Val Thr Arg Tyr  
35 40 45  
Tyr Val Ile Leu Glu Gly Phe Phe Met Val Glu Asn Val Arg Lys Ala  
50 55 60  
Ile Arg Ile Asp Glu His Val Pro Asp Ser Leu Thr Thr Ser Met Val  
65 70 75 80  
Asp Asp Val Phe Tyr Val Leu Gln Ser Cys Leu Arg Arg Ala Ile Ser  
85 90 95  
Thr Ser Asn Ile Ser Ser Val Ile Ala Val Leu Ser Tyr Ala Gly Ser  
100 105 110  
Leu Leu Gly Asn Asp Tyr His Glu Ala Leu Gln Gln Lys Ile Arg Glu  
115 120 125  
Pro Asn Leu Gly Ala Arg Leu Phe Leu Gly Gly Ile Gly Met Glu Asn

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |  |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|--|--|-----|
| 130 |     |     |     |     |     |     |     |     |     |     | 135 |     |     |     |     |  |  |  |  |  |  | 140 |
| Thr | Gly | Thr | Glu | Ile | Ala | Thr | Ala | Leu | Asn | Asn | Met | Asp | Val | Ser | Cys |  |  |  |  |  |  |     |
| 145 |     |     |     |     |     |     |     |     |     |     | 150 |     |     |     |     |  |  |  |  |  |  | 155 |
| Glu | Tyr | Ile | Leu | Lys | Leu | Lys | His | Glu | Ile | Glu | Glu | Gln | Cys | Thr | Glu |  |  |  |  |  |  |     |
| 165 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |  |     |
| Val | Phe | Pro | Ala | Pro | Ala | Asp | Arg | Glu | Arg | Ile | Lys | Ser | Cys | Leu | Ser |  |  |  |  |  |  |     |
| 180 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |  |     |
| Glu | Leu | Gly | Glu | Leu | Ser | Ser | Thr | Phe | Lys | Gln | Leu | Leu | Asn | Ser | Gly |  |  |  |  |  |  |     |
| 195 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |  |     |
| Met | Glu | Gln | Leu | Val | Ala | Thr | Val | Thr | Pro | Arg | Ile | Arg | Pro | Val | Leu |  |  |  |  |  |  |     |
| 210 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |  |     |
| Asp | Thr | Val | Ala | Thr | Ile | Ser | Tyr | Glu | Leu | Thr | Glu | Thr | Glu | Tyr | Ala |  |  |  |  |  |  |     |
| 225 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |  |     |
| Glu | Asn | Glu | Val | Asn | Asp | Pro | Trp | Val | Gln | Arg | Leu | Leu | His | Ser | Val |  |  |  |  |  |  |     |
| 240 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |  |     |
| Glu | Thr | Asn | Ala | Ala | Trp | Leu | Gln | Pro | Leu | Met | Thr | Ser | Asn | Asn | Tyr |  |  |  |  |  |  |     |
| 255 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |  |     |
| Asp | Ser | Phe | Leu | His | Leu | Ile | Ile | Asp | Phe | Ile | Val | Lys | Arg | Glu | Leu |  |  |  |  |  |  |     |
| 270 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |  |     |
| Val | Ile | Met | Met | Gln | Lys | Arg | Phe | Xaa | Gln | Leu | Gly | Gly | Leu | Gln | Leu |  |  |  |  |  |  |     |
| 285 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |  |     |
| Asp | Arg | Asp | Thr | Arg | Ala | Leu | Val | Ser | His | Phe | Ser | Gly | Met | Thr | Gln |  |  |  |  |  |  |     |
| 300 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |  |     |
| 305 |     |     |     |     |     |     |     |     |     |     | 310 |     |     |     |     |  |  |  |  |  |  | 315 |
| Arg | Thr | Val | Arg | Asp | Lys | Phe | Ala | Arg | Leu | Thr | Gln | Met | Ala | Thr | Ile |  |  |  |  |  |  |     |
| 330 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |  |     |
| Leu | Asn | Leu | Glu | Lys | Val | Ser | Glu | Ile | Leu | Asp | Phe | Trp | Gly | Glu | Asn |  |  |  |  |  |  |     |
| 345 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |  |     |
| Ser | Gly | Pro | Met | Thr | Trp | Arg | Leu | Thr | Pro | Ala | Glu | val | Arg | Arg | Val |  |  |  |  |  |  |     |
| 360 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |  |     |
| Leu | Gly | Leu | Arg | Val | Glu | Phe | Lys | Pro | Glu | Ser | Ile | Ala | Ala | Leu | Lys |  |  |  |  |  |  |     |
| 375 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |  |  |  |     |
|     |     |     |     |     |     |     |     |     |     | 380 |     |     |     |     |     |  |  |  |  |  |  |     |

Leu  
385

(2) INFORMATION FOR SEQ ID NO:1029:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- ```
(A) NAME/KEY: peptide
(B) LOCATION: 1..375
```

(D) OTHER INFORMATION: / Ceres Seq. ID 1499461

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1029:

Met	Val	Ser	Lys	Ile	Lys	Ser	Leu	Thr	Ser	Val	Asp	Pro	Glu	Leu	Leu
1			5						10					15	
Pro	Thr	Ala	Thr	Lys	Ala	Phe	Arg	Asn	Lys	Ser	Phe	Ser	Lys	Ala	Ile
			20					25					30		
Gln	Asp	Val	Thr	Arg	Tyr	Tyr	Val	Ile	Leu	Glu	Gly	Phe	Phe	Met	Val
		35					40					45			
Glu	Asn	Val	Arg	Lys	Ala	Ile	Arg	Ile	Asp	Glu	His	Val	Pro	Asp	Ser
		50				55					60				
Leu	Thr	Thr	Ser	Met	Val	Asp	Asp	Val	Phe	Tyr	Val	Leu	Gln	Ser	Cys
65					70					75				80	
Leu	Arg	Arg	Ala	Ile	Ser	Thr	Ser	Asn	Ile	Ser	Ser	Val	Ile	Ala	Val
				85					90					95	
Leu	Ser	Tyr	Ala	Gly	Ser	Leu	Leu	Gly	Asn	Asp	Tyr	His	Glu	Ala	Leu
			100					105					110		
Gln	Gln	Lys	Ile	Arg	Glu	Pro	Asn	Leu	Gly	Ala	Arg	Leu	Phe	Leu	Gly
		115					120					125			

Gly Ile Gly Met Glu Asn Thr Gly Thr Glu Ile Ala Thr Ala Leu Asn
130 135 140
Asn Met Asp Val Ser Cys Glu Tyr Ile Leu Lys Leu Lys His Glu Ile
145 150 155 160
Glu Glu Gln Cys Thr Glu Val Phe Pro Ala Pro Ala Asp Arg Glu Arg
165 170 175
Ile Lys Ser Cys Leu Ser Glu Leu Gly Glu Leu Ser Ser Thr Phe Lys
180 185 190
Gln Leu Leu Asn Ser Gly Met Glu Gln Leu Val Ala Thr Val Thr Pro
195 200 205
Arg Ile Arg Pro Val Leu Asp Thr Val Ala Thr Ile Ser Tyr Glu Leu
210 215 220
Thr Glu Thr Glu Tyr Ala Glu Asn Glu Val Asn Asp Pro Trp Val Gln
225 230 235 240
Arg Leu Leu His Ser Val Glu Thr Asn Ala Ala Trp Leu Gln Pro Leu
245 250 255
Met Thr Ser Asn Asn Tyr Asp Ser Phe Leu His Leu Ile Ile Asp Phe
260 265 270
Ile Val Lys Arg Leu Glu Val Ile Met Met Gln Lys Arg Phe Xaa Gln
275 280 285
Leu Gly Gly Leu Gln Leu Asp Arg Asp Thr Arg Ala Leu Val Ser His
290 295 300
Phe Ser Gly Met Thr Gln Arg Thr Val Arg Asp Lys Phe Ala Arg Leu
305 310 315 320
Thr Gln Met Ala Thr Ile Leu Asn Leu Glu Lys Val Ser Glu Ile Leu
325 330 335
Asp Phe Trp Gly Glu Asn Ser Gly Pro Met Thr Trp Arg Leu Thr Pro
340 345 350
Ala Glu Val Arg Arg Val Leu Gly Leu Arg Val Glu Phe Lys Pro Glu
355 360 365
Ser Ile Ala Ala Leu Lys Leu
370 375

(2) INFORMATION FOR SEQ ID NO:1030:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..348

- (D) OTHER INFORMATION: / Ceres Seq. ID 1499462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1030:

atattattca	cgatttctcat	caaatcatct	ccgatactca	caaccgaaat	aactaacccc	60
tcctcaacaa	aaaacaacaa	aacatgtaca	ctccatcata	cttaaaatat	tcaataatct	120
caattatata	cgtattattc	ctccaaggaa	ctcatggaga	cgacggagggt	tggaaggtgt	180
gtcacgcgt	aaaacgtggc	gtgaccacct	tgccaacctc	cgctgctccct	tattaaaatt	240
acctgccagt	ttacttttct	ctcttcttgt	tttctgtgtt	ggaagattct	caagttattt	300
attccgcaaa	aaacggttta	tcattttacaa	ttagttgaat	tttggttcg		

(2) INFORMATION FOR SEQ ID NO:1031:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..34

- (D) OTHER INFORMATION: / Ceres Seq. ID 1499463

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1031:
Ile Leu Phe Thr Ile Leu Ile Lys Ser Ser Pro Ile Leu Thr Thr Glu
1 5 10 15
Ile Thr Asn Pro Ser Ser Thr Lys Asn Asn Lys Thr Cys Thr Leu His
20 25 30
His Thr

(2) INFORMATION FOR SEQ ID NO:1032:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..50

(D) OTHER INFORMATION: / Ceres Seq. ID 1499464

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1032:

Met Tyr Thr Pro Ser Tyr Leu Lys Tyr Ser Ile Ile Ser Ile Ile Ser
1 5 10 15
Val Leu Phe Leu Gln Gly Thr His Gly Asp Asp Gly Gly Trp Gln Gly
20 25 30
Gly His Ala Val Lys Arg Gly Val Thr Thr Leu Pro Thr Ser Val Val
35 40 45

Pro Tyr

50

(2) INFORMATION FOR SEQ ID NO:1033:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1004 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1004

(D) OTHER INFORMATION: / Ceres Seq. ID 1499465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1033:

aaagaccaaa agaaaaaaaa atctttttct tttctgatga atcgtatcta ttagctatga 60
gacctaggtg atgatcatgt caacataacc atcaacgttc taccatggct agtccataga 120
acaaggccaa aggcataagca gaaggatcgt ctcaaccgca atcgcaaccg caaccacaaac 180
cacaccaact gcaatcaoct cctaaccgcg cagcggttaa cgggtacgag tcacagaaac 240
gacgagactg gaacacggtt tgtcaatacc tgcgtaacca acagccaccg gttcacatct 300
cgacagtggg atcaaacacc atcctcgatt tccctcaata tctcgaccag ttgtgggaaga 360
caaaagttca tatccatgga tgcgctttct tcggacaggt tgagccagcg ggacagtgtta 420
actgtccttt aaaaacaagcg tgggggagtt tagatgcttt gatcggaagg ctaagagcgg 480
ctttcgagga gaacggagga ttgccggaga gaaacccttt tgcggcgccg ggaattaggg 540
ttttttcag ggaagtggaga gattcacagg cgaaggcaag aggagttccg tacaagaaaa 600
gaaaaaagag gaagaagagg aatcctatga agagtcatga tgggtgaagat ggtactacgg 660
gaactagtag tagctccaac ttggcttctt agcgggaagca acaaaaaaat ctataataaa 720
acaaaagtgg aattagttaa tggtaagcat ttaatactct ccaataatct tatataattt 780
cagtcattta atctctattt gtgatctatt tacaatttta catatagagt gaaaagaaac 840
aattctacat ttgtttcttg atagtcagct cttaatgcatt agttgaattt tatacgtatc 900
atacccaaac tataagatta atcttgatct tagatcatat acatatatca tcatgtgtgtg 960
taccctaaagt ttcataatca tttttcttaa ctatttatgt ggat

(2) INFORMATION FOR SEQ ID NO:1034:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..195
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499466
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1034:
Met Ala Ser Pro Ser Asn Lys Gly Lys Gly Ile Ala Glu Gly Ser Ser
1 5 10 15
Gln Pro Gln Ser Gln Pro Gln Pro Gln Pro His Gln Leu Gln Ser Pro
 20 25 30
Pro Asn Pro Pro Ala Leu Ser Arg Tyr Glu Ser Gln Lys Arg Arg Asp
 35 40 45
Trp Asn Thr Phe Cys Gln Tyr Leu Arg Asn Gln Gln Pro Pro Val His
 50 55 60
Ile Ser Gln Cys Gly Ser Asn His Ile Leu Asp Phe Leu Gln Tyr Leu
65 70 75 80
Asp Gln Phe Gly Lys Thr Lys Val His Ile His Gly Cys Val Phe Phe
 85 90 95
Gly Gln Val Glu Pro Ala Gly Gln Cys Asn Cys Pro Leu Lys Gln Ala
 100 105 110
Trp Gly Ser Leu Asp Ala Leu Ile Gly Arg Leu Arg Ala Ala Phe Glu
 115 120 125
Glu Asn Gly Gly Leu Pro Glu Arg Asn Pro Phe Ala Gly Gly Gly Ile
 130 135 140
Arg Val Phe Leu Arg Glu Val Arg Asp Ser Gln Ala Lys Ala Arg Gly
145 150 155 160
Val Pro Tyr Lys Lys Arg Lys Lys Arg Lys Lys Arg Asn Pro Met Lys
 165 170 175
Ser His Asp Gly Glu Asp Gly Thr Thr Gly Thr Ser Ser Ser Ser Asn
 180 185 190
Leu Ala Ser
 195

(2) INFORMATION FOR SEQ ID NO:1035:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1049 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1049
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499467

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1035:

actttgtaat aataaccaca acttcccaat cttcttcate agattttgct agttcgtcac 60
acacacggat caacgtctate atctctctct cttcttctcc acaagcccac ctacaaatttc 120
catttcgcgc cttctctctgt tcccaacttac atcaattccg ctcgatttgc aatttgcagc 180
tcaattctcc ctttgatcgc aagaagaaga agaagaatct ggtctgtctc tggctttaaa 240
tctatggccc atttagtaaa aaccaatgct cgcagagacg gtgaagaacg atttcaagcg 300
cttgagcaag aggccttcat caataattcg tctccggagc tccagaacga gttggtatcc 360
gacgcggagc gttggattga agcaatcgct aatcgtctga ctgcattttt gtcaaatggc 420
agagcaaatg gattgtagca gctctgtttt gatccgttct gcttctacga catgatgggt 480
cagctttgtg ggctgtgatt ggcctcgttt caaattccgt gctctcagta gctttgaaac 540
gtataacttaa ccaagagaga cctgttgcta ctctccgttc tgatcctggg atgcctcttt 600
ctcatgccca atccatttct ttcattctct tgttttctgt cttctccgtt agggatgggc 660
ttggaaccaa tgtactctct ctgttcctta cggcgttcat cctcgcattg gttcttatt 720
tcacgtggtt aagggtttct cagaagcttc acacgacaag tcaagtggtc gtaggtgcaa 780
tcgtgggttc tgtttactcc accttatggt atgtaacttg gaactctctt gttcttgaag 840
cctttacctc aacatttcca gtacaaatag ctgtctttct ggttgcgtct gcgtctgctt 900
taggttttgc agtttatgtg ctacttaact ggtttaaaga tgacagatga cagatgacag 960

aatgataatt ttacgtactt aggatgtata aggaatgcat ttgattctcc ttataattca 1020
tattgattga gctatttttaa cattcaatg

(2) INFORMATION FOR SEQ ID NO:1036:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1499468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1036:

Phe	Val	Ile	Ile	Thr	Thr	Thr	Ser	Gln	Ser	Ser	Ser	Asp	Phe	Ala
1				5				10					15	
Ser	Ser	Ser	Ser	His	Thr	Arg	Ile	Asn	Val	Ile	Ile	Phe	Ser	Ser
				20				25				30		
Pro	Gln	Ala	His	Leu	Gln	Phe	Pro	Phe	Arg	Arg	Phe	Leu	Cys	Ser
				35				40				45		
Leu	His	Gln	Phe	Arg	Ser	Ile	Ser	Asn	Phe	Glu	Leu	Asn	Leu	Pro
				50				55			60			
Gly	Ser	Lys	Lys	Lys	Lys	Lys	Asn	Leu	Val	Cys	Leu	Trp	Leu	
65				70				75						

(2) INFORMATION FOR SEQ ID NO:1037:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..119

(D) OTHER INFORMATION: / Ceres Seq. ID 1499469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1037:

Met	Pro	Ser	Ser	His	Ala	Gln	Ser	Ile	Ser	Phe	Ile	Ser	Val	Phe	Ser
1				5				10					15		
Val	Phe	Ser	Val	Met	Glu	Trp	Leu	Gly	Thr	Asn	Val	Leu	Ser	Leu	Phe
				20				25					30		
Leu	Ser	Gly	Phe	Ile	Leu	Ala	Leu	Gly	Ser	Tyr	Phe	Thr	Trp	Leu	Arg
				35				40					45		
Val	Ser	Gln	Lys	Leu	His	Thr	Thr	Ser	Gln	Val	Val	Val	Gly	Ala	Ile
				50				55				60			
Val	Gly	Ser	Val	Tyr	Ser	Thr	Leu	Trp	Tyr	Val	Thr	Trp	Asn	Ser	Leu
				65				70				75			80
Val	Leu	Glu	Ala	Phe	Thr	Ser	Thr	Phe	Ser	Val	Gln	Ile	Ala	Val	Phe
				85				90					95		
Leu	Val	Ala	Ala	Ala	Ser	Ala	Leu	Gly	Phe	Ala	Val	Tyr	Val	Leu	Leu
				100				105					110		
Asn	Trp	Phe	Lys	Asp	Asp	Arg									
				115											

(2) INFORMATION FOR SEQ ID NO:1038:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1499470

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1038:

Met	Glu	Trp	Leu	Gly	Thr	Asn	Val	Leu	Ser	Leu	Phe	Leu	Ser	Gly	Phe
1				5					10					15	
Ile	Leu	Ala	Leu	Gly	Ser	Tyr	Phe	Thr	Trp	Leu	Arg	Val	Ser	Gln	Lys
				20				25					30		
Leu	His	Thr	Thr	Thr	Ser	Gln	Val	Val	Val	Gly	Ala	Ile	Val	Gly	Ser
				35			40					45			
Tyr	Ser	Thr	Leu	Trp	Tyr	Val	Thr	Trp	Asn	Ser	Leu	Val	Leu	Glu	Ala
				50			55				60				
Phe	Thr	Ser	Thr	Phe	Ser	Val	Gln	Ile	Ala	Val	Phe	Leu	Val	Ala	Ala
				65			70				75			80	
Ala	Ser	Ala	Leu	Gly	Phe	Ala	Val	Tyr	Val	Leu	Leu	Asn	Trp	Phe	Lys
				85				90						95	

Asp Asp Arg

(2) INFORMATION FOR SEQ ID NO:1039:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1232 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1232

(D) OTHER INFORMATION: / Ceres Seq. ID 1499474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1039:

tctttcttctt	ccacacagct	agaaacacag	tctctctatc	tcttgagcaa	aaaaatggaa	60
gtggctctctt	tatnvtcttc	tcttctcttg	tctctctctt	gtcaccagcg	aatctcaact	120
ctcacaccca	aaacctcgaa	tcccccaaat	taccctcgcc	tcccggtcat	cagatccgcg	180
gtgacagaga	ggagacaaag	aagaagagaa	ggagatgttg	aactaggggg	acaacaaggt	240
ggagatcaag	gattggaaag	tttttttcaa	aaaggttcaa	gtgattgaca	aacagtatga	300
taagctagac	aagcttctaa	agaaactgca	ggcttcccat	gaggagtcaa	aatctgtgac	360
caaaagctcct	gccatgaag	cgataaaagaa	gacaatggaa	aaagacgttg	atgaagtggg	420
aagtattgcc	cgtttcttaa	aggggaaact	cgaggagtgt	gacagagaga	acttggggcaa	480
atagacaaaa	acctggatgt	gcataaaggat	ctgggttgga	tcgatcaaga	acagcaacaa	540
cactttcctt	aaagaagaag	ttgaaagaca	agatggccga	gtttcaggtt	ctacgagaga	600
acattcaaca	agagtatcgc	gatgttgttg	atagggcagt	ttatacagta	actggggagc	660
ggggcgtaga	agatactatt	gatgaattga	tgtaaatctg	aaacagcgaa	cagatcttcc	720
agaaaagcgt	tcaggagcaa	ggaagaggac	aggtaatgga	caccttggcg	gaaatccaag	780
aacgtcatga	tgctgtcaga	gacttggaag	agaaaacttc	tgacttacaa	caaatattct	840
tggatatggc	agtttttggt	gtgacacaag	gagaaatgct	tgacaatata	gaatctcagg	900
tgtcaagtgc	agtagatcac	gtgcaatcgg	gaaacacggc	acttcaaga	gcaaaagagct	960
tgcaagaaga	actcaagaata	attgatgtgt	attgcaatta	tcattctctc	catgttggtt	1020
gcagtgtatg	tgtgtgtgtg	tctcaagcct	tggaaaaaca	aagagtgcct	gagggaaagaa	1080
agaaagtaca	aaaaagaatat	caaatctcta	ttcacggctt	tgagtggagag	tgttttgttt	1140
atgatgtgtg	tgtttttttt	ttaccaagaa	acgaaaaaaa	aagaaacara	attctacatt	1200
cttttaattg	gatcaaacaa	accaatttcc	cc			

(2) INFORMATION FOR SEQ ID NO:1040:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1499475

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1040:

Ser	Ser	Ser	Ser	Thr	Gln	Leu	Glu	Thr	Gln	Ser	Pro	His	Leu	Leu	Ser	
1				5				10					15			
Lys	Lys	Met	Glu	Val	Ala	Leu	Leu	Xaa	Phe	Ser	Ser	Ser	Leu	Ser	Pro	
		20						25					30			
Leu	Cys	His	Gln	Arg	Ile	Ser	Thr	Leu	Thr	Pro	Lys	Thr	Ser	Asn	Ser	
		35						40				45				
Pro	Asn	Tyr	Pro	Arg	Leu	Pro	Val	Ile	Arg	Ser	Ala	Val	Thr	Glu	Arg	
		50				55					60					
Arg	Gln	Gly	Arg	Arg	Glu	Gly	Asp	Val	Glu	Leu	Gly	Glu	Gln	Gln	Gly	
65					70					75					80	
Gly	Asp	Gln	Gly	Leu	Glu	Asp	Phe	Phe	Gln	Lys	Gly	Ser	Ser	Asp		
				85					90					95		

(2) INFORMATION FOR SEQ ID NO:1041:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..184
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499476

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1041:

Met	Ala	Glu	Phe	Gln	Val	Leu	Arg	Glu	Asn	Ile	Gln	Gln	Glu	Tyr	Arg	
1				5				10					15			
Asp	Val	Val	Asp	Arg	Arg	Val	Tyr	Thr	Val	Thr	Gly	Glu	Arg	Ala	Asp	
			20					25				30				
Glu	Asp	Thr	Ile	Asp	Glu	Leu	Ile	Glu	Thr	Gly	Asn	Ser	Glu	Gln	Ile	
		35						40				45				
Phe	Gln	Lys	Ala	Ile	Gln	Glu	Gln	Gly	Arg	Gly	Gln	Val	Met	Asp	Thr	
		50				55				60						
Leu	Ala	Glu	Ile	Gln	Glu	Arg	His	Asp	Ala	Val	Arg	Asp	Leu	Glu	Lys	
65				70					75					80		
Lys	Leu	Leu	Asp	Leu	Gln	Gln	Ile	Phe	Leu	Asp	Met	Ala	Val	Leu	Val	
			85					90					95			
Asp	Ala	Gln	Gly	Glu	Met	Leu	Asp	Asn	Ile	Glu	Ser	Gln	Val	Ser	Ser	
		100						105				110				
Ala	Val	Asp	His	Val	Gln	Ser	Gly	Asn	Thr	Ala	Leu	Gln	Arg	Ala	Lys	
		115					120					125				
Ser	Leu	Xaa	Glu	Glu	Leu	Lys	Lys	Met	Asp	Val	Tyr	Cys	Asn	Tyr	His	
		130				135					140					
Pro	Pro	His	Cys	Gly	Cys	Ser	Asp	Arg	Cys	Trp	Cys	Ser	Gln	Ala	Leu	
145				150						155					160	
Glu	Lys	Gln	Arg	Val	Leu	Glu	Glu	Arg	Lys	Asn	Val	Gln	Lys	Glu	Tyr	
				165				170						175		
Gln	Ile	Leu	Ile	His	Gly	Phe	Glu									
				180												

(2) INFORMATION FOR SEQ ID NO:1042:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..123
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1042:

Met Asp Thr Leu Ala Glu Ile Gln Glu Arg His Asp Ala Val Arg Asp
1 5 10 15
Leu Glu Lys Lys Leu Leu Asp Leu Gln Ile Phe Leu Asp Met Ala
20 25 30
Val Leu Val Asp Ala Gln Gly Glu Met Leu Asp Asn Ile Glu Ser Gln
35 40 45
Val Ser Ser Ala Val Asp His Val Gln Ser Gly Asn Thr Ala Leu Gln
50 55 60
Arg Ala Lys Ser Leu Xaa Glu Glu Leu Lys Lys Met Asp Val Tyr Cys
65 70 75 80
Asn Tyr His Pro Pro His Cys Gly Cys Ser Asp Arg Cys Trp Cys Ser
85 90 95
Gln Ala Leu Glu Lys Gln Arg Val Leu Glu Glu Arg Lys Asn Val Gln
100 105 110
Lys Glu Tyr Gln Ile Leu Ile His Gly Phe Glu
115 120

(2) INFORMATION FOR SEQ ID NO:1043:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..591
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1043:

gccttagttt	aaaccacacg	atctaaaaat	cccttctctc	tttctttctt	tctttttttc	60
tctccctctc	ttctcaggcg	agtatgcaaa	gcaagaacat	gatcgtggct	tcactctcat	120
agcagcaaca	acaacagcaa	cgcgacgacg	cacaacgcga	acttaaatgc	cctcgtttgc	180
attcttccaa	cacaaagttc	tgctactaca	acaactacag	cctctctcaa	ccacggcgact	240
tttgcaaggc	ttgcaagagg	tactggacga	gaggtggggc	tctcaggaac	gttcccggtan	300
gggntagtag	tgggaagaac	aaacgtgtaa	agcggccatc	aaccgcgaac	acaaccactg	360
cctccacagt	ctcgacgact	aattcttcat	cccttaataa	ccctcatcag	atctctcatt	420
tctcttccat	gaatcatcat	cctttgttct	atggtttatc	agatcatatg	agcagttgta	480
ataataaatc	ttccaatgat	cccaagccgt	ttcagtgatt	cttcaaaagac	ttgttcatca	540
agtggtttag	agagtgagtt	tctctcatct	ggktttagca	gtcttagtgc	b	

(2) INFORMATION FOR SEQ ID NO:1044:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1044:

Met Gln Ser Lys Asn Met Ile Val Ala Ser Ser His Gln Gln Gln Glu
1 5 10 15
Gln Gln Gln Pro Gln Gln Pro Gln Pro Gln Leu Lys Cys Pro Arg Cys
20 25 30
Asp Ser Ser Asn Thr Lys Phe Cys Tyr Tyr Asn Asn Tyr Ser Leu Ser
35 40 45
Gln Pro Arg His Phe Cys Lys Ala Cys Lys Arg Tyr Trp Thr Arg Gly
50 55 60
Gly Thr Leu Arg Asn Val Pro Val Xaa Xaa Ser Tyr Arg Lys Asn Lys
65 70 75 80
Arg Val Lys Arg Pro Ser Thr Ala Thr Thr Thr Thr Ala Ser Thr Val

85										90					95			
Ser	Thr	Thr	Asn	Ser	Ser	Ser	Pro	Asn	Asn	Pro	His	Gln	Ile	Ser	His			
			100						105						110			
Phe	Ser	Ser	Met	Asn	His	His	Pro	Leu	Phe	Tyr	Gly	Leu	Ser	Asp	His			
			115				120						125					
Met	Ser	Ser	Cys	Asn	Asn	Lys	Ser	Ser	Asn	Asp	Pro	Lys	Pro	Phe	Gln			
			130				135											

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..139
(D) OTHER INFORMATION

(D) OTHER INFORMATION: / Ceres Seq. ID 1499488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1045:

Met	ile	Val	Ala	Ser	Ser	His	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Pro	Gln
1				5				10						15	
Gln	Pro	Gln	Pro	Gln	Leu	Lys	Cys	Pro	Arg	Cys	Asp	Ser	Ser	Asn	Thr
			20					25						30	
Lys	Phe	Cys	Tyr	Tyr	Asn	Asn	Tyr	Ser	Leu	Ser	Gln	Pro	Arg	His	Phe
		35					40					45			
Cys	Lys	Ala	Cys	Lys	Arg	Tyr	Trp	Thr	Arg	Gly	Gly	Thr	Leu	Arg	Asn
		50				55					60				
Val	Pro	Val	Xaa	Xaa	Ser	Tyr	Arg	Lys	Asn	Lys	Arg	Val	Lys	Arg	Pro
65					70					75					80
Ser	Thr	Ala	Thr	Thr	Thr	Ala	Ser	Thr	Val	Ser	Thr	Thr	Asn	Ser	
				85				90					95		
Ser	Ser	Pro	Asn	Asn	Pro	His	Gln	Ile	Ser	His	Phe	Ser	Ser	Met	Asn
			100					105					110		
Lis	His	Pro	Leu	Phe	Tyr	Gly	Leu	Ser	Asp	His	Met	Ser	Ser	Cys	Asn
		115				120						125			
Asn	Lys	Ser	Ser	Asn	Asp	Pro	Lys	Pro	Phe	Gln					
		130				135									

(2) INFORMATION FOR SEQ ID NO:1046:

- ### (i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 1762 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1

(D) OTHER INFORMATION: / Ceres Seq. ID 1499501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1046:

agacccgctag	tgtttttttt	ccactctctt	cgctctctct	ctctagaaga	cgccgtcttt	60
ctccaccagat	ctgttcggcga	tcctctcttc	gagattacga	ttccaaagaa	aagcacaatt	120
ctccaaagcat	tgctctcttc	tcacaaagat	ctccattctc	aagctcccat	tatctcaact	180
tcacaggacga	gaatcctcaa	acgggtctct	cagaaattct	ctgtagctat	agctgcttca	240
ctccaaagcta	gtatgatgtg	tggtgagagt	gttgcacaaa	catcagaaaa	agatggtgtt	300
agggctcttgt	gcacgattat	tgatctgat	tttgggaacg	atattgttct	ttgtgtgttt	360
gtgaaagatt	tcgggattaa	tgaagcttgt	ggtaggtttt	cgctccgttt	ggagctgcaga	420
acaccgcgat	tcggcgtcaa	agacatgttt	gagaaacaag	caaatagagt	agttgcagcc	480
ctccaaagctg	tgaagaaggt	aaatctgaca	atgtcagcac	aaccagccaa	gcccattttt	540
cgcaqcgagc	ttccctttgg	attatcaaga	ttttcgaaca	tcacgtcgct	ttctatgttg	600

aagggtggtg	ttgggaatc	aacagtagct	gtaaatcttg	cttatacatt	agctggtatg	660
ggtgctagag	ttggtatctt	tgatgctgat	gtctatggtc	caagtctacc	aacctaggtc	720
aatcctgaga	gccgtatatt	ggaaatgaac	ccggagaaga	agaccatcat	tccaacagaa	780
tacatggggc	tcaagtagat	ctcatttgga	tttgaggagc	aagggcggtg	cattatgaga	840
ggctctatgg	tgctctggtg	tataaaccaa	ctccttacaa	caactgaagt	gggagagctg	900
gactatcttg	ttatcgacat	gcctcctgga	actggtgata	tacaactgac	cttatgccag	960
gttgcgcat	tgacagcagc	ggtaattgtc	accacccctc	aaaagttggc	gtttattgat	1020
gttgcaaaag	gtgtaaggat	gtctcctgga	cttaaggtgc	cttgcgttgc	tggtgtggag	1080
aatatgtgcc	actttgacgc	tgatggggaa	cgttattacc	cttttgggaa	aggttcaggt	1140
tctgagtggt	tcaagcaatt	cgccatccct	cacctctttg	acctcccat	tagaccaacg	1200
ttatctgtct	cgggggatag	cggaactcct	gaagttagtg	cggtatcctc	aagtgcagtt	1260
gccagaacgt	tccaggatct	tggtgtatgt	gtagtgcac	aatgcgccaa	gatacgcag	1320
caagatcaaa	cgcccgtag	atacgacaag	tatctcaagg	caattagagt	gaaggtacca	1380
aactcagacg	aagagtctct	actgcaccct	gcaaccgtca	gaagaaatga	tagatctgca	1440
caaatgttgg	atgaatggag	tgagagacaa	aaagtcttat	atggcgatgt	agcggaagat	1500
atcgaaacct	aggacatacg	accaatggga	aactacgctg	tctcgataac	ctggcccgag	1560
gggttttagc	agattgtctc	atatgaccag	ttggaagaaa	ttgaaaggct	agtagatggt	1620
cctccattgt	ctccagtcga	agtcctagtc	ttgaacaata	tgttttcgct	ttacgatatc	1680
ctctgaaaat	gaaatttgta	tattcatatt	aagagcattg	ttatgaatct	tacaatgatg	1740

(2) INFORMATION FOR SEQ ID NO:1047:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 548 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..548
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1047:

Arg	Pro	Leu	Val	Phe	Phe	Cys	His	Ser	Leu	Arg	Leu	Ser	Leu	Val	Ala
1				5				10						15	
Met	Pro	Leu	Leu	His	Pro	Gln	Ser	Leu	Arg	His	Pro	Ser	Phe	Glu	Ile
				20				25					30		
Gln	Thr	Gln	Arg	Arg	Ser	Asn	Ser	Thr	Arg	Leu	Leu	Leu	Ser	His	
				35			40					45			
Lys	Phe	Leu	His	Ser	Gln	Ala	Ser	Ile	Ile	Ser	Ile	Ser	Arg	Thr	Arg
				50			55				60				
Ile	Leu	Lys	Arg	Val	Ser	Gln	Asn	Leu	Ser	Val	Ala	Lys	Ala	Ala	Ser
65				70				75					80		
Ala	Gln	Ala	Ser	Ser	Ser	Val	Gly	Glu	Ser	Val	Ala	Gln	Thr	Ser	Glu
				85				90					95		
Lys	Asp	Val	Leu	Lys	Ala	Leu	Ser	Gln	Ile	Ile	Asp	Pro	Asp	Phe	Gly
				100			105					110			
Thr	Asp	Ile	Val	Ser	Cys	Gly	Phe	Val	Lys	Asp	Leu	Gly	Ile	Asn	Glu
				115			120					125			
Ala	Leu	Gly	Glu	Val	Ser	Phe	Arg	Leu	Glu	Leu	Thr	Thr	Pro	Ala	Cys
				130			135				140				
Pro	Val	Lys	Asp	Met	Phe	Glu	Asn	Lys	Ala	Asn	Glu	Val	Val	Ala	Ala
145				150				155					160		
Leu	Pro	Trp	Val	Lys	Lys	Val	Asn	Leu	Thr	Met	Ser	Ala	Gln	Pro	Ala
				165				170					175		
Lys	Pro	Ile	Phe	Ala	Gly	Gln	Leu	Pro	Phe	Gly	Leu	Ser	Arg	Ile	Ser
				180				185					190		
Asn	Ile	Ile	Ala	Val	Ser	Ser	Cys	Lys	Gly	Gly	Val	Gly	Lys	Ser	Thr
				195			200					205			
Val	Ala	Val	Asn	Leu	Ala	Tyr	Thr	Leu	Ala	Gly	Met	Gly	Ala	Arg	Val
				210			215				220				
Gly	Ile	Phe	Asp	Ala	Asp	Val	Tyr	Gly	Pro	Ser	Leu	Pro	Thr	Met	Val

```

225          230          235          240
Asn Pro Glu Ser Arg Ile Leu Glu Met Asn Pro Glu Lys Lys Thr Ile
          245          250          255
Ile Pro Thr Glu Tyr Met Gly Val Lys Leu Val Ser Phe Gly Phe Ala
          260          265          270
Gly Gln Gly Arg Ala Ile Met Arg Gly Pro Met Val Ser Gly Val Ile
          275          280          285
Asn Gln Leu Leu Thr Thr Thr Glu Trp Gly Glu Leu Asp Tyr Leu Val
          290          295          300
Ile Asp Met Pro Pro Gly Thr Gly Asp Ile Gln Leu Thr Leu Cys Gln
          305          310          315          320
Val Ala Pro Leu Thr Ala Ala Val Ile Val Thr Thr Pro Gln Lys Leu
          325          330          335
Ala Phe Ile Asp Val Ala Lys Gly Val Arg Met Phe Ser Lys Leu Lys
          340          345          350
Val Pro Cys Val Ala Val Val Glu Asn Met Cys His Phe Asp Ala Asp
          355          360          365
Gly Lys Arg Tyr Tyr Pro Phe Gly Lys Gly Ser Gly Ser Glu Val Val
          370          375          380
Lys Gln Phe Gly Ile Pro His Leu Phe Asp Leu Pro Ile Arg Pro Thr
          385          390          395          400
Leu Ser Ala Ser Gly Asp Ser Gly Thr Pro Glu Val Val Ser Asp Pro
          405          410          415
Leu Ser Asp Val Ala Arg Thr Phe Gln Asp Leu Gly Val Cys Val Val
          420          425          430
Gln Gln Cys Ala Lys Ile Arg Gln Gln Val Ser Thr Ala Val Thr Tyr
          435          440          445
Asp Lys Tyr Leu Lys Ala Ile Arg Val Lys Val Pro Asn Ser Asp Glu
          450          455          460
Glu Phe Leu Leu His Pro Ala Thr Val Arg Arg Asn Asp Arg Ser Ala
          465          470          475          480
Gln Ser Val Asp Glu Trp Thr Gly Glu Gln Lys Val Leu Tyr Gly Asp
          485          490          495
Val Ala Glu Asp Ile Glu Pro Glu Asp Ile Arg Pro Met Gly Asn Tyr
          500          505          510
Ala Val Ser Ile Thr Trp Pro Asp Gly Phe Ser Gln Ile Ala Pro Tyr
          515          520          525
Asp Gln Leu Glu Glu Ile Glu Arg Leu Val Asp Val Pro Pro Leu Ser
          530          535          540
Pro Val Glu Val
545

```

(2) INFORMATION FOR SEQ ID NO:1048:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..532

(D) OTHER INFORMATION: / Ceres Seq. ID 1499503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1048:

```

Met Pro Leu Leu His Pro Gln Ser Leu Arg His Pro Ser Phe Glu Ile
1          5          10          15
Gln Thr Gln Arg Arg Ser Asn Ser Thr Thr Arg Leu Leu Ser His
          20          25          30
Lys Phe Leu His Ser Gln Ala Ser Ile Ile Ser Ile Ser Arg Thr Arg
          35          40          45
Ile Leu Lys Arg Val Ser Gln Asn Leu Ser Val Ala Lys Ala Ala Ser
          50          55          60

```

Ala Gln Ala Ser Ser Ser Val Gly Glu Ser Val Ala Gln Thr Ser Glu
65 70 75 80
Lys Asp Val Leu Lys Ala Leu Ser Gln Ile Asp Pro Asp Phe Gly
85 90 95
Thr Asp Ile Val Ser Cys Gly Phe Val Lys Asp Leu Gly Ile Asn Glu
100 105 110
Ala Leu Gly Glu Val Ser Phe Arg Leu Glu Leu Thr Thr Pro Ala Cys
115 120 125
Pro Val Lys Asp Met Phe Glu Asn Lys Ala Asn Glu Val Val Ala Ala
130 135 140
Leu Pro Trp Val Lys Lys Val Asn Leu Thr Met Ser Ala Gln Pro Ala
145 150 155 160
Lys Pro Ile Phe Ala Gly Gln Leu Pro Phe Gly Leu Ser Arg Ile Ser
165 170 175
Asn Ile Ile Ala Val Ser Ser Cys Lys Gly Gly Val Gly Lys Ser Thr
180 185 190
Val Ala Val Asn Leu Ala Tyr Thr Leu Ala Gly Met Gly Ala Arg Val
195 200 205
Gly Ile Phe Asp Ala Asp Val Tyr Gly Pro Ser Leu Pro Thr Met Val
210 215 220
Asn Pro Glu Ser Arg Ile Leu Glu Met Asn Pro Glu Lys Lys Thr Ile
225 230 235 240
Ile Pro Thr Glu Tyr Met Gly Val Lys Leu Val Ser Phe Gly Phe Ala
245 250 255
Gly Gln Gly Arg Ala Ile Met Arg Gly Pro Met Val Ser Gly Val Ile
260 265 270
Asn Gln Leu Leu Thr Thr Thr Glu Trp Gly Glu Leu Asp Tyr Leu Val
275 280 285
Ile Asp Met Pro Pro Gly Thr Gly Asp Ile Gln Leu Thr Leu Cys Gln
290 295 300
Val Ala Pro Leu Thr Ala Ala Val Ile Val Thr Thr Pro Gln Lys Leu
305 310 315 320
Ala Phe Ile Asp Val Ala Lys Gly Val Arg Met Phe Ser Lys Leu Lys
325 330 335
Val Pro Cys Val Ala Val Val Glu Asn Met Cys His Phe Asp Ala Asp
340 345 350
Gly Lys Arg Tyr Tyr Pro Phe Gly Lys Gly Ser Gly Ser Glu Val Val
355 360 365
Lys Gln Phe Gly Ile Pro His Leu Phe Asp Leu Pro Ile Arg Pro Thr
370 375 380
Leu Ser Ala Ser Gly Asp Ser Gly Thr Pro Glu Val Val Ser Asp Pro
385 390 395 400
Leu Ser Asp Val Ala Arg Thr Phe Gln Asp Leu Gly Val Cys Val Val
405 410 415
Gln Gln Cys Ala Lys Ile Arg Gln Gln Val Ser Thr Ala Val Thr Tyr
420 425 430
Asp Lys Tyr Leu Lys Ala Ile Arg Val Lys Val Pro Asn Ser Asp Glu
435 440 445
Glu Phe Leu Leu His Pro Ala Thr Val Arg Arg Asn Asp Arg Ser Ala
450 455 460
Gln Ser Val Asp Glu Trp Thr Gly Glu Gln Lys Val Leu Tyr Gly Asp
465 470 475 480
Val Ala Glu Asp Ile Glu Pro Glu Asp Ile Arg Pro Met Gly Asn Tyr
485 490 495
Ala Val Ser Ile Thr Trp Pro Asp Gly Phe Ser Gln Ile Ala Pro Tyr
500 505 510
Asp Gln Leu Glu Glu Ile Glu Arg Leu Val Asp Val Pro Pro Leu Ser
515 520 525
Pro Val Glu Val
530

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..400
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1049:

Met Phe Glu Asn Lys Ala Asn Glu Val Val Ala Ala Leu Pro Trp Val
1 5 10 15
Lys Lys Val Asn Leu Thr Met Ser Ala Gln Pro Ala Lys Pro Ile Phe
20 25 30
Ala Gly Gln Leu Pro Phe Gly Leu Ser Arg Ile Ser Asn Ile Ile Ala
35 40 45
Val Ser Ser Cys Lys Gly Gly Val Gly Lys Ser Thr Val Ala Val Asn
50 55 60
Leu Ala Tyr Thr Leu Ala Gly Met Gly Ala Arg Val Gly Ile Phe Asp
65 70 75 80
Ala Asp Val Tyr Gly Pro Ser Leu Pro Thr Met Val Asn Pro Glu Ser
85 90 95
Arg Ile Leu Glu Met Asn Pro Glu Lys Lys Thr Ile Ile Pro Thr Glu
100 105 110
Tyr Met Gly Val Lys Leu Val Ser Phe Gly Phe Ala Gly Gln Gly Arg
115 120 125
Ala Ile Met Arg Gly Pro Met Val Ser Gly Val Ile Asn Gln Leu Leu
130 135 140
Thr Thr Thr Glu Trp Gly Glu Leu Asp Tyr Leu Val Ile Asp Met Pro
145 150 155 160
Pro Gly Thr Gly Asp Ile Gln Leu Thr Leu Cys Gln Val Ala Pro Leu
165 170 175
Thr Ala Ala Val Ile Val Thr Thr Pro Gln Lys Leu Ala Phe Ile Asp
180 185 190
Val Ala Lys Gly Val Arg Met Phe Ser Lys Leu Lys Val Pro Cys Val
195 200 205
Ala Val Val Glu Asn Met Cys His Phe Asp Ala Asp Gly Lys Arg Tyr
210 215 220
Tyr Pro Phe Gly Lys Gly Ser Gly Ser Glu Val Val Lys Gln Phe Gly
225 230 235 240
Ile Pro His Leu Phe Asp Leu Pro Ile Arg Pro Thr Leu Ser Ala Ser
245 250 255
Gly Asp Ser Gly Thr Pro Glu Val Val Ser Asp Pro Leu Ser Asp Val
260 265 270
Ala Arg Thr Phe Gln Asp Leu Gly Val Cys Val Val Gln Gln Cys Ala
275 280 285
Lys Ile Arg Gln Gln Val Ser Thr Ala Val Thr Tyr Asp Lys Tyr Leu
290 295 300
Lys Ala Ile Arg Val Lys Val Pro Asn Ser Asp Glu Phe Leu Leu
305 310 315 320
His Pro Ala Thr Val Arg Arg Asn Asp Arg Ser Ala Gln Ser Val Asp
325 330 335
Glu Trp Thr Gly Glu Gln Lys Val Leu Tyr Gly Asp Val Ala Glu Asp
340 345 350
Ile Glu Pro Glu Asp Ile Arg Pro Met Gly Asn Tyr Ala Val Ser Ile
355 360 365
Thr Trp Pro Asp Gly Phe Ser Gln Ile Ala Pro Tyr Asp Gln Leu Glu
370 375 380
Glu Ile Glu Arg Leu Val Asp Val Pro Pro Leu Ser Pro Val Glu Val
385 390 395 400

(2) INFORMATION FOR SEQ ID NO:1050:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1211
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499509

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1050:

```
aagcatctct ccctcatatt caoctaaaaa tcagggttaat aaaaaagaat aatgatgttt 60
tcggtgacgg ttgcgatctt tgtttgtctt attgggtaca ttaccgatc atttaagcct 120
ccaccaccgc gaatctgcgg ccactcctaac ggtcctccgg ttacttctcc gagaatcaag 180
ctcagtgatg gaagatatct tgcttataga gaatctgggg ttgatagaga caatgctaac 240
tacaagatca ttgtcgttca tggcttcaac agctccaaag acactgaatt ttccatccct 300
aaggatgtaa ttgaggagct tgggatatata ttgtgttct acgatagagc aggatattgga 360
gaaagtgtgt cacaccctac acgcactgtt aagagtgaag cacacgacat tcaagaactc 420
gccgataaac tcaagatcgg accaaaagttc tacgttcttg gtatatcact cgggtgcttac 480
tcggtttata gttgcctcaa atacattccc cacagactag ctggagcagt cttaagggtt 540
ccatttgtga actattgttg gactaaaagt cctcaagaaa aattgagtaa agcgttggag 600
ctaagtccaa agaaagacca atggacgttt aaagtggctc attatgttcc gtggttgtta 660
tattggtgtt tgacccaaaa actatttcgc tcttcgagta tgatcacggg gaacaatgcs 720
ttatgcagcg acaaaagattt ggtcgtcata aagaagaaaa tggagaatcc acgcctctgc 780
ttggaaaaaa tagacaaca aggtgacctt gaatgtcttc accgggacat gatagccgga 840
ttcgcgcact gggaattcca cccgactgaa ttagaataat cgtttgcgga aggcgaagga 900
tcggtccacg ttgtgcgaag gatggaagac agaattcatt catcacgaaat taatcgatat 960
atatcagaga agcttccatg gattaagtac catgaggtct taggttatgg acatcttcta 1020
aacgccgagg aggagaaagt caaagacatt atcaaggcac ttcttgcgaa ctgatgatca 1080
tctctacaca agatgccaca aaaaatatag catatttaat agattttatt tttattttat 1140
ggattataat attatagcat attataagtt tgtaagtaag atgaaaacca cttgaaagtc 1200
attaatttac t
```

(2) INFORMATION FOR SEQ ID NO:1051:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..340
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499510

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1051:

```
Met Met Phe Ser Val Thr Val Ala Ile Leu Val Cys Leu Ile Gly Tyr
1 5 10 15
Ile Tyr Arg Ser Phe Lys Pro Pro Pro Arg Ile Cys Gly His Pro
20 25 30
Asn Gly Pro Pro Val Thr Ser Pro Arg Ile Lys Leu Ser Asp Gly Arg
35 40 45
Tyr Leu Ala Tyr Arg Glu Ser Gly Val Asp Arg Asp Asn Ala Asn Tyr
50 55 60
Lys Ile Ile Val Val His Gly Phe Asn Ser Ser Lys Asp Thr Glu Phe
65 70 75 80
Ser Ile Pro Lys Asp Val Ile Glu Glu Leu Gly Ile Tyr Phe Val Phe
85 90 95
Tyr Asp Arg Ala Gly Tyr Gly Glu Ser Asp Pro His Pro Ser Arg Thr
100 105 110
```

Val Lys Ser Glu Ala His Asp Ile Gln Glu Leu Ala Asp Lys Leu Lys
115 120 125
Ile Gly Pro Lys Phe Tyr Val Leu Gly Ile Ser Leu Gly Ala Tyr Ser
130 135 140
Val Tyr Ser Cys Leu Lys Tyr Ile Pro His Arg Leu Ala Gly Ala Val
145 150 155 160
Leu Met Val Pro Phe Val Asn Tyr Trp Trp Thr Lys Val Pro Gln Glu
165 175
Lys Leu Ser Lys Ala Leu Glu Leu Met Pro Lys Lys Asp Gln Trp Thr
180 185 190
Phe Lys Val Ala His Tyr Val Pro Trp Leu Leu Tyr Trp Trp Leu Thr
195 200 205
Gln Lys Leu Phe Pro Ser Ser Ser Met Ile Thr Gly Asn Asn Ala Leu
210 215 220
Cys Ser Asp Lys Asp Leu Val Val Ile Lys Lys Lys Met Glu Asn Pro
225 230 235 240
Arg Pro Gly Leu Glu Lys Val Arg Gln Gln Gly Asp His Glu Cys Leu
245 250 255
His Arg Asp Met Ile Ala Gly Phe Ala Thr Trp Glu Phe Asp Pro Thr
260 265 270
Glu Leu Glu Asn Pro Phe Ala Glu Gly Glu Ser Val His Val Trp
275 280 285
Gln Gly Met Glu Asp Arg Ile Ile Pro Tyr Glu Ile Asn Arg Tyr Ile
290 295 300
Ser Glu Lys Leu Pro Trp Ile Lys Tyr His Glu Val Leu Gly Tyr Gly
305 310 315 320
His Leu Leu Asn Ala Glu Glu Glu Lys Cys Lys Asp Ile Ile Lys Ala
325 330 335
Leu Leu Val Asn
340

(2) INFORMATION FOR SEQ ID NO:1052:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..339
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499511

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1052:

Met Phe Ser Val Thr Val Ala Ile Leu Val Cys Leu Ile Gly Tyr Ile
1 5 10 15
Tyr Arg Ser Phe Lys Pro Pro Pro Arg Ile Cys Gly His Pro Asn
20 25 30
Gly Pro Pro Val Thr Ser Pro Arg Ile Lys Leu Ser Asp Gly Arg Tyr
35 40 45
Leu Ala Tyr Arg Glu Ser Gly Val Asp Arg Asp Asn Ala Asn Tyr Lys
50 55 60
Ile Ile Val Val His Gly Phe Asn Ser Ser Lys Asp Thr Glu Phe Ser
65 70 75 80
Ile Pro Lys Asp Val Ile Glu Glu Leu Gly Ile Tyr Phe Val Phe Tyr
85 90 95
Asp Arg Ala Gly Tyr Gly Glu Ser Asp Pro His Pro Ser Arg Thr Val
100 105 110
Lys Ser Glu Ala His Asp Ile Gln Glu Leu Ala Asp Lys Leu Lys Ile
115 120 125
Gly Pro Lys Phe Tyr Val Leu Gly Ile Ser Leu Gly Ala Tyr Ser Val
130 135 140
Tyr Ser Cys Leu Lys Tyr Ile Pro His Arg Leu Ala Gly Ala Val Leu

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1192 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1192
(D) OTHER INFORMATION: / Ceres Seq. ID 1499513

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1054:

(X1) SEQUENCE DESCRIPTION						
atctacgact	gaaaatatga	tctctgtcttt	ttttgtgttg	tctatctttc	aaatcatttaa	60
aaagtgtatt	tctagaggcg	atttgcattc	tcocgaatag	gaattttgag	aaaaaaaaca	120
ctctctgttt	tcttcccaat	aatatccaat	cgggcaatat	agttcccaac	attctttatt	180
ctctgtctgc	actcggaaat	ttttaaataa	tagagctcgt	ttaataatat	aatctctata	240
atttatagat	ctcttttcca	tattggcgct	tcogttgaag	ctttccacaa	attctcaatt	300
tgtttggaga	ctctcaaaat	tatcctcttc	tcgacaaatg	ttctgcctct	gtattttgtt	360
ctgctgatca	aagcaatgga	cgacaaatct	atgattaacac	acagttttgt	gtaattttgt	420
agactgatca	agagattacc	tttccagatt	tttgtcatca	tgtgtgtgaat	tgcgcagcgg	480
agccgataag	agcttttagc	atttggagct	ctccaaatga	ttttctctcg	tataattgag	540
ttttgtcact	agagccagaa	caggtggggc	aacaagattg	tgaagtttgc	caggagaaga	600
aaagttagat	caattctgtg	tcactctggt	agaggtttaa	tgagcaaacg	gaacctttag	660
atagcagtg	ctccagaaag	cgggcaagtg	ctggactaat	tagcacagag	ggaggaacta	720
acagcgtctg	tgaaaatgag	agggaggaag	agctaaatga	gaggttttat	gatttagact	780
cggttttggg	gcctggggagg	ctccttaaga	ctgataaac	gggtatactc	gatgatgcaa	840
tcctgatatt	gaatcaacct	agagatgaag	ctcttaagct	tgaagaaact	aaccagaagc	900
ttttgaggga	ctgcaagatg	ctcaagcggc	aggaagaacg	ctcgaggagc	gaaaacgtgg	960
tgttgaagcg	ggataaagag	aagacacagc	aacagtttaa	gtctatgagc	gttccatctt	1020
cagggttctc	acctcatatt	cgactcgcat	ttaaccacaa	caaaatggct	gtttatccaa	1080
gttacaggtt	catgccaatg	tgcattataa	tgctccatac	cgttctgtgac	acatctcgtg	1140
atcaagaaact	cagcgcctct	cgtctctaaa	ctctcaaatg	tttttttttt	gt	

(2) INFORMATION FOR SEQ ID NO:1055:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..283
(D) OTHER INFORMATION: / Ceres Seq. ID 1499514

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1055:

Met	Tyr	Pro	Ser	Leu	Asp	Asn	Asp	Phe	Val	Ser	Asp	Leu	Phe	Cys	Phe
1				5					10					15	
Asp	Gln	Ser	Asn	Gly	Ala	Glu	Leu	Asp	Asp	Tyr	Thr	Gln	Phe	Gly	Val
			20					25					30		
Asn	Leu	Gln	Thr	Asp	Gln	Glu	Asp	Thr	Phe	Pro	Asp	Phe	Val	Ser	Tyr
			35				40					45			
Gly	Val	Asn	Leu	Gln	Gln	Glu	Pro	Asp	Glu	Val	Phe	Ser	Ile	Gly	Ala
	50					55					60				
Ser	Gln	Leu	Asp	Leu	Ser	Ser	Tyr	Asn	Gly	Val	Leu	Ser	Leu	Glu	Pro
65				70						75				80	
Glu	Gln	Val	Gly	Gln	Gln	Asp	Cys	Glu	Val	Val	Gln	Glu	Glu	Glu	Val
				85					90					95	
Glu	Ile	Asn	Ser	Gly	Ser	Ser	Gly	Gly	Ala	Val	Lys	Glu	Glu	Gln	Glu
			100					105					110		
His	Leu	Asp	Asp	Asp	Cys	Ser	Arg	Lys	Arg	Ala	Arg	Thr	Gly	Ser	Cys
			115					120				125			
Ser	Arg	Gly	Gly	Gly	Thr	Lys	Ala	Cys	Arg	Glu	Arg	Leu	Arg	Arg	Glu

130	135	140
Lys Leu Asn Glu Arg Phe Met Asp Leu Ser Ser Val Leu Glu Pro Gly		
145	150	155
Arg Thr Pro Lys Thr Asp Lys Pro Ala Ile Leu Asp Asp Ala Ile Arg		
	165	175
Ile Leu Asn Gln Leu Arg Asp Glu Ala Leu Lys Leu Glu Glu Thr Asn		
	180	190
Gln Lys Leu Leu Glu Glu Ile Lys Ser Leu Lys Ala Glu Lys Asn Glu		
	195	205
Leu Arg Glu Glu Lys Leu Val Leu Lys Ala Asp Lys Glu Lys Thr Glu		
	210	220
Gln Gln Leu Lys Ser Met Thr Ala Pro Ser Ser Gly Phe Ile Pro His		
	215	235
225 Gln Lys Leu Lys Ser Met Thr Ala Pro Ser Ser Gly Phe Ile Pro His		
	230	240
Ile Pro Ala Ala Phe Asn His Asn Lys Met Ala Val Tyr Pro Ser Tyr		
	245	255
Gly Tyr Met Pro Met Trp His Tyr Met Pro Gln Ser Val Arg Asp Thr		
	260	270
Ser Arg Asp Gln Glu Leu Arg Pro Pro Ala Ala		
	275	280

(2) INFORMATION FOR SEQ ID NO:1056:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1191 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1191

(D) OTHER INFORMATION: / Ceres Seq. ID 1499519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1056:

attctaaacc	acacaggcaa	gcattgtggc	tggtgccttg	tagagtgttg	tctgtctaac	60
gaagcaaaaga	tgctgttgga	aacgaaaaac	ggcgaatatt	tgaacgattg	caagattttt	120
cttggaagtgg	ctaagatggc	tccataccct	ccaccaagt	attgcattga	tcacaagggt	180
tggtacgaag	actaccttcg	acgagaaatc	cttctgatag	aagaaaatga	ggcagaggaa	240
ggacttgatg	acaactccgc	tcttgttgag	gaatttgcg	taagaaaaaa	gacgctcttt	300
gttgccaatc	tctcaccag	aactaaaata	tcacatatca	tcaagttttt	taaatgatgt	360
gcagaaattg	ttcgtgttcg	acttattgta	aaccacagg	gtgagcatgt	gggctgtggc	420
ttgtgttgat	ttgcttctgt	taacgaagca	cagaaggcgc	tgcaaaagaa	gaatggtgaa	480
aatttgcgca	gtcgtgagat	ttttcttgac	gtgctgagat	tagctccata	ccctctccga	540
cccaagtaca	accatgcaga	gaaacttttg	cacgaacgag	aaagtcttct	gaagaaacag	600
aaggaatatg	agatgttgag	cgagaggacc	gaattctgcg	gtcctttagg	gttttcggat	660
tcgagcaaaa	acaaaatctc	cgcaatcgag	agaaactctg	agatcggaat	caatggagtc	720
cacaatatcg	ttgaaggtca	acaaaggaaa	aggcaaaagg	tcaaaggggag	cttctctctc	780
cgatgacaaa	tccaagtgtg	atgtcgttaa	ggaatggacc	aattggtcat	tgaagaaggc	840
taaaagtcgt	actactatg	gcttcatccc	tctggtcatc	ttcgtcggca	tgaactccga	900
tcccaaacct	catctcttcc	agctccttag	ccctgtcttc	tccatccaat	tccatcatca	960
acctaaatca	atcgaatcgg	tcttctctgt	gtttggcttc	tccatatctt	tacgctgtgt	1020
cttagattcg	ccgaatcttc	ttttatgctt	ttttcattag	ctagtttttg	aataactttct	1080
ctatggtact	gtattgaata	acttttagatt	atgatataat	gtgaaatcga	attttatgtt	1140
ttgaaaatct	gggaattgct	ttaaagattg	aagtttggg	gaatgtcttg	t	

(2) INFORMATION FOR SEQ ID NO:1057:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..261

(D) OTHER INFORMATION: / Ceres Seq. ID 1499520

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1057:

Ile Leu Asn His Thr Gly Lys His Val Gly Cys Ala Phe Val Glu Phe
1 5 10 15
Gly Ser Ala Asn Glu Ala Lys Met Ser Leu Glu Thr Lys Asn Gly Glu
20 25 30
Tyr Leu Asn Asp Cys Lys Ile Phe Leu Glu Val Ala Lys Met Ala Pro
35 40 45
Tyr Pro Pro Pro Lys Tyr Cys Ile Asp His Lys Val Trp Tyr Glu Asp
50 55 60
Tyr Leu Arg Arg Glu Ile Leu Leu Ile Glu Glu Asn Glu Ala Glu Glu
65 70 75 80
Gly Leu Asp Asp Thr Pro Ala Leu Val Glu Glu Phe Ala Val Arg Lys
85 90 95
Lys Thr Leu Phe Val Ala Asn Leu Ser Pro Arg Thr Lys Ile Ser His
100 105 110
Ile Ile Lys Phe Phe Lys Asp Val Ala Glu Val Val Arg Val Arg Leu
115 120 125
Ile Val Asn His Arg Gly Glu His Val Gly Cys Gly Phe Val Glu Phe
130 135 140
Ala Ser Val Asn Glu Ala Gln Lys Ala Leu Gln Lys Lys Asn Gly Glu
145 150 155 160
Asn Leu Arg Ser Arg Glu Ile Phe Leu Asp Val Ala Glu Leu Ala Pro
165 170 175
Tyr Pro Leu Arg Pro Lys Tyr Asn His Ala Glu Lys Leu Trp His Glu
180 185 190
Arg Glu Ser Leu Leu Lys Lys Gln Lys Glu Tyr Glu Met Leu Ser Glu
195 200 205
Arg Thr Glu Phe Cys Gly Pro Leu Gly Phe Ser Asp Ser Ser Lys Asn
210 215 220
Lys Ile Ser Ala Ile Glu Arg Asn Ser Glu Ile Gly Ile Asn Gly Val
225 230 235 240
His Asn Ile Val Glu Gly Gln Gln Arg Lys Arg Gln Arg Ile Lys Gly
245 250 255
Ser Phe Leu Phe Arg
260

(2) INFORMATION FOR SEQ ID NO:1058:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 238 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..238

(D) OTHER INFORMATION: / Ceres Seq. ID 1499521

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1058:

Met Ser Leu Glu Thr Lys Asn Gly Glu Tyr Leu Asn Asp Cys Lys Ile
1 5 10 15
Phe Leu Glu Val Ala Lys Met Ala Pro Tyr Pro Pro Pro Lys Tyr Cys
20 25 30
Ile Asp His Lys Val Trp Tyr Glu Asp Tyr Leu Arg Arg Glu Ile Leu
35 40 45
Leu Ile Glu Glu Asn Glu Ala Glu Glu Gly Leu Asp Asp Thr Pro Ala
50 55 60
Leu Val Glu Glu Phe Ala Val Arg Lys Lys Thr Leu Phe Val Ala Asn
65 70 75 80
Leu Ser Pro Arg Thr Lys Ile Ser His Ile Ile Lys Phe Phe Lys Asp
85 90 95
Val Ala Glu Val Val Arg Val Arg Leu Ile Val Asn His Arg Gly Glu

100 105 110
His Val Gly Cys Gly Phe Val Glu Phe Ala Ser Val Asn Glu Ala Gln
115 120 125
Lys Ala Leu Gln Lys Lys Asn Gly Glu Asn Leu Arg Ser Arg Glu Ile
130 135 140
Phe Leu Asp Val Ala Glu Leu Ala Pro Tyr Pro Leu Arg Pro Lys Tyr
145 150 155
Asn His Ala Glu Lys Leu Trp His Glu Arg Glu Ser Leu Leu Lys Lys
160 165 170 175
Gln Lys Glu Tyr Glu Met Leu Ser Glu Arg Thr Glu Phe Cys Gly Pro
180 185 190
Leu Gly Phe Ser Asp Ser Ser Lys Asn Lys Ile Ser Ala Ile Glu Arg
195 200 205
Asn Ser Glu Ile Gly Ile Asn Gly Val His Asn Ile Val Glu Gly Gln
210 215 220
Gln Arg Lys Arg Gln Arg Ile Lys Gly Ser Phe Leu Phe Arg
225 230 235

(2) INFORMATION FOR SEQ ID NO:1059:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..216
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1059:

Met Ala Pro Tyr Pro Pro Lys Tyr Cys Ile Asp His Lys Val Trp
1 5 10 15
Tyr Glu Asp Tyr Leu Arg Arg Glu Ile Leu Leu Ile Glu Glu Asn Glu
20 25 30
Ala Glu Glu Gly Leu Asp Asp Thr Pro Ala Leu Val Glu Phe Ala
35 40 45
Val Arg Lys Lys Thr Leu Phe Val Ala Asn Leu Ser Pro Arg Thr Lys
50 55 60
Ile Ser His Ile Ile Lys Phe Phe Lys Asp Val Ala Glu Val Val Arg
65 70 75 80
Val Arg Leu Ile Val Asn His Arg Gly Glu His Val Gly Cys Gly Phe
85 90 95
Val Glu Phe Ala Ser Val Asn Glu Ala Gln Lys Ala Leu Gln Lys Lys
100 105 110
Asn Gly Glu Asn Leu Arg Ser Arg Glu Ile Phe Leu Asp Val Ala Glu
115 120 125
Leu Ala Pro Tyr Pro Leu Arg Pro Lys Tyr Asn His Ala Glu Lys Leu
130 135 140
Trp His Glu Arg Glu Ser Leu Leu Lys Lys Gln Lys Glu Tyr Glu Met
145 150 155 160
Leu Ser Glu Arg Thr Glu Phe Cys Gly Pro Leu Gly Phe Ser Asp Ser
165 170 175
Ser Lys Asn Lys Ile Ser Ala Ile Glu Arg Asn Ser Glu Ile Gly Ile
180 185 190
Asn Gly Val His Asn Ile Val Glu Gly Gln Gln Arg Lys Arg Gln Arg
195 200 205
Ile Lys Gly Ser Phe Leu Phe Arg
210 215

(2) INFORMATION FOR SEQ ID NO:1060:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1673 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1673
(D) OTHER INFORMATION: / Ceres Seq. ID 1499523
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1060:

ataatttgct	attgttcttg	ggcgagccaa	taaaagcctc	tcttttgaat	ccccacaca	60
gattctatgc	ctcttcttcc	ctctgtctcg	ccagaatttt	tgtttccgt	tgataaagg	120
tttatctttg	gtggatgatt	agtgaaactt	tttaaggaga	tattagtcca	catgttttag	180
ttaaaaatg	caggttcaag	cggtctgggt	ttggaagctg	aggaggggga	aataagtata	240
gacatggaag	aagacatgga	tctaacagaa	gatgatttca	gaaatgtgtc	tggccagttt	300
tcaggacaag	catcgatcgt	ggaggttggg	gatgctgttg	atgtgagagt	cgaaaaccgtg	360
aaagttagat	ttagtcttaa	atctgggtgt	aaaagagcca	gaacaatctc	ctctggaacag	420
caaccttcag	tccatgttac	ttataaacac	ttacaacag	atagtaagca	gaagctggaa	480
agttttattac	agcaatggtc	agaatgggag	atctcttctc	cgaggatcaa		540
gaacaagtac	tagaagctgg	tgatgagaca	tactttcctg	ctttgcgtgt	gggattgcag	600
aagacatcat	ctgtatcatt	ttggtttgac	taccaaaactg	gtcacagttc	ttcgaagaag	660
ctctgttccag	tggaaagtag	cactactcct	ctttataacc	gtggatttac	aattgggttta	720
gattcaggtt	caaataacgt	ggaaggaggc	ttggagatta	ttgatgatcc	tccacgttgc	780
ttcaactgtg	ggcgatacag	tcatcttatt	agagaatgtc	caaggccctt	tgtatcgatca	840
gcagtttagta	atgctcggag	gcaacataaa	agaaaaagaa	atcacagctc	tgatcccgct	900
ctaccatcca	gatattatca	gagccttcaa	cggtgaaaaa	aatgatggct	gaagcctggc	960
tcacttgatg	cagagacgcg	taagcttctc	ggctctaaag	aactcgatcc	tcctccatgg	1020
cttaacagaa	tggcagagat	tggatatcca	ccaggatatt	ttgctgtaga	agaagacagt	1080
gatgatcact	cgagaataac	tatatgttgt	gaggaagaga	ctaaagaaga	ggaagaagtt	1140
aagactgaag	aaggtgaaat	cttggaaaaa	gcaagcctcc	aagagccaa	aaagataatg	1200
acagttggat	ttcccgggat	taacgcaccc	attccagaaa	acgcagattc	gtggctatgg	1260
gaacagagga	atagttaacac	aggacatact	aattatcata	atcaccttcg	accacaaat	1320
gagatggggc	ctctagtgat	tcaactgtct	tcaagcttcc	ctccaatgca	tggcattaga	1380
tatgatcata	ggttcgggtt	atgaccaata	agcccgggat	cgaaaagagt	taagatccat	1440
tttagtttta	gcagcagaag	atagattcat	tagtgaatgt	gggatgtatg	ataaccatta	1500
gttaaaagagt	taaccacacag	ccaactacgg	ttaaaacatt	caggcctaag	ccaaagtatg	1560
ctatgcttaa	ggcagaatcg	aacttttacg	tctttgtgtg	taaaactgga	atcgtgatta	1620
tacacgtttg	gtgtgttaac	atgtccatca	atgtacaaga	tttttgtttt	ggt	

(2) INFORMATION FOR SEQ ID NO:1061:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 405 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..405
(D) OTHER INFORMATION: / Ceres Seq. ID 1499524

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1061:

Met	Ala	Ala	Ser	Ser	Gly	Ser	Gly	Leu	Glu	Ala	Glu	Glu	Gly	Glu	Ile
1			5						10					15	
Ser	Ile	Asp	Met	Glu	Glu	Asp	Met	Asp	Leu	Thr	Glu	Asp	Asp	Phe	Arg
			20					25					30		
Asn	Val	Ser	Gly	Gln	Phe	Ser	Gly	Gln	Ala	Ser	Ile	Val	Glu	Val	Gly
			35				40					45			
Asp	Ala	Val	Asp	Val	Arg	Val	Glu	Thr	Val	Lys	Val	Asp	Val	Ser	Ser
			50				55				60				
Lys	Ser	Gly	Val	Lys	Arg	Ala	Arg	Thr	Ile	Ser	Leu	Glu	Gln	Gln	Pro
			65				70				75			80	
Ser	Val	His	Val	Thr	Tyr	Lys	His	Leu	Thr	Arg	Asp	Ser	Lys	Gln	Lys
							85				90			95	
Leu	Glu	Ser	Leu	Leu	Gln	Gln	Trp	Ser	Glu	Trp	Glu	Ala	Glu	Gln	Asn

Met	Glu	Glu	Asp	Met	Asp	Leu	Thr	Glu	Asp	Asp	Phe	Arg	Asn	Val	Ser
1			5					10						15	
Gly	Gln	Phe	Ser	Gly	Gln	Ala	Ser	Ile	Val	Glu	Val	Gly	Asp	Ala	Val
			20					25					30		
Asp	Val	Arg	Val	Glu	Thr	Val	Lys	Val	Asp	Val	Ser	Ser	Lys	Ser	Gly
			35				40					45			
Val	Lys	Arg	Ala	Arg	Thr	Ile	Ser	Leu	Glu	Gln	Gln	Pro	Ser	Val	His
			50				55				60				
Val	Thr	Tyr	Lys	His	Leu	Thr	Arg	Asp	Ser	Lys	Gln	Lys	Leu	Glu	Ser
65					70					75				80	

Leu Leu Gln Gln Trp Ser Glu Trp Glu Ala Glu Gln Asn Ser Leu Ser
85 90 95
Glu Asp Gln Glu Gln Val Leu Glu Ala Gly Asp Glu Thr Tyr Phe Pro
100 105 110
Ala Leu Arg Val Gly Leu Gln Lys Thr Ser Ser Val Ser Phe Trp Phe
115 120 125
Asp Tyr Gln Thr Gly His Ser Ser Ser Lys Lys Ser Val Pro Val Glu
130 135 140
Ser Ser Thr Thr Pro Leu Tyr Asn Arg Gly Phe Thr Ile Gly Leu Asp
145 150 155 160
Ser Gly Ser Asn Asn Val Glu Gly Gly Leu Glu Ile Ile Asp Asp Pro
165 170 175
Pro Arg Cys Phe Asn Cys Gly Ala Tyr Ser His Ser Ile Arg Glu Cys
180 185 190
Pro Arg Pro Phe Asp Arg Ser Ala Val Ser Asn Ala Arg Arg Gln His
195 200 205
Lys Arg Lys Arg Asn Gln Thr Pro Gly Ser Arg Leu Pro Ser Arg Tyr
210 215 220
Tyr Gln Ser Leu Gln Arg Gly Lys Tyr Asp Gly Leu Lys Pro Gly Ser
225 230 235 240
Leu Asp Ala Glu Thr Arg Lys Leu Leu Gly Leu Lys Glu Leu Asp Pro
245 250 255
Pro Pro Trp Leu Asn Arg Met Arg Glu Ile Gly Tyr Pro Pro Gly Tyr
260 265 270
Phe Ala Val Glu Glu Asp Asp Asp Asp His Ser Arg Ile Thr Ile Phe
275 280 285
Gly Glu Glu Glu Thr Lys Glu Glu Glu Val Lys Thr Glu Glu Gly
290 295 300
Glu Ile Leu Glu Lys Ala Ser Pro Gln Glu Pro Arg Lys Ile Met Thr
305 310 315 320
Val Gly Phe Pro Gly Ile Asn Ala Pro Ile Pro Glu Asn Ala Asp Ser
325 330 335
Trp Leu Trp Glu Gln Arg Asn Ser Asn Thr Gly His Thr Asn Tyr His
340 345 350
Asn His Leu Arg Pro Gln Tyr Glu Met Gly Pro Leu Gly Ile Gln Leu
355 360 365
Ser Ser Ser Phe Pro Pro Met His Gly Ile Arg Tyr Asp His Arg Phe
370 375 380
Gly Leu
385

(2) INFORMATION FOR SEQ ID NO:1063:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 382 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..382

(D) OTHER INFORMATION: / Ceres Seq. ID 1499526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1063:

Met Asp Leu Thr Glu Asp Asp Phe Arg Asn Val Ser Gly Gln Phe Ser
1 5 10 15
Gly Gln Ala Ser Ile Val Glu Val Gly Asp Ala Val Asp Val Arg Val
20 25 30
Glu Thr Val Lys Val Asp Val Ser Ser Lys Ser Gly Val Lys Arg Ala
35 40 45
Arg Thr Ile Ser Leu Glu Gln Gln Pro Ser Val His Val Thr Tyr Lys
50 55 60
His Leu Thr Arg Asp Ser Lys Gln Lys Leu Glu Ser Leu Leu Gln Gln

65	70	75	80
Trp Ser Glu Trp Glu Ala Glu Gln Asn Ser Leu Ser Glu Asp Gln Glu	85	90	95
Gln Val Leu Glu Ala Gly Asp Glu Thr Tyr Phe Pro Ala Leu Arg Val	100	105	110
Gly Leu Gln Lys Thr Ser Ser Val Ser Phe Trp Phe Asp Tyr Gln Thr	115	120	125
Gly His Ser Ser Ser Lys Lys Ser Val Pro Val Glu Ser Ser Thr Thr	130	135	140
Pro Leu Tyr Asn Arg Gly Phe Thr Ile Gly Leu Asp Ser Gly Ser Asn	145	150	155
Asn Val Glu Gly Gly Leu Glu Ile Ile Asp Asp Pro Pro Arg Cys Phe	160	165	170
Asn Cys Gly Ala Tyr Ser His Ser Ile Arg Glu Cys Pro Arg Pro Phe	175	180	185
Asp Arg Ser Ala Val Ser Asn Ala Arg Arg Gln His Lys Arg Lys Arg	190	195	200
Asn Gln Thr Pro Gly Ser Arg Leu Pro Ser Arg Tyr Tyr Gln Ser Leu	205	210	215
Gln Arg Gly Lys Tyr Asp Gly Leu Lys Pro Gly Ser Leu Asp Ala Glu	220	225	230
Thr Arg Lys Leu Leu Gly Leu Lys Glu Leu Asp Pro Pro Pro Trp Leu	235	240	245
Asn Arg Met Arg Glu Ile Gly Tyr Pro Pro Gly Tyr Phe Ala Val Glu	250	255	260
Glu Asp Asp Asp Asp His Ser Arg Ile Thr Ile Phe Gly Glu Glu Glu	265	270	275
Thr Lys Glu Glu Glu Glu Val Lys Thr Glu Glu Gly Glu Ile Leu Glu	280	285	290
Lys Ala Ser Pro Gln Glu Pro Arg Lys Ile Met Thr Val Gly Phe Pro	295	300	305
Gly Ile Asn Ala Pro Ile Pro Glu Asn Ala Asp Ser Trp Leu Trp Glu	310	315	320
Gln Arg Asn Ser Asn Thr Gly His Thr Asn Tyr His Asn His Leu Arg	325	330	335
Pro Gln Tyr Glu Met Gly Pro Leu Gly Ile Gln Leu Ser Ser Ser Phe	340	345	350
Pro Pro Met His Gly Ile Arg Tyr Asp His Arg Phe Gly Leu	355	360	365
	370	375	380

(2) INFORMATION FOR SEQ ID NO:1064:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1043 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1043

(D) OTHER INFORMATION: / Ceres Seq. ID 1499527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1064:

gaaatttcct	ctctcttctt	tttgcttgag	cttttaggttt	tgagagcaaa	gaaaaacgaa	60
gacgcgtcaa	agagcttttg	tggagaggtt	ctgcttgctt	gctacaatgg	gttacgccca	120
tgtagtattt	ggtcacgacg	gcagtggaaa	gtcaacttat	tgctcgcttt	tgatgaaca	180
ttgtgaaact	atcggctcgaa	caatgcattg	tgtaaacttt	gatcctgctg	cggagatcct	240
caactatcct	gtggctatgg	atatcacaga	acttatttct	ttggaagatg	tgatggagga	300
tctaaagctt	ggctcctaag	gtgcccttat	gtattgcatt	gagtatcttg	aggatagctt	360
acatgatggg	gtggatgaag	aattggagaa	ctacagggat	gacgattaac	ttatctttga	420
ttgtccaggc	cagatagagc	gttttacaca	tgttccctgtg	ctcaagaact	ttgtggagca	480
tttgaagcag	aagaacttca	acgtctgtgt	tgtttatctg	cttgattcac	agttcatcac	540
agatgtaacc	aagtttatca	gtgggttgcat	gtcatctctc	gctgcataga	tccagcttga	600

attaccacat	gtcaacatcc	tctcaaaaaa	ggacctcttg	caggacaaaa	gcaacattga	660
tgattacttg	aatccggagc	ctcgcacatt	gctagcagag	ttaacaaaaa	ggatgggtcc	720
tcaattacga	aaactaaaaa	aagccttgat	tgagatgggt	ggagagtatg	ggatgggtgaa	780
tttcaatacc	attaacttga	ggaagaagaa	gagcattcaa	tatgttctgt	cacaatacga	840
cgctctgatt	cagtttggag	aagatgctga	tgtgaacatc	aaagatgatg	acgatttttag	900
tgacgatggt	cctgacctat	aattgttata	ttoggtttct	acaacttttg	ttaaaaagtct	960
aaacaagcgt	ggctctcatg	ttctgttcag	ttaccaatgg	cgtttgtgag	aacttttgtt	1020
gaatatcaaa	agccttcaat	gtg				

(2) INFORMATION FOR SEQ ID NO:1065:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..271

(D) OTHER INFORMATION: / Ceres Seq. ID 1499528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1065:

Met	Gly	Tyr	Ala	Gln	Leu	Val	Ile	Gly	Pro	Ala	Gly	Ser	Gly	Lys	Ser
1				5				10					15		
Thr	Tyr	Cys	Ser	Ser	Leu	Tyr	Glu	His	Cys	Glu	Thr	Ile	Gly	Arg	Thr
			20				25						30		
Met	His	Val	Val	Asn	Leu	Asp	Pro	Ala	Ala	Glu	Ile	Phe	Asn	Tyr	Pro
			35				40					45			
Val	Ala	Met	Asp	Ile	Arg	Glu	Leu	Ile	Ser	Leu	Glu	Asp	Val	Met	Glu
			50				55				60				
Asp	Leu	Lys	Leu	Gly	Pro	Asn	Gly	Ala	Leu	Met	Tyr	Cys	Met	Glu	Tyr
65					70					75				80	
Leu	Glu	Asp	Ser	Leu	His	Asp	Trp	Val	Asp	Glu	Glu	Leu	Glu	Asn	Tyr
			85					90					95		
Arg	Asp	Asp	Asp	Tyr	Leu	Ile	Phe	Asp	Cys	Pro	Gly	Gln	Ile	Glu	Leu
			100					105					110		
Phe	Thr	His	Val	Pro	Val	Leu	Lys	Asn	Phe	Val	Glu	His	Leu	Lys	Gln
			115					120					125		
Lys	Asn	Phe	Asn	Val	Cys	Val	Val	Tyr	Leu	Leu	Asp	Ser	Gln	Phe	Ile
			130					135				140			
Thr	Asp	Val	Thr	Lys	Phe	Ile	Ser	Gly	Cys	Met	Ser	Ser	Leu	Ala	Ala
145					150					155				160	
Met	Ile	Gln	Leu	Glu	Leu	Pro	His	Val	Asn	Ile	Leu	Ser	Lys	Met	Asp
			165							170				175	
Leu	Leu	Gln	Asp	Lys	Ser	Asn	Ile	Asp	Asp	Tyr	Leu	Asn	Pro	Glu	Pro
			180					185					190		
Arg	Thr	Leu	Leu	Ala	Glu	Leu	Asn	Lys	Arg	Met	Gly	Pro	Gln	Tyr	Ala
			195					200					205		
Lys	Leu	Asn	Lys	Ala	Leu	Ile	Glu	Met	Val	Gly	Glu	Tyr	Gly	Met	Val
			210					215				220			
Asn	Phe	Ile	Pro	Ile	Asn	Leu	Arg	Lys	Glu	Lys	Ser	Ile	Gln	Tyr	Val
225					230					235				240	
Leu	Ser	Gln	Ile	Asp	Val	Cys	Ile	Gln	Phe	Gly	Glu	Asp	Ala	Asp	Val
			245							250				255	
Asn	Ile	Lys	Asp	Asp	Asp	Asp	Phe	Ser	Asp	Asp	Gly	Pro	Asp	Leu	
			260					265							

(2) INFORMATION FOR SEQ ID NO:1066:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..239

(D) OTHER INFORMATION: / Ceres Seq. ID 1499529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1066:

```
Met His Val Val Asn Leu Asp Pro Ala Ala Glu Ile Phe Asn Tyr Pro
1      5      10      15
Val Ala Met Asp Ile Arg Glu Leu Ile Ser Leu Glu Asp Val Met Glu
20      25      30
Asp Leu Lys Leu Gly Pro Asn Gly Ala Leu Met Tyr Cys Met Glu Tyr
35      40      45
Leu Glu Asp Ser Leu His Asp Trp Val Asp Glu Glu Leu Glu Asn Tyr
50      55      60
Arg Asp Asp Asp Tyr Leu Ile Phe Asp Cys Pro Gly Gln Ile Glu Leu
65      70      75      80
Phe Thr His Val Pro Val Leu Lys Asn Phe Val Glu His Leu Lys Gln
85      90      95
Lys Asn Phe Asn Val Cys Val Val Tyr Leu Leu Asp Ser Gln Phe Ile
100      105      110
Thr Asp Val Thr Lys Phe Ile Ser Gly Cys Met Ser Ser Leu Ala Ala
115      120      125
Met Ile Gln Leu Glu Leu Pro His Val Asn Ile Leu Ser Lys Met Asp
130      135      140
Leu Leu Gln Asp Lys Ser Asn Ile Asp Asp Tyr Leu Asn Pro Glu Pro
145      150      155      160
Arg Thr Leu Leu Ala Glu Leu Asn Lys Arg Met Gly Pro Gln Tyr Ala
165      170      175
Lys Leu Asn Lys Ala Leu Ile Glu Met Val Gly Glu Tyr Gly Met Val
180      185      190
Asn Phe Ile Pro Ile Asn Leu Arg Lys Glu Lys Ser Ile Gln Tyr Val
195      200      205
Leu Ser Gln Ile Asp Val Cys Ile Gln Phe Gly Glu Asp Ala Asp Val
210      215      220
Asn Ile Lys Asp Asp Asp Phe Ser Asp Asp Gly Pro Asp Leu
225      230      235
```

(2) INFORMATION FOR SEQ ID NO:1067:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 221 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..221

(D) OTHER INFORMATION: / Ceres Seq. ID 1499530

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1067:

```
Met Asp Ile Arg Glu Leu Ile Ser Leu Glu Asp Val Met Glu Asp Leu
1      5      10      15
Lys Leu Gly Pro Asn Gly Ala Leu Met Tyr Cys Met Glu Tyr Leu Glu
20      25      30
Asp Ser Leu His Asp Trp Val Asp Glu Glu Leu Glu Asn Tyr Arg Asp
35      40      45
Asp Asp Tyr Leu Ile Phe Asp Cys Pro Gly Gln Ile Glu Leu Phe Thr
50      55      60
His Val Pro Val Leu Lys Asn Phe Val Glu His Leu Lys Gln Lys Asn
65      70      75      80
Phe Asn Val Cys Val Val Tyr Leu Leu Asp Ser Gln Phe Ile Thr Asp
85      90      95
Val Thr Lys Phe Ile Ser Gly Cys Met Ser Ser Leu Ala Ala Met Ile
100      105      110
```

Gln Leu Glu Leu Pro His Val Asn Ile Leu Ser Lys Met Asp Leu Leu
115 120 125
Gln Asp Lys Ser Asn Ile Asp Asp Tyr Leu Asn Pro Glu Pro Arg Thr
130 135 140
Leu Leu Ala Glu Leu Asn Lys Arg Met Gly Pro Gln Tyr Ala Lys Leu
145 150 155 160
Asn Lys Ala Leu Ile Glu Met Val Gly Glu Tyr Gly Met Val Asn Phe
165 170 175
Ile Pro Ile Asn Leu Arg Lys Glu Lys Ser Ile Gln Tyr Val Leu Ser
180 185 190
Gln Ile Asp Val Cys Ile Gln Phe Gly Glu Asp Ala Asp Val Asn Ile
195 200 205
Lys Asp Asp Asp Asp Phe Ser Asp Asp Gly Pro Asp Leu
210 215 220

(2) INFORMATION FOR SEQ ID NO:1068:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..444

(D) OTHER INFORMATION: / Ceres Seq. ID 1499538

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1068:

aaaatttagt	tcttttctca	tttatccact	gctcttaact	caacttcaat	atctctctat	60
cctcacaaata	tttgtttgt	ttctmettca	actttcaact	gataaaagttt	aaacctttat	120
gctctttact	ctctgatctc	aaaagggttt	tggttagttc	nmctcaaaac	catggrgatt	180
tgcttaagt	ctmagattaa	agctgtgagt	ccaggttaagc	cagggtgcaag	tccgaagatt	240
atgagctcag	aggctaata	ttcactggga	agtaaaaagc	ctctctgtgc	aatcagaaca	300
aaccacaagaa	ctgaaggaga	gatcttggca	tctcctaact	tcaaaagttt	cacttttgt	360
gagcttaaa	cagcanctag	gnattttaga	ccagatagtg	ttcttggtga	agggtggttt	420
ggtctgtgtt	tcaaaggttg	gatt				

(2) INFORMATION FOR SEQ ID NO:1069:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..91

(D) OTHER INFORMATION: / Ceres Seq. ID 1499539

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1069:

Met Xaa Ile Cys Leu Ser Ala Xaa Ile Lys Ala Val Ser Pro Gly Lys	
1 5 10 15	
Pro Gly Ala Ser Pro Lys Tyr Met Ser Ser Glu Ala Asn Asp Ser Leu	
20 25 30	
Gly Ser Lys Ser Ser Ser Val Ser Ile Arg Thr Asn Pro Arg Thr Glu	
35 40 45	
Gly Glu Ile Leu Gln Ser Pro Asn Leu Lys Ser Phe Thr Phe Ala Glu	
50 55 60	
Leu Lys Ala Ala Xaa Arg Xaa Phe Arg Pro Asp Ser Val Leu Gly Glu	
65 70 75 80	
Gly Gly Phe Gly Ser Val Phe Lys Gly Trp Ile	
85 90	

(2) INFORMATION FOR SEQ ID NO:1070:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..68
(D) OTHER INFORMATION: / Ceres Seq. ID 1499540
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1070:
Met Ser Ser Glu Ala Asn Asp Ser Leu Gly Ser Lys Ser Ser Val
1 5 10 15
Ser Ile Arg Thr Asn Pro Arg Thr Glu Gly Glu Ile Leu Gln Ser Pro
20 25 30
Asn Leu Lys Ser Phe Thr Phe Ala Glu Leu Lys Ala Ala Xaa Arg Xaa
35 40 45
Phe Arg Pro Asp Ser Val Leu Gly Glu Gly Gly Phe Gly Ser Val Phe
50 55 60
Lys Gly Trp Ile
65

(2) INFORMATION FOR SEQ ID NO:1071:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..62
(D) OTHER INFORMATION: / Ceres Seq. ID 1499541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1071:

Met Ile His Trp Glu Val Lys Ala Leu Leu Cys Gln Ser Glu Gln Thr
1 5 10 15
Gln Glu Leu Lys Glu Arg Ser Cys Asn Leu Leu Ile Ser Lys Val Ser
20 25 30
Leu Leu Leu Ser Leu Lys Gln Xaa Leu Xaa Ile Leu Asp Gln Ile Val
35 40 45
Phe Leu Val Lys Val Val Leu Val Leu Phe Ser Lys Val Gly
50 55 60

(2) INFORMATION FOR SEQ ID NO:1072:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1396 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1396
(D) OTHER INFORMATION: / Ceres Seq. ID 1499542

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1072:

agaaccaaatt cctcggcggc gattgaagaa acctttcoga tggatctgct caggggaagag 60
attctgaaga aacgtaagag tctagtctgag gaattctggt gtaagaagtt cttcaagcgg 120
tctgagatcg agcagaagaa aatccagaag ctctgagagg aagaacgacg cgagcacgag 180
cttaagcttc agcggagagc cgcccgcgcc gcttcocggt gagatggaaa atcatccggc 240
gtgtgtgcta tcggcgattc aaaaagcccta accgacgaaa acctaatctt cccgagggag 300
gaagtgattc gtctgttag attccttaag cagccgatga ctctctctcg agaagatgat 360
caatcgccgg tcgattcgact caagtacgtt ttgaaggaag gattgttcga gtttgatgat 480
gatatgactg aaggacagac gaatgatttc ttgcgtgaca tcgcagagct taagaagagg 540
cagaagatgt gtatgatggg agataggaag aggaagagta gagatgagag aggaagagac 600

(2) INFORMATION FOR SEQ ID NO:1073:

(A) LENGTH: 433 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..433

(D) OTHER INFORMATION: / Ceres Seq. ID 1499543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1073:

Arg	Thr	Lys	Leu	Ser	Ser	Ala	Ala	Ile	Glu	Glu	Thr	Phe	Pro	Met	Asp	Leu
1	5	10	15	20	25	30	35	40	45	50	55	60	65	70	75	80
Leu	Arg	Glu	Glu	Ile	Leu	Lys	Lys	Arg	Lys	Ser	Leu	Ala	Glu	Glu	Ser	
Gly	Gly	Lys	Lys	Phe	Phe	Lys	Arg	Ser	Glu	Ile	Glu	Gln	Lys	Lys	Ile	
Gln	Lys	Leu	Arg	Glu	Glu	Glu	Arg	Arg	Glu	His	Glu	Leu	Lys	Ala	Gln	
Arg	Arg	Ala	Ala	Ala	Ala	Ala	Ser	Gly	Gly	Asp	Gly	Lys	Ser	Ser	Gly	
65	70	75	80	85	90	95	100	105	110	115	120	125	130	135	140	145
Ser	Ala	Pro	Gly	Ser	Ser	Asn	Ala	Ala	Thr	Ser	Ala	Ser	Ser	Lys	Ser	
Ser	Ala	Ser	Asp	Ala	Ala	Ala	Ile	Ala	Asp	Ser	Lys	Ala	Leu	Thr	Asp	
Glu	Asn	Leu	Ile	Leu	Pro	Arg	Gln	Glu	Val	Ile	Arg	Arg	Leu	Arg	Phe	
Leu	Lys	Gln	Pro	Met	Thr	Leu	Phe	Gly	Glu	Asp	Asp	Gln	Ser	Arg	Leu	
130	135	140	145	150	155	160	165	170	175	180	185	190	195	200	205	210
Asp	Arg	Leu	Tyr	Val	Val	Lys	Glu	Gly	Leu	Phe	Glu	Val	Asp	Ser	Ala	
Asp	Met	Thr	Glu	Gly	Gln	Thr	Asn	Asp	Phe	Leu	Arg	Asp	Ile	Ala	Glu	
Leu	Lys	Lys	Arg	Gln	Lys	Ser	Gly	Met	Met	Gly	Asp	Arg	Lys	Arg	Lys	
Ser	Arg	Asp	Glu	Arg	Gly	Arg	Asp	Glu	Gly	Asp	Arg	Gly	Glu	Thr	Arg	
Glu	Tyr	Glu	Leu	Ser	Gly	Gly	Glu	Ser	Ser	Asp	Val	Asp	Ala	Asp	Lys	
210	215	220	225	225	230	235	240	245	250	255	260	265	270	275	280	285
Asp	Met	Lys	Arg	Leu	Lys	Ala	Asn	Phe	Glu	Asp	Leu	Cys	Asp	Glu	Asp	
Lys	Ile	Leu	Val	Phe	Thr	Lys	Lys	Leu	Leu	Ile	Glu	Trp	Lys	Gln	Glu	
Leu	Asp	Ala	Met	Glu	Asn	Thr	Glu	Arg	Arg	Thr	Ala	Lys	Gly	Lys	Gln	
Met	Val	Ala	Thr	Phe	Lys	Gln	Cys	Ala	Arg	Tyr	Leu	Val	Pro	Leu	Phe	

275	280	285
Asn Leu Cys Arg Lys Lys Gly Leu Pro Ala Asp Ile Arg Gln Ala Leu		
290	295	300
Met Val Met Val Asn His Cys Ile Lys Arg Asp Tyr Leu Ala Ala Met		
305	310	315
Asp His Tyr Ile Lys Leu Ala Ile Gly Asn Ala Pro Trp Pro Ile Gly		
325	330	335
Val Thr Met Val Gly Ile His Glu Arg Ser Ala Arg Glu Lys Ile Tyr		
340	345	350
Thr Asn Ser Val Ala His Ile Met Asn Asp Glu Thr Thr Arg Lys Tyr		
355	360	365
Leu Gln Ser Val Lys Arg Leu Met Thr Phe Cys Gln Arg Arg Tyr Pro		
370	375	380
Thr Met Pro Ser Lys Ala Val Glu Phe Asn Ser Leu Ala Asn Gly Ser		
385	390	395
Asp Leu Gln Ser Leu Leu Ala Glu Glu Arg Phe Phe Gly Asn Arg		
405	410	415
Glu Gln Val Ser Glu Glu Arg Leu Arg Leu Met Pro Ser Gln Ser Glu		
420	425	430
Ser		

(2) INFORMATION FOR SEQ ID NO:1074:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..420

(D) OTHER INFORMATION: / Ceres Seq. ID 1499544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1074:

Met Asp Leu Leu Arg Glu Glu Ile Leu Lys Lys Arg Lys Ser Leu Ala	
1	5 10 15
Glu Glu Ser Gly Gly Lys Lys Phe Phe Lys Arg Ser Glu Ile Glu Gln	
20	25 30
Lys Lys Ile Gln Lys Leu Arg Glu Glu Glu Arg Arg Glu His Glu Leu	
35	40 45
Lys Ala Gln Arg Arg Ala Ala Ala Ala Ser Gly Gly Asp Gly Lys	
50	55 60
Ser Ser Gly Ser Ala Pro Gly Ser Ser Asn Ala Ala Thr Ser Ala Ser	
65	70 75 80
Ser Lys Ser Ser Ala Ser Asp Ala Ala Ala Ile Ala Asp Ser Lys Ala	
85	90 95
Leu Thr Asp Glu Asn Leu Ile Leu Pro Arg Gln Glu Val Ile Arg Arg	
100	105 110
Leu Arg Phe Leu Lys Gln Pro Met Thr Leu Phe Gly Glu Asp Asp Gln	
115	120 125
Ser Arg Leu Asp Arg Leu Lys Tyr Val Leu Lys Glu Gly Leu Phe Glu	
130	135 140
Val Asp Ser Asp Met Thr Glu Gly Gln Thr Asn Asp Phe Leu Arg Asp	
145	150 155 160
Ile Ala Glu Leu Lys Lys Arg Gln Lys Ser Gly Met Met Gly Asp Arg	
165	170 175
Lys Arg Lys Ser Arg Asp Glu Arg Gly Arg Asp Glu Gly Asp Arg Gly	
180	185 190
Glu Thr Arg Glu Tyr Glu Leu Ser Gly Gly Glu Ser Ser Asp Val Asp	
195	200 205
Ala Asp Lys Asp Met Lys Arg Leu Lys Ala Asn Phe Glu Asp Leu Cys	
210	215 220

Asp Glu Asp Lys Ile Leu Val Phe Tyr Lys Lys Leu Leu Ile Glu Trp
225 230 235 240
Lys Gln Glu Leu Asp Ala Met Glu Asn Thr Glu Arg Arg Thr Ala Lys
245 250 255
Gly Lys Gln Met Val Ala Thr Phe Lys Gln Cys Ala Arg Tyr Leu Val
260 265 270
Pro Leu Phe Asn Leu Cys Arg Lys Lys Gly Leu Pro Ala Asp Ile Arg
275 280 285
Gln Ala Leu Met Val Met Val Asn His Cys Ile Lys Arg Asp Tyr Leu
290 295 300
Ala Ala Met Asp His Tyr Ile Lys Leu Ala Ile Gly Asn Ala Pro Trp
305 310 315 320
Pro Ile Gly Val Thr Met Val Gly Ile His Glu Arg Ser Ala Arg Glu
325 330 335
Lys Ile Tyr Thr Asn Ser Val Ala His Ile Met Asn Asp Glu Thr Thr
340 345 350
Arg Lys Tyr Leu Gln Ser Val Lys Arg Leu Met Thr Phe Cys Gln Arg
355 360 365
Arg Tyr Pro Thr Met Pro Ser Lys Ala Val Glu Phe Asn Ser Leu Ala
370 375 380
Asn Gly Ser Asp Leu Gln Ser Ser Leu Leu Ala Glu Glu Arg Phe Phe Gly
385 390 395 400
Gly Asn Arg Glu Gln Val Ser Glu Glu Arg Leu Arg Leu Met Pro Ser
405 410 415
Gln Ser Glu Ser
420

(2) INFORMATION FOR SEQ ID NO:1075:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..301
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499545

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1075:

Met Thr Leu Phe Gly Glu Asp Asp Gln Ser Arg Leu Asp Arg Leu Lys
1 5 10 15
Tyr Val Leu Lys Glu Gly Leu Phe Glu Val Asp Ser Asp Met Thr Glu
20 25 30
Gly Gln Thr Asn Asp Phe Leu Arg Asp Ile Ala Glu Leu Lys Lys Arg
35 40 45
Gln Lys Ser Gly Met Met Gly Asp Arg Lys Arg Lys Ser Arg Asp Glu
50 55 60
Arg Gly Arg Asp Glu Gly Asp Arg Gly Glu Thr Arg Glu Tyr Glu Leu
65 70 75 80
Ser Gly Gly Glu Ser Ser Asp Val Asp Ala Asp Lys Asp Met Lys Arg
85 90 95
Leu Lys Ala Asn Phe Glu Asp Leu Cys Asp Glu Asp Lys Ile Leu Val
100 105 110
Phe Tyr Lys Lys Leu Leu Ile Glu Trp Lys Gln Glu Leu Asp Ala Met
115 120 125
Glu Asn Thr Glu Arg Arg Thr Ala Lys Gly Lys Gln Met Val Ala Thr
130 135 140
Phe Lys Gln Cys Ala Arg Tyr Leu Val Pro Leu Phe Asn Leu Cys Arg
145 150 155 160
Lys Lys Gly Leu Pro Ala Asp Ile Arg Gln Ala Leu Met Val Met Val
165 170 175
Asn His Cys Ile Lys Arg Asp Tyr Leu Ala Ala Met Asp His Tyr Ile

[illegible]

100

(2) INFORMATION FOR SEQ ID NO:1078:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1078:

Met	Asn	Glu	Leu	Lys	Ile	Arg	Asp	Asp	Lys	Glu	Val	Glu	Ala	Thr	Ile
1				5					10					15	
Ile	Asn	Gly	Lys	Gly	Thr	Glu	Thr	Gly	His	Ile	Ile	Val	Thr	Thr	
			20					25					30		
Gly	Gly	Lys	Asn	Gly	Gln	Pro	Lys	Gln	Thr	Val	Ser	Tyr	Met	Ala	Glu
			35				40					45			
Arg	Ile	Val	Gly	Gln	Gly	Ser	Phe	Gly	Ile	Val	Phe	Gln	Ala	Lys	Cys
			50			55					60				
Leu	Glu	Thr	Gly	Glu	Thr	Val	Ala	Ile	Lys	Lys					
65					70				75						

(2) INFORMATION FOR SEQ ID NO:1079:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..398
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499558

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1079:

aaagctcccg	cacaccctgc	ctgatccctc	ccaataagct	ccccagctcc	acgccggcag	60
cagcagcagc	agcagtagag	atggccgccc	tcgccgcctc	ctccacggcc	gccttcgccg	120
ccaagccgcg	cctccacagc	gcgcgcctca	ccgtggccgt	ctccgccaac	ggcgcgcgac	180
gcaacggcag	cagcagcagt	gtgtcgctcg	catcctccgt	gaagacgttc	tcggccgcgc	240
tggtctgtgc	gtcgggtgctt	ctctcctcgg	cgcscacctc	cmctscctccc	gcggccgcgtg	300
acatcgccgg	gctgaccccg	tqcaaggagt	ccaagcgctt	gcgcaagcgc	gagaagaact	360
cgatcaagaa	gstcaccgcg	tcgctcaaga	agtcacgcg			

(2) INFORMATION FOR SEQ ID NO:1080:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499559

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1080:

Ser	Ser	Arg	Thr	Pro	Cys	Leu	Ile	Pro	Pro	Asn	Lys	Leu	Pro	Ser	Ser
1				5					10					15	
Thr	Pro	Asp	Ala	Ala	Ala	Ala	Ala	Val	Glu	Met	Ala	Ala	Leu	Ala	Ala
			20					25					30		
Ser	Ser	Thr	Ala	Ala	Phe	Ala	Ala	Lys	Pro	Arg	Leu	Pro	Arg	Ala	Arg
			35			40				45					
Leu	Thr	Val	Ala	Cys	Ser	Ala	Thr	Gly	Xaa	Asp	Gly	Asn	Gly	Ser	Ser

50 55 60
Ser Ser Val Ser Leu Ala Ser Ser Val Lys Thr Phe Ser Ala Ala Leu
65 70 75 80
Ala Leu Ser Ser Val Leu Leu Ser Ser Ala Xaa Thr Ser Xaa Xaa Pro
85 90 95
Ala Ala Ala Asp Ile Ala Gly Leu Thr Pro Cys Lys Glu Ser Lys Ala
100 105 110
Phe Ala Lys Arg Glu Lys Asn Ser Ile Lys Lys Xaa Thr Ala Ser Leu
115 120 125
Lys Lys Tyr Ala
130

(2) INFORMATION FOR SEQ ID NO:1081:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..106
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499560

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1081:

Met Ala Ala Leu Ala Ala Ser Ser Thr Ala Ala Phe Ala Ala Lys Pro
1 5 10 15
Arg Leu Pro Arg Ala Arg Leu Thr Val Ala Cys Ser Ala Thr Gly Xaa
20 25 30
Asp Gly Asn Gly Ser Ser Ser Ser Val Ser Leu Ala Ser Ser Val Lys
35 40 45
Thr Phe Ser Ala Ala Leu Ala Leu Ser Ser Val Leu Leu Ser Ser Ala
50 55 60
Xaa Thr Ser Xaa Xaa Pro Ala Ala Ala Asp Ile Ala Gly Leu Thr Pro
65 70 75 80
Cys Lys Glu Ser Lys Ala Phe Ala Lys Arg Glu Lys Asn Ser Ile Lys
85 90 95
Lys Xaa Thr Ala Ser Leu Lys Lys Tyr Ala
100 105

(2) INFORMATION FOR SEQ ID NO:1082:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..439
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1082:

atcctcaagt catcagctag ctagccttcc ctacagcaac tgcatcata caacacttcc 60
atctgcccgc tegtcttcga tcaattccca agtcaaataa tataacagca atgggtgttc 120
ccgtgatcga ctcttccaag ctggacggcg ctgagagggc cgaaacctcg gcgcagatcg 180
ccaatggctg cgaggagtg gattcttccc agctcgtgaa ccacggcatc ccgctggagc 240
tgctcgagcg cgtcaagaag gtgtgctccc acagctaccg cctccgggag gccgggttca 300
aggcgctcga gccggtgcgc acgctggagg cgctcgtcga cgcggasrcg ccgskttgaa 360
gtgtggcgcg cgttggagca cctggactgg gaggacatct tctacattca tgacgatgc 420
cagtdgcgct ccgacccgc

(2) INFORMATION FOR SEQ ID NO:1083:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..82
(D) OTHER INFORMATION: / Ceres Seq. ID 1499568
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1083:
Met Val Val Pro Val Ile Asp Phe Ser Lys Leu Asp Gly Ala Glu Arg
1 5 10 15
Ala Glu Thr Leu Ala Gln Ile Ala Asn Gly Cys Glu Glu Trp Gly Phe
20 25 30
Phe Gln Leu Val Asn His Gly Ile Pro Leu Glu Leu Glu Arg Val
35 40 45
Lys Lys Val Cys Ser Asp Ser Tyr Arg Leu Arg Glu Ala Gly Phe Lys
50 55 60
Ala Ser Glu Pro Val Arg Thr Leu Glu Ala Leu Val Asp Ala Xaa Xaa
65 70 75 80
Pro Xaa

(2) INFORMATION FOR SEQ ID NO:1084:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..471
(D) OTHER INFORMATION: / Ceres Seq. ID 1499576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1084:

accaaaccaga tcaaatcaga gatggcaagt cgtagtagct ctgcagaagg tgcaggcgagg 60
acgtgtgcctg tcaatctcaa gttgatcacc gtgctgagca tgcattggcg cgccatcaga 120
gggatactcc cgccaccat cctcgcttc ctggaagcga actccaggaa ctggacgggc 180
cagacgctcg tatcgcgac tacttcgacg tcgtcgccgg caccagcacc ggcgtctccc 240
tgacggcgat gctcaccgg ccggacacga acgaacggcc gctgttcgcc gccaaaggacc 300
tgcgcggtt ctacatccag cactcgccca aatcttccg gcagaagaat gctatgggggt 360
ccaagctcgt cgccaaagctg aggatggctt gtgggcccac gtacgacgcg acctacctcc 420
atgcgcavtc cgacggcttc ttgtaatat gaggctggac aggacactga c

(2) INFORMATION FOR SEQ ID NO:1085:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..80
(D) OTHER INFORMATION: / Ceres Seq. ID 1499577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1085:

Thr Lys Gln Ile Lys Ser Glu Met Ala Ser Arg Ser Ser Ser Ala Glu
1 5 10 15
Gly Ala Gly Arg Thr Leu Pro Val Asn Leu Lys Leu Ile Thr Val Leu
20 25 30
Ser Ile Asp Gly Gly Gly Ile Arg Gly Ile Ile Pro Ala Thr Ile Leu
35 40 45
Ala Phe Leu Glu Ala Asn Ser Arg Asn Trp Thr Gly Gln Thr Leu Val
50 55 60
Ser Arg Thr Thr Ser Thr Ser Ser Pro Ala Arg Ala Pro Ala Val Ser

65

70

75

80

(2) INFORMATION FOR SEQ ID NO:1086:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 73 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..73

(D) OTHER INFORMATION: / Ceres Seq. ID 1499578

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1086:

Met	Ala	Ser	Arg	Ser	Ser	Ser	Ala	Glu	Gly	Ala	Gly	Arg	Thr	Leu	Pro
1				5					10					15	
Val	Asn	Leu	Lys	Leu	Ile	Thr	Val	Leu	Ser	Ile	Asp	Gly	Gly	Gly	Ile
			20					25					30		
Arg	Gly	Ile	Ile	Pro	Ala	Thr	Ile	Leu	Ala	Phe	Leu	Glu	Ala	Asn	Ser
		35					40					45			
Arg	Asn	Trp	Thr	Gly	Gln	Thr	Leu	Val	Ser	Arg	Thr	Thr	Ser	Thr	Ser
	50					55					60				
Ser	Pro	Ala	Arg	Ala	Pro	Ala	Val	Ser							
65						70									

(2) INFORMATION FOR SEQ ID NO:1087:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 122 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1499579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1087:

Met	Ala	Ala	Ala	Ser	Glu	Gly	Ser	Ser	Arg	Pro	Pro	Ser	Ser	Pro	Ser
1				5					10					15	
Trp	Lys	Arg	Thr	Pro	Gly	Thr	Gly	Arg	Ala	Arg	Arg	Ser	Tyr	Arg	Gly
			20					25					30		
Leu	Leu	Arg	Arg	Arg	Arg	Arg	His	Glu	His	Arg	Arg	Ser	Pro	Asp	Gly
		35				40						45			
Asp	Ala	His	Gly	Pro	Gly	His	Glu	Arg	Thr	Ala	Ala	Val	Arg	Arg	Gln
	50					55					60				
Gly	Pro	Gly	Ala	Val	Leu	His	Pro	Ala	Leu	Ala	Gln	Asn	Leu	Pro	Ala
	65					70				75				80	
Glu	Glu	Cys	Tyr	Gly	Val	Gln	Ala	Arg	Arg	Gln	Ala	Glu	Asp	Gly	Leu
				85					90				95		
Trp	Ala	Gln	Val	Arg	Arg	Gln	Val	Pro	Pro	Cys	Ala	Xaa	Arg	Arg	Leu
			100					105					110		
Leu	Gly	Asn	Met	Arg	Leu	Asp	Arg	Thr	Leu						
	115					120									

(2) INFORMATION FOR SEQ ID NO:1088:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 477 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..477

(D) OTHER INFORMATION: / Ceres Seq. ID 1499591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1088:

aactcgggtgc	gaaaccacac	caccatcgc	caccaccaat	caatccatca	cggtagtctgc	60
acctgcgcct	ctccttgavg	tcgcgcasca	gcaatggcgt	gctccaaagc	ngtgcgtctc	120
gcmgcgctcc	tagcgcgtgc	aggagcgcctc	tcctccgctg	cggtgtggga	ggactacgac	180
caccacatgt	accacaagtgc	ctacaggctcc	tgcatgagga	agtgcgacga	cgacgatgcc	240
gatgatgcct	tgaagaatag	catcagcccc	gttgtaacct	ctgtgtccga	tgatcacgac	300
catgacgacg	atcacgacca	ccacgatgat	cacaaccacg	accacgacga	ccacatgat	360
gatcacgacc	acgaccacca	tcacgatgat	cacgaccacg	accatgatga	tcacgaccac	420
gaccataatg	acaaccacgg	cgaacaccat	gacgacgacg	atgaggatga	cgattac	

(2) INFORMATION FOR SEQ ID NO:1089:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1499592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1089:

Met	Ala	Cys	Ser	Lys	Xaa	Val	Leu	Leu	Xaa	Ala	Leu	Leu	Ala	Val	Ala
1			5						10					15	
Gly	Ala	Leu	Ser	Ser	Ala	Ala	Val	Trp	Glu	Asp	Tyr	Asp	His	His	Met
			20					25					30		
Tyr	His	Lys	Cys	Tyr	Arg	Ser	Cys	Met	Arg	Lys	Cys	Asp	Asp	Asp	Asp
			35				40					45			
Ala	Asp	Asp	Ala	Leu	Lys	Asn	Ser	Ile	Ser	Pro	Val	Val	Thr	Ser	Val
			50				55				60				
Ser	Asp	Asp	His	Asp	His	Asp	Asp	Asp	His	Asp	His	His	Asp	Asp	His
			65			70				75			80		
Asn	His	Asp	His	Asp	Asp	His	His	Asp	Asp	His	Asp	His	Asp	His	His
						85				90			95		
His	Asp	Asp	His	Asp	His	Asp	His	Asp	Asp	His	Asp	His	Asp	His	Asn
			100				105					110			
Asp	Asn	His	Gly	Glu	His	His	Asp	Asp	Asp	Glu	Asp	Asp	Asp	Tyr	
			115				120					125			

(2) INFORMATION FOR SEQ ID NO:1090:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1499593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1090:

Met	Tyr	His	Lys	Cys	Tyr	Arg	Ser	Cys	Met	Arg	Lys	Cys	Asp	Asp	Asp
1			5						10				15		
Asp	Ala	Asp	Asp	Ala	Leu	Lys	Asn	Ser	Ile	Ser	Pro	Val	Val	Thr	Ser
			20					25					30		
Val	Ser	Asp	Asp	His	Asp	His	Asp	Asp	Asp	His	Asp	His	His	Asp	Asp
			35				40					45			
His	Asn	Gis	Asp	His	Asp	Asp	His	His	Asp	Asp	His	Asp	His	Asp	His

50 55 60
His His Asp Asp His Asp His Asp His Asp His Asp His Asp His
65 70 75 80
Asn Asp Asn His Gly Glu His His Asp Asp Asp Asp Glu Asp Asp Asp
85 90 95
Tyr

(2) INFORMATION FOR SEQ ID NO:1091:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1091:

Met Arg Lys Cys Asp Asp Asp Ala Asp Asp Ala Leu Lys Asn Ser
1 5 10 15
Ile Ser Pro Val Val Thr Ser Val Ser Asp Asp His Asp His Asp Asp
20 25 30
Asp His Asp His His Asp Asp His Asn His Asp His Asp Asp His His
35 40 45
Asp Asp His Asp His Asp His His Asp Asp His Asp His Asp His
50 55 60
Asp Asp His Asp His Asp His Asn Asp Asn His Gly Glu His His Asp
65 70 75 80
Asp Asp Asp Glu Asp Asp Tyr
85

(2) INFORMATION FOR SEQ ID NO:1092:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..347
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499605

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1092:

tctccttttcg gargargcgg accargtaag cagcagcagg aaccctagca ccgccgcattc 60
cccagccatg ggtatcgacc tcgttgccgg tgggaggaa aagaagacca agcgacacagc 120
gccgaagtcc gacgatgttt attccaccgg gatggargtc gccgagatcg acggcgccccc 180
gaggatgggg ccgacgtttcg gcgcattgat gatctcggcg cagaaggcgg cgacactrgc 240
gctgaaggca ctggngcagg cccaacgcgg tggacgggac catccccgar gtgtgcggcg 300
cgctckmga rgagttctgtg attdrtcca aggcacgacga ggctcgtg

(2) INFORMATION FOR SEQ ID NO:1093:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1093:

Leu Leu Ser Xaa Xaa Ala Asp Xaa Val Ser Ser Ser Arg Asn Pro Ser
1 5 10 15
Thr Ala Ala Ser Pro Ala Met Gly Ile Asp Leu Val Ala Gly Gly Arg
20 25 30
Asn Lys Lys Thr Lys Arg Thr Ala Pro Lys Ser Asp Asp Val Tyr Leu
35 40 45
Thr Gly Met Xaa Val Ala Glu Ile Asp Gly Ala Pro Arg Met Gly Pro
50 55 60
Thr Phe Gly Ala Met Met Ile Ser Gly Gln Lys Ala Ala His Xaa Ala
65 70 75 80
Leu Lys Ala Leu Xaa Gln Ala Gln Arg Arg Gly Arg Asp His Pro Arg
85 90 95
Xaa Val Ala Gly Ala Xaa Xaa Xaa Val Arg Asp Xaa Xaa Gln Gly Arg
100 105 110
Arg Gly Arg
115

(2) INFORMATION FOR SEQ ID NO:1094:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..93
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499607

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1094:

Met Gly Ile Asp Leu Val Ala Gly Gly Arg Asn Lys Lys Thr Lys Arg
1 5 10 15
Thr Ala Pro Lys Ser Asp Asp Val Tyr Leu Thr Gly Met Xaa Val Ala
20 25 30
Glu Ile Asp Gly Ala Pro Arg Met Gly Pro Thr Phe Gly Ala Met Met
35 40 45
Ile Ser Gly Gln Lys Ala Ala His Xaa Ala Leu Lys Ala Leu Xaa Gln
50 55 60
Ala Gln Arg Arg Gly Arg Asp His Pro Arg Xaa Val Ala Gly Ala Xaa
65 70 75 80
Xaa Xaa Val Arg Asp Xaa Xaa Gln Gly Arg Arg Gly Arg
85 90

(2) INFORMATION FOR SEQ ID NO:1095:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..65
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499608

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1095:

Met Xaa Val Ala Glu Ile Asp Gly Ala Pro Arg Met Gly Pro Thr Phe
1 5 10 15
Gly Ala Met Met Ile Ser Gly Gln Lys Ala Ala His Xaa Ala Leu Lys
20 25 30
Ala Leu Xaa Gln Ala Gln Arg Arg Gly Arg Asp His Pro Arg Xaa Val
35 40 45
Ala Gly Ala Xaa Xaa Xaa Val Arg Asp Xaa Xaa Gln Gly Arg Arg Gly
50 55 60
Arg

65

(2) INFORMATION FOR SEQ ID NO:1096:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..503
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499627

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1096:

ctctaaaaagt	ggctgtgttct	gcaggtttact	cctgtgtact	aagtaccgca	ggcttccagt	60
ggctgatagc	tcaggcaaac	tggttgggat	cattacaaga	gggaacgtcg	tccaagccgc	120
cctcgaaatc	aagaaaaaag	ttgaaggggac	actctgagat	gactaccctcc	aggtatcctt	180
tttctgccca	catgggggggc	ttaggacttg	gacacatctc	tagttggcaa	ctgatcaate	240
aaagcgactg	tcagagtgag	cgatgaaagt	cgctatgttt	atgaagattt	gcccggagaa	300
gcacaggtgt	atgtgtagt	ttgtttatat	atgctgatgc	agtccttgct	ggccaaaaca	360
caggtttaccg	attgtttctg	tttctctggc	ttctttggac	accaaattct	taacctaggt	420
cttgtttggg	tcacacagta	tctagtcca	cttacttgta	ttgaggttca	ttgaagtggg	480
aaatcaacta	gttttcgcac	ttc				

(2) INFORMATION FOR SEQ ID NO:1097:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..51
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499628

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1097:

Ser	Lys	Ser	Gly	Leu	Phe	Cys	Arg	Leu	Leu	Pro	Val	Thr	Lys	Tyr	Arg
1				5						10				15	
Arg	Leu	Pro	Val	Val	Asp	Ser	Ser	Gly	Lys	Leu	Val	Gly	Ile	Ile	Thr
			20					25					30		
Arg	Gly	Asn	Val	Val	Gln	Ala	Ala	Leu	Glu	Ile	Lys	Lys	Lys	Val	Glu
		35				40						45			
Gly	Thr	Leu													
		50													

(2) INFORMATION FOR SEQ ID NO:1098:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..47
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499629

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1098:

Met	Leu	Met	Gln	Ser	Leu	Leu	Ala	Lys	Thr	Gln	Val	Thr	Asp	Cys	Ser
1				5						10				15	
Gly	Phe	Leu	Gly	Phe	Phe	Gly	His	Gln	Ile	Leu	Asn	Leu	Gly	Leu	Val
			20					25					30		
Trp	Val	His	Thr	Tyr	Leu	Val	Gln	Leu	Thr	Cys	Ile	Glu	Val	His	
		35				40						45			

(2) INFORMATION FOR SEQ ID NO:1099:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..45
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499630
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1099:
Met Gln Ser Leu Leu Ala Lys Thr Gln Val Thr Asp Cys Ser Gly Phe
1 5 10 15
Leu Gly Phe Phe Gly His Gln Ile Leu Asn Leu Gly Leu Val Trp Val
 20 25 30
His Thr Tyr Leu Val Gln Leu Thr Cys Ile Glu Val His
 35 40 45

(2) INFORMATION FOR SEQ ID NO:1100:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 476 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..476
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499649
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1100:
aattactgtg cctttatctt caacccaac catcattac catattccta agctatcatg 60
gtgcaccgga ctcccatagc cgatgtgcat gtgatgtgca tggatctaag cccaagaaaa 120
cccaacaagg ccagcgccas sancggcgga gctactacga ctggtcctccc gccgatctgc 180
ccatgctcgg cggtgcctcc attgggtgcc ccaagctctg cctccaccgc ggaggctctg 240
ccctaccagc ctactccgac tctgccaaaga tcgcctacgt cctccaaggc aaaggatat 300
tcggcggtgt tctcccgagg gcgaccaagg agaaggtcat ctccgtcaag gaaggcgacg 360
cgctggcgct ccctctcggc gtgcgtcacct ggtggcacia caacgccgac gccgctatct 420
ccgacctcgt ggtgctcttc ctcgcgacga cctccacggg ccacaagccg ggccag

(2) INFORMATION FOR SEQ ID NO:1101:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 158 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..158
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499650
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1101:
Leu Leu Cys Leu Tyr Leu Gln Pro Lys Pro Ser Ile Thr Ile Phe Leu
1 5 10 15
Ser Tyr His Gly Ala Pro Asp Phe His Ser Arg Cys Ala Cys Asp Val
 20 25 30
His Gly Ser Lys Pro Lys Glu Thr Gln Gln Gly Gln Arg Xaa Xaa Arg
 35 40 45
Arg Ser Tyr Tyr Asp Trp Ser Pro Ala Asp Leu Pro Met Leu Gly Val
 50 55 60
Ala Ser Ile Gly Ala Ala Lys Leu Cys Leu Thr Ala Gly Gly Leu Ala
65 70 75 80
Leu Pro Ser Tyr Ser Asp Ser Ala Lys Ile Ala Tyr Val Leu Gln Gly
 85 90 95

Lys Gly Ile Phe Gly Val Val Leu Pro Glu Ala Thr Lys Glu Lys Val
100 105 110
Ile Ser Val Lys Glu Gly Asp Ala Leu Ala Leu Pro Phe Gly Val Val
115 120 125
Thr Trp Trp His Asn Asn Ala Asp Ala Ala Ile Ser Asp Leu Val Val
130 135 140
Leu Phe Leu Gly Asp Thr Ser Thr Gly His Lys Pro Gly Gln
145 150 155

(2) INFORMATION FOR SEQ ID NO:1102:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1499651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1102:

Met Val His Arg Thr Ser Ile Ala Asp Val His Val Met Cys Met Asp
1 5 10 15
Leu Ser Pro Lys Lys Pro Asn Lys Ala Ser Ala Xaa Xaa Gly Ala
20 25 30
Thr Thr Thr Gly Pro Pro Pro Ile Cys Pro Cys Ser Ala Leu Pro Pro
35 40 45
Leu Val Pro Pro Ser Ser Ala Ser Pro Pro Glu Val Leu Pro Tyr Pro
50 55 60
Ala Thr Pro Thr Leu Pro Arg Ser Pro Thr Ser Ser Lys Ala Lys Val
65 70 75 80
Tyr Ser Ala Trp Phe Ser Arg Arg Arg Pro Arg Arg Ser Ser Pro
85 90 95
Ser Arg Lys Ala Thr Arg Trp Arg Ser Pro Ser Ala Ser Ser Pro Gly
100 105 110
Gly Thr Thr Thr Pro Thr Pro Leu Ser Pro Thr Ser Trp Cys Ser Ser
115 120 125
Ser Ala Thr Pro Pro Arg Ala Thr Ser Arg Ala
130 135

(2) INFORMATION FOR SEQ ID NO:1103:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1499652

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1103:

Met Cys Met Asp Leu Ser Pro Lys Lys Pro Asn Lys Ala Ser Ala Xaa
1 5 10 15
Xaa Gly Gly Ala Thr Thr Thr Gly Pro Pro Ile Cys Pro Cys Ser
20 25 30
Ala Leu Pro Pro Leu Val Pro Pro Ser Ser Ala Ser Pro Pro Glu Val
35 40 45
Leu Pro Tyr Pro Ala Thr Pro Thr Leu Pro Arg Ser Pro Thr Ser Ser
50 55 60
Lys Ala Lys Val Tyr Ser Ala Trp Phe Ser Arg Arg Arg Pro Arg Arg
65 70 75 80
Arg Ser Ser Pro Ser Arg Lys Ala Thr Arg Trp Arg Ser Pro Ser Ala

	85						90								95
Ser	Ser	Pro	Gly	Gly	Thr	Thr	Thr	Pro	Leu	Ser	Pro	Thr	Ser		
	100						105					110			
Trp	Cys	Ser	Ser	Ser	Ala	Thr	Pro	Pro	Arg	Ala	Thr	Ser	Arg	Ala	
	115						120					125			

(2) INFORMATION FOR SEQ ID NO:1104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..476
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499655

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1104:

ctactaacgc	cgtctctctc	ccagcgccgc	ccgtcgccgc	cgcctctctc	ttggctccgc	60
cgctccgcga	ggatcatcatg	gtgagggtca	gtgtgctcaa	cgatgcgctc	aagtccatgt	120
acaatgcaga	gaagaggggc	aagaggcagg	tcatgatcac	gccgtcgctc	aaggatgatca	180
tcaagttctc	gacgggtcaag	acctgggctt	ctttgccaat	ttctggggca	tcttcatctt	240
tgtcttggtt	attgcgtacc	acttcgtgat	ggcagaccgc	aagtacgaag	gaaactgatg	300
tcctctagtg	caaatgctct	attatctgca	ggcggaaata	gggctatact	gttagctaat	360
gctagtgcga	tgcgttgaca	ctttgagtcg	atatcatgga	agctggacat	gcagttctctg	420
gcattttggt	tttgcccatg	ttttaatctg	ctgaattagt	aaatcctgga	gaatcc	

(2) INFORMATION FOR SEQ ID NO:1105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499656

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1105:

Thr	Asn	Arg	Val	Ser	Ser	Pro	Ala	Pro	Ala	Val	Ala	Ala	Ala	Leu	Leu
1		5						10						15	
Leu	Val	Pro	Pro	Ser	Val	Glu	Val	Ile	Met	Val	Arg	Val	Ser	Val	Leu
		20					25					30			
Asn	Asp	Ala	Leu	Lys	Ser	Met	Tyr	Asn	Ala	Glu	Lys	Arg	Gly	Lys	Arg
		35					40				45				
Gln	Val	Met	Ile	Arg	Pro	Ser	Ser	Lys	Val	Ile	Ile	Lys	Phe	Leu	Thr
		50				55					60				
Val	Lys	Thr	Trp	Ala	Ser	Leu	Pro	Ile	Ser	Trp	Ala	Ser	Ser	Ser	Leu
		65				70				75					80
Ser	Trp	Leu	Leu	Arg	Thr	Thr	Ser								
						85									

(2) INFORMATION FOR SEQ ID NO:1106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..63
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499657

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1106:

Met Val Arg Val Ser Val Leu Asn Asp Ala Leu Lys Ser Met Tyr Asn
1 5 10 15
Ala Glu Lys Arg Gly Lys Arg Gln Val Met Ile Arg Pro Ser Ser Lys
20 25 30
Val Ile Ile Lys Phe Leu Thr Val Lys Thr Trp Ala Ser Leu Pro Ile
35 40 45
Ser Trp Ala Ser Ser Ser Leu Ser Trp Leu Arg Thr Thr Ser
50 55 60

(2) INFORMATION FOR SEQ ID NO:1107:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..50

(D) OTHER INFORMATION: / Ceres Seq. ID 1499658

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1107:

Met Tyr Asn Ala Glu Lys Arg Gly Lys Arg Gln Val Met Ile Arg Pro
1 5 10 15
Ser Ser Lys Val Ile Ile Lys Phe Leu Thr Val Lys Thr Trp Ala Ser
20 25 30
Leu Pro Ile Ser Trp Ala Ser Ser Leu Ser Trp Leu Arg Thr
35 40 45
Thr Ser
50

(2) INFORMATION FOR SEQ ID NO:1108:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 514 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..514

(D) OTHER INFORMATION: / Ceres Seq. ID 1499667

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1108:

agaggatttc tattgtagaa atgcagttag gccattagg ttttgctct ttttttttca 60
gactcggatt ggtctgccgt ccttggtctc cgccggcaat ggcgctccacc gccgtcaagc 120
tcactgcacat cgcagtcacac ttcacagatg gcatgtttcaa ggccatctac cacggcgaagc 180
agtgcacacg cggcgacatc cggcgccgtac ttgcgcgcgc gtggggtgca gccgtcgacc 240
gcatcatgtt caccggaggg tccctgaaag agtccagaga ggcatgtcag atcgccgaga 300
ccgacgggag actgtttctgc actgtgggag tgcacccaac aagatgcggg gaattcgagg 360
agagtggaga tcccgarggt cattttcagg cactgtgggc tctagcgaag gagggtttag 420
ataaaggcaa ggtcgtttrct gttggtgaat gtggtttgga ttatgacaga cttcagttct 480
gtccsgcgag atatgcaaaa gaagtacttc gagg

(2) INFORMATION FOR SEQ ID NO:1109:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 140 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1499668

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1109:

Glu Asp Phe Tyr Cys Arg Asn Ala Val Arg Pro Ile Arg Phe Cys Leu
1 5 10 15
Phe Phe Phe Gln Thr Arg Ile Gly Leu Pro Ser Leu Cys Ser Ala Gly
20 25 30
Asn Gly Val His Arg Arg Gln Ala His Arg His Arg Ser Gln Leu His
35 40 45
Arg Trp His Val Gln Gly His Leu Pro Arg Gln Ala Val Pro Arg Arg
50 55 60
Arg His Pro Gly Arg Thr Cys Ala Arg Val Gly Cys Arg Arg Arg Pro
65 70 75 80
His His Cys His Arg Arg Leu Pro Glu Arg Val Gln Arg Gly Ile Ala
85 90 95
Asp Arg Arg Asp Arg Arg Glu Thr Val Leu His Cys Gly Ser Ala Pro
100 105 110
Asn Lys Met Arg Gly Ile Arg Gly Glu Trp Arg Ser Arg Xaa Ser Phe
115 120 125
Ser Gly Thr Ala Gly Ser Ser Glu Gly Gly Phe Arg
130 135 140

(2) INFORMATION FOR SEQ ID NO:1110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..170

(D) OTHER INFORMATION: / Ceres Seq. ID 1499669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1110:

Arg Ile Ser Ile Val Glu Met Gln Leu Gly Pro Leu Gly Phe Ala Ser
1 5 10 15
Phe Phe Phe Arg Leu Gly Leu Val Cys Arg Pro Cys Ala Pro Pro Ala
20 25 30
Met Ala Ser Thr Ala Val Lys Leu Ile Asp Ile Ala Val Asn Phe Thr
35 40 45
Asp Gly Met Phe Lys Gly Ile Tyr His Gly Lys Gln Cys His Ala Ala
50 55 60
Asp Ile Pro Ala Val Leu Ala Arg Ala Trp Ala Ala Gly Val Asp Arg
65 70 75 80
Ile Ile Val Thr Gly Gly Ser Leu Lys Glu Ser Arg Glu Ala Leu Gln
85 90 95
Ile Ala Glu Thr Asp Gly Arg Leu Phe Cys Thr Val Gly Val His Pro
100 105 110
Thr Arg Cys Gly Glu Phe Glu Glu Ser Gly Asp Pro Xaa Gly His Phe
115 120 125
Gln Ala Leu Leu Ala Leu Ala Lys Glu Gly Leu Asp Lys Gly Lys Val
130 135 140
Val Xaa Val Gly Glu Cys Gly Leu Asp Tyr Asp Arg Leu Gln Phe Cys
145 150 155 160
Xaa Gly Arg Tyr Ala Lys Glu Val Leu Arg
165 170

(2) INFORMATION FOR SEQ ID NO:1111:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 1499670

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1111:

```
Met Gln Leu Gly Pro Leu Gly Phe Ala Ser Phe Phe Phe Arg Leu Gly
1      5      10      15
Leu Val Cys Arg Pro Cys Ala Pro Pro Ala Met Ala Ser Thr Ala Val
20     25     30
Lys Leu Ile Asp Ile Ala Val Asn Phe Thr Asp Gly Met Phe Lys Gly
35     40     45
Ile Tyr His Gly Lys Gln Cys His Ala Ala Asp Ile Pro Ala Val Leu
50     55     60
Ala Arg Ala Trp Ala Ala Gly Val Asp Arg Ile Ile Val Thr Gly Gly
65     70     75     80
Ser Leu Lys Glu Ser Arg Glu Ala Leu Gln Ile Ala Glu Thr Asp Gly
85     90     95
Arg Leu Phe Cys Thr Val Gly Val His Pro Thr Arg Cys Gly Glu Phe
100    105    110
Glu Glu Ser Gly Asp Pro Xaa Gly His Phe Gln Ala Leu Leu Ala Leu
115    120    125
Ala Lys Glu Gly Leu Asp Lys Gly Lys Val Val Xaa Val Gly Glu Cys
130    135    140
Gly Leu Asp Tyr Asp Arg Leu Gln Phe Cys Xaa Gly Arg Tyr Ala Lys
145    150    155    160
Glu Val Leu Arg
```

(2) INFORMATION FOR SEQ ID NO:1112:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 540 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..540

(D) OTHER INFORMATION: / Ceres Seq. ID 1499671

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1112:

```
atagaagaag agcaggcagg agctataagt accccgcccc ctccaccct ctccctccac 60
ctccctccct tgctgectca tccattccag agctgcgaag acagacagac agagagaaag 120
agggatcgac ggagcaaggc ggggcccgtgt ccggtcacac acgagcgagc cctctcgggcc 180
gcgcgtttgt gaattgtgaa cvgcgagcgg cgggcggagc cggagtgcaac gcgggcgtcg 240
ctgtctgggga ggtatgagat cggcgcgacc ctgcgcgagg gcaacttcgg caaggtgaag 300
tacgcgcgcc acatgcgccag cgggggccac ttgcgccatca agatcctcga ccgcagcaag 360
atccctctccc tccgcatcga cgaccagatc aggagggaga tcgggacgct caagctcctc 420
aagaccacga atgtcgtccc ctgcacagag gttcgtgcca gtaaacgaa gatctacatg 480
tgtcgttagt ttgtcaacgg cggcgagctc ttcgacaaga tcgctatcaa ggggaaactg 540
```

(2) INFORMATION FOR SEQ ID NO:1113:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..63

(D) OTHER INFORMATION: / Ceres Seq. ID 1499672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1113:

```
Ile Glu Glu Glu Gln Ala Gly Ala Ile Ser Thr Pro Pro Pro Ser Thr
1      5      10      15
```

Leu Ser Phe His Leu Pro Pro Leu Leu Pro His Pro Phe Gln Ser Cys
20 25 30
Glu Asp Arg Gln Thr Glu Arg Lys Arg Asp Arg Arg Ser Lys Ala Gly
35 40 45
Pro Cys Pro Val Thr His Glu Arg Ala Leu Ser Ala Ala Arg Leu
50 55 60

(2) INFORMATION FOR SEQ ID NO:1114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1114:

Arg Arg Arg Ala Gly Arg Ser Tyr Lys Tyr Pro Ala Pro Phe His Pro
1 5 10 15
Leu Leu Pro Pro Ser Leu Ala Ala Ser Ser Ile Pro Glu Leu Arg
20 25 30
Arg Gln Thr Asp Arg Glu Lys Glu Gly Ser Thr Glu Gln Gly Gly Ala
35 40 45
Val Ser Gly His Thr Arg Ala Ser Pro Leu Gly Arg Ala Phe Val Asn
50 55 60
Gly Glu Xaa Arg Ala Ala Gly Gly Arg Gly Val His Ala Gly Val Ala
65 70 75 80
Ala Gly Glu Val

(2) INFORMATION FOR SEQ ID NO:1115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..116
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499674

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1115:

Met Val Asn Xaa Glu Arg Arg Ala Asp Ala Glu Cys Thr Arg Ala Ser
1 5 10 15
Leu Leu Gly Arg Tyr Glu Ile Gly Arg Thr Leu Gly Glu Gly Asn Phe
20 25 30
Gly Lys Val Lys Tyr Ala Arg His Ile Ala Ser Gly Xaa His Phe Ala
35 40 45
Ile Lys Ile Leu Asp Arg Ser Lys Ile Leu Ser Leu Arg Ile Asp Asp
50 55 60
Gln Ile Arg Arg Glu Ile Gly Thr Leu Lys Leu Lys His Pro Asn
65 70 75 80
Val Val Arg Leu His Glu Val Ala Ala Ser Lys Thr Lys Ile Tyr Met
85 90 95
Val Leu Glu Phe Val Asn Gly Gly Glu Leu Phe Asp Lys Ile Ala Ile
100 105 110
Lys Gly Lys Leu
115

(2) INFORMATION FOR SEQ ID NO:1116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..478
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499675
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1116:
aaaaaccaca acacaagaac gggaagcgtg catgcacacg cacgagcacg aacctgagct 60
gtagcgccct ctgcgtcgtc cccgcgcgcg aatggccacg gtascgccag tcccatgcaa 120
accagccatg cctcacgcgg gccgatccct acagctacag gccccgtgcc cgtggccgtg 180
cttctcgcgc cgcgcgcgcg cggcctcctc gcgctgctgc cgtcgtctgc cgaggccgtg 240
tgggaggtgc cgcacctctt cctcctcggc gcgcgtatct ccttcggcgt cttcacgcag 300
aggaacacgc acgcccacgc ccgcgccaaag gacagctcac aggcgtggag cgcggtgtgc 360
caccccgatg ccccccctcgt cgtgatcgcg gatcacacgc cgcgcgagca cgacgacgac 420
aacgacgact acgggctgga actggaagaa ggcgacacg agacgccgct ttcggttc
(2) INFORMATION FOR SEQ ID NO:1117:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 158 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..158
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499676
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1117:
Lys Pro Gln His Lys Asn Gly Lys Arg Ala Cys Thr Arg Thr Ser Thr
1 5 10 15
Asn Leu Ser Cys Ser Ala Leu Ser Leu Ala Pro Arg Ala Gln Trp Pro
20 25 30
Ala Xaa Pro Arg Ser His Ala Asn Gln Pro Cys Leu Thr Ala Ala Asp
35 40 45
Pro Tyr Ser Tyr Arg Pro Arg Ala Arg Gly Arg Ala Ser Arg Arg Arg
50 55 60
Arg Arg Arg Pro Pro Arg Ala Ala Val Ala Gly Arg Gly Arg Val
65 70 75 80
Gly Gly Ala Ala Pro Leu Pro Pro Arg Arg His Leu Leu Arg Arg
85 90 95
Leu His Ala Glu Glu Gln Arg Arg Arg Pro Arg Gln Gly Gln Leu
100 105 110
Thr Gly Val Glu Arg Gly Val Pro Pro Arg Cys Pro Pro Arg Arg Asp
115 120 125
Arg Gly Ser His Gly Ala Glu Arg Arg Arg Gln Arg Arg Leu Arg
130 135 140
Ala Gly Thr Gly Arg Arg Arg Thr Arg Asp Ala Ala Phe Val
145 150 155
(2) INFORMATION FOR SEQ ID NO:1118:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 97 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..97
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499677
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1118:

```
Met Ala Ser Val Xaa Gln Val Pro Cys Lys Pro Ala Met Pro His Gly
1          5          10          15
Gly Arg Ser Leu Gln Leu Gln Ala Pro Cys Pro Trp Pro Cys Phe Ser
          20          25          30
Pro Pro Pro Pro Ser Ala Ser Arg Cys Cys Arg Arg Trp Pro Arg
          35          40          45
Pro Cys Gly Arg Cys Arg Thr Ser Ser Ser Ser Ala Pro Ser Ser Pro
          50          55          60
Ser Ala Ser Ser Arg Arg Gly Thr Ala Thr Pro Thr Ala Ala Pro Arg
65          70          75          80
Thr Ala His Arg Arg Gly Ala Arg Cys Ala Thr Pro Met Pro Pro Ser
          85          90          95
Ser
```

(2) INFORMATION FOR SEQ ID NO:1119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..121
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499678

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1119:

```
Met Gln Thr Ser His Ala Ser Arg Arg Pro Ile Pro Thr Ala Thr Gly
1          5          10          15
Pro Val Pro Val Ala Val Leu Leu Ala Ala Ala Val Gly Leu Leu
          20          25          30
Ala Leu Leu Pro Ser Leu Ala Glu Ala Val Trp Glu Val Pro His Leu
          35          40          45
Phe Leu Leu Gly Ala Val Ile Ser Phe Gly Val Phe Thr Gln Arg Asn
          50          55          60
Ser Asp Ala Asp Gly Arg Ala Lys Asp Ser Ser Gln Ala Trp Ser Ala
65          70          75          80
Val Cys His Pro Asp Ala Pro Leu Val Val Ile Ala Asp His Thr Ala
          85          90          95
Pro Ser Asp Asp Asp Asn Asp Asp Tyr Gly Leu Glu Leu Glu Glu
          100          105          110
Gly Ala Arg Glu Thr Pro Leu Ser Leu
          115          120
```

(2) INFORMATION FOR SEQ ID NO:1120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..518
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499686

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1120:

```
aggcgagaca ctgcacgccca cttatctct aaccggagat caaagaagta gccgttaacg 60
atggcttccg acgagctcgc aaaggccgc gagcccagga agaagggccaa cgtaaatgat 120
gcctccatat gtgccatcct ggcctccatg gcctctgtca tccttggtta tgacattggg 180
gtgatgagtg gagcgcccat gtacatcaag aaggacctga atatacagga cgtkacgtcg 240
gagatcctga tcgggatcct cagctctctac tcgctgttcg gatccttcgc tggcgcgcg 300
acgtccgaca ggaatcgggc cgcgttgacc gtcgtgttcg ccgctgtcat cttcttcgtg 360
ggtcgtgttc tcatgggttt cgccgtcaac tacggcatgc tcatggcggg ccgcttcgtg 420
```

480

(1) SEQUENCE CHARACTERISTICS:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1121:

(2) INFORMATION FOR SEQ ID NO:1122:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1122:

[illegible]

115

(2) INFORMATION FOR SEQ ID NO:1123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..106
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1123:

Met	Ser	Gly	Ala	Ala	Met	Tyr	Ile	Lys	Lys	Asp	Leu	Asn	Ile	Thr	Asp
1			5					10						15	
Xaa	Gln	Leu	Glu	Ile	Leu	Ile	Gly	Ile	Leu	Ser	Leu	Tyr	Ser	Leu	Phe
			20				25						30		
Gly	Ser	Phe	Ala	Gly	Ala	Arg	Thr	Ser	Asp	Arg	Ile	Gly	Arg	Arg	Leu
		35				40					45				
Thr	Val	Val	Phe	Ala	Ala	Val	Ile	Phe	Phe	Val	Gly	Ser	Leu	Leu	Met
		50				55					60				
Gly	Phe	Ala	Val	Asn	Tyr	Gly	Met	Leu	Met	Ala	Gly	Arg	Phe	Val	Ala
				70						75				80	
Gly	Val	Gly	Val	Gly	Tyr	Gly	Gly	Met	Ile	Xaa	Pro	Val	Tyr	Thr	Ala
				85						90				95	
Glu	Ile	Ser	Pro	Xaa	Xaa	Pro	Val	Ala	Ser						
				100				105							

(2) INFORMATION FOR SEQ ID NO:1124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..861
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1124:

aagcaagcga	asatcgccag	attggtatat	cgatcgattg	awcrghnnnn	gavgaangrg	60
aggacggrgg	gcagatggcg	gcgtgccggg	gcttcttcga	gtgcttgctc	aggctgctca	120
acttcatect	cacgcgtgcc	ggcctcgcta	tgggttggtta	cgggatctac	ctgctcgctcg	180
agtggatgaa	gatatccgan	gacggcator	gcggggcttc	gacggcgbag	gtgctcgctct	240
ctdgccggcc	gttggtgggg	gctgtcattc	tgggtgacag	cttctcgacg	aatctaccca	300
aagcatggtt	tatttatttg	ttttattggt	tggcaaccat	cgctcatctg	gtgtctctgt	360
ttgttcgcatt	tgagcagagg	acaagaaaca	cctgctgttt	gtgtttctat	gctttcttgg	420
tcattattgtt	gatccctgct	gaagctgcag	ctgctgcatt	cattttcttt	gacctatggt	480
ggaaagatgt	aattccagtg	gacaaaacac	ataactttga	tgttatgtat	gactttctga	540
aggaaaactg	ggagattgca	agatgggtcg	ctctggggcgt	tggtgttttt	gaggcagtcg	600
tcttgctgtt	agctctggct	gtcaggggcaa	tgaacaaacc	tgctgagtat	gacagtgtat	660
acgaaattat	agcaattggc	cgaagcccta	ccatcccgga	gccactgata	catacccaaa	720
atgttctctg	cactgggtgt	cctgtcccaa	cacttgatca	acgtgcaagt	agaaatgatg	780
cctggagcca	aaggatgcga	gagaagatat	gtctggacac	gagccagttc	acatacaaac	840
cttcagacc	aagcagggtac	c				

(2) INFORMATION FOR SEQ ID NO:1125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..262

(D) OTHER INFORMATION: / Ceres Seq. ID 1499691

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1125:

Met Ala Ala Cys Arg Gly Phe Phe Glu Cys Leu Leu Arg Leu Leu Asn
1 5 10 15
Phe Ile Leu Thr Val Ala Gly Leu Ala Met Val Gly Tyr Gly Ile Tyr
20 25 30
Leu Leu Val Glu Trp Met Lys Ile Ser Xaa Asp Gly Ile Xaa Gly Ala
35 40 45
Ser Thr Ala Xaa Val Leu Val Ser Xaa Arg Pro Leu Leu Gly Ala Val
50 55 60
Ile Leu Gly Asp Ser Phe Leu Asp Asn Leu Pro Lys Ala Trp Phe Ile
65 70 75 80
Tyr Leu Phe Ile Gly Val Gly Thr Ile Val Ile Leu Val Ser Leu Phe
85 90 95
Gly Cys Ile Gly Ala Gly Thr Arg Asn Thr Cys Cys Leu Cys Phe Tyr
100 105 110
Ala Phe Leu Val Ile Leu Leu Ile Leu Ala Glu Ala Ala Ala Ala
115 120 125
Phe Ile Phe Phe Asp His Gly Trp Lys Asp Val Ile Pro Val Asp Lys
130 135 140
Thr His Asn Phe Asp Val Met Tyr Asp Phe Leu Lys Glu Asn Trp Glu
145 150 155 160
Ile Ala Arg Trp Val Ala Leu Gly Val Val Val Phe Glu Ala Val Leu
165 170 175
Leu Leu Leu Ala Leu Ala Val Arg Ala Met Asn Lys Pro Ala Glu Tyr
180 185 190
Asp Ser Asp Asp Glu Ile Ile Ala Ile Gly Arg Ser Pro Thr Ile Arg
195 200 205
Gln Pro Leu Ile His Thr Gln Asn Val Pro Ala Thr Gly Val Pro Val
210 215 220
Pro Thr Leu Asp Gln Arg Ala Ser Arg Asn Asp Ala Trp Ser Gln Arg
225 230 235 240
Met Arg Glu Lys Tyr Gly Leu Asp Thr Ser Gln Phe Thr Tyr Asn Pro
245 250 255
Ser Asp Pro Ser Arg Tyr
260

(2) INFORMATION FOR SEQ ID NO:1126:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..237

(D) OTHER INFORMATION: / Ceres Seq. ID 1499692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1126:

Met Val Gly Tyr Gly Ile Tyr Leu Leu Val Glu Trp Met Lys Ile Ser
1 5 10 15
Xaa Asp Gly Ile Xaa Gly Ala Ser Thr Ala Xaa Val Leu Val Ser Xaa
20 25 30
Arg Pro Leu Leu Gly Ala Val Ile Leu Gly Asp Ser Phe Leu Asp Asn
35 40 45
Leu Pro Lys Ala Trp Phe Ile Tyr Leu Phe Ile Gly Val Gly Thr Ile
50 55 60
Val Ile Leu Val Ser Leu Phe Gly Cys Ile Gly Ala Gly Thr Arg Asn
65 70 75 80

Thr	Cys	Cys	Leu	Cys	Phe	Tyr	Ala	Phe	Leu	Val	Ile	Leu	Leu	Ile	Leu		
			85						90					95			
Ala	Glu	Ala	Ala	Ala	Ala	Phe	Ile	Phe	Phe	Asp	His	Gly	Trp	Lys			
			100				105					110					
Asp	Val	Ile	Pro	Val	Asp	Lys	Thr	His	Asn	Phe	Asp	Val	Met	Tyr	Asp		
		115					120					125					
Phe	Leu	Lys	Glu	Asn	Trp	Glu	Ile	Ala	Arg	Trp	Val	Ala	Leu	Gly	Val		
		130				135					140						
Val	Val	Phe	Glu	Ala	Val	Leu	Leu	Leu	Ala	Leu	Ala	Val	Arg	Ala			
		145				150				155				160			
Met	Asn	Lys	Pro	Ala	Glu	Tyr	Asp	Ser	Asp	Asp	Glu	Ile	Ile	Ala	Ile		
			165						170					175			
Gly	Arg	Ser	Pro	Thr	Ile	Arg	Gln	Pro	Leu	Ile	His	Thr	Gln	Asn	Val		
			180					185					190				
Pro	Ala	Thr	Gly	Val	Pro	Val	Pro	Thr	Leu	Asp	Gln	Arg	Ala	Ser	Arg		
		195					200					205					
Asn	Asp	Ala	Trp	Ser	Gln	Arg	Met	Arg	Glu	Lys	Tyr	Gly	Leu	Asp	Thr		
		210				215					220						
Ser	Gln	Phe	Thr	Tyr	Asn	Pro	Ser	Asp	Pro	Ser	Arg	Tyr					
		225			230					235							

(2) INFORMATION FOR SEQ ID NO:1127:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 225 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..225

(D) OTHER INFORMATION: / Ceres Seq. ID 1499693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1127:

Met	Lys	Ile	Ser	Xaa	Asp	Gly	Ile	Xaa	Gly	Ala	Ser	Thr	Ala	Xaa	Val		
1			5					10					15				
Leu	Val	Ser	Xaa	Arg	Pro	Leu	Leu	Gly	Ala	Val	Ile	Leu	Gly	Asp	Ser		
		20						25					30				
Phe	Leu	Asp	Asn	Leu	Pro	Lys	Ala	Trp	Phe	Ile	Tyr	Leu	Phe	Ile	Gly		
		35					40					45					
Val	Gly	Thr	Ile	Val	Ile	Leu	Val	Ser	Leu	Phe	Gly	Cys	Ile	Gly	Ala		
		50				55					60						
Gly	Thr	Arg	Asn	Thr	Cys	Cys	Leu	Cys	Phe	Tyr	Ala	Phe	Leu	Val	Ile		
		65			70				75				80				
Leu	Leu	Ile	Leu	Ala	Glu	Ala	Ala	Ala	Ala	Phe	Ile	Phe	Phe	Asp			
			85					90				95					
His	Gly	Trp	Lys	Asp	Val	Ile	Pro	Val	Asp	Lys	Thr	His	Asn	Phe	Asp		
		100					105					110					
Val	Met	Tyr	Asp	Phe	Leu	Lys	Glu	Asn	Trp	Glu	Ile	Ala	Arg	Trp	Val		
		115				120					125						
Ala	Leu	Gly	Val	Val	Val	Phe	Glu	Ala	Val	Leu	Leu	Leu	Ala	Leu			
		130				135					140						
Ala	Val	Arg	Ala	Met	Asn	Lys	Pro	Ala	Glu	Tyr	Asp	Ser	Asp	Asp	Glu		
		145				150				155				160			
Ile	Ile	Ala	Ile	Gly	Arg	Ser	Pro	Thr	Ile	Arg	Gln	Pro	Leu	Ile	His		
			165						170				175				
Thr	Gln	Asn	Val	Pro	Ala	Thr	Gly	Val	Pro	Val	Pro	Thr	Leu	Asp	Gln		
		180						185					190				
Arg	Ala	Ser	Arg	Asn	Asp	Ala	Trp	Ser	Gln	Arg	Met	Arg	Glu	Lys	Tyr		
		195				200					205						
Gly	Leu	Asp	Thr	Ser	Gln	Phe	Thr	Tyr	Asn	Pro	Ser	Asp	Pro	Ser	Arg		
		210				215					220						

Tyr

225

(2) INFORMATION FOR SEQ ID NO:1128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..435
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499694

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1128:

aatatcatgc gcaggggctg aaagctgaag ctgctcaaga cgccaccgtc ttctctccgcg	60
atcttcagatt ctctgtctct cctctctctt ttctcttagc tcccaaccaa gccaaagagta	120
cgctgctcaag cgcgcgcgcs tngtgtgtgt cagtaggcta cagggctcgg aggaacgcgc	180
tcattgagctt gatcagcatg atggaggcgc ggctgcccgc ggggttccgg ttccaccgca	240
gggacgacga gctcgtgctc gactacctct gccgcaagct ctccggcaaa ggcggcgcg	300
gasgtacggc ggcacgcgat ggctgacgtc gacctcaaca agtcgcgagc gtgggatctt	360
ccagacgagg cgtrcrtggg cggccgcgag tggactctt tcagcctgca cgaccgcaag	420
tacgccacgg ggcag	

(2) INFORMATION FOR SEQ ID NO:1129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499695

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1129:

Tyr	His	Ala	Gln	Gly	Leu	Lys	Ala	Glu	Thr	Ala	Gln	Asp	Ala	Thr	Val
1				5					10					15	
Phe	Leu	Arg	Asp	Leu	Gln	Phe	Ser	Val	Ser	Pro	Ser	Leu	Phe	Pro	Leu
				20				25					30		
Ala	Pro	Asn	Gln	Ala	Lys	Ser	Thr	Ser	Ser	Ser	Ala	Pro	Xaa	Xaa	Cys
				35			40					45			
Val	Ser	Val	Gly	Tyr	Arg	Ala	Arg	Arg	Asn	Ala	Val	Met	Ser	Leu	Ile
				50			55				60				
Ser	Met	Met	Glu	Ala	Arg	Leu	Pro	Pro	Gly	Phe	Arg	Phe	His	Pro	Arg
65				70					75					80	
Asp	Asp	Glu	Leu	Val	Leu	Asp	Tyr	Leu	Cys	Arg	Lys	Leu	Ser	Gly	Lys
				85					90				95		
Gly	Gly	Gly	Gly	Xaa	Thr	Ala	Ala	Ser	His	Gly	Arg	Arg	Arg	Pro	Gln
				100				105					110		
Gln	Val	Arg	Ala	Val	Gly	Ser	Ser	Arg	Arg	Gly	Xaa	Xaa	Gly	Arg	Pro
				115			120					125			
Arg	Val	Val	Leu	Leu	Gln	Pro	Ala	Arg	Pro	Gln	Val	Arg	His	Gly	Ala
				130			135					140			

(2) INFORMATION FOR SEQ ID NO:1130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..84
(D) OTHER INFORMATION: / Ceres Seq. ID 1499696
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1130:
Met Ser Leu Ile Ser Met Met Glu Ala Arg Leu Pro Pro Gly Phe Arg
1 5 10 15
Phe His Pro Arg Asp Asp Glu Leu Val Leu Asp Tyr Leu Cys Arg Lys
20 25 30
Leu Ser Gly Lys Gly Gly Gly Gly Xaa Thr Ala Ala Ser His Gly Arg
35 40 45
Arg Arg Pro Gln Gln Val Arg Ala Val Gly Ser Ser Arg Arg Gly Xaa
50 55 60
Xaa Gly Arg Pro Arg Val Val Leu Leu Gln Pro Ala Arg Pro Gln Val
65 70 75 80
Arg His Gly Ala

(2) INFORMATION FOR SEQ ID NO:1131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..79
(D) OTHER INFORMATION: / Ceres Seq. ID 1499697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1131:
Met Met Glu Ala Arg Leu Pro Pro Gly Phe Arg Phe His Pro Arg Asp
1 5 10 15
Asp Glu Leu Val Leu Asp Tyr Leu Cys Arg Lys Leu Ser Gly Lys Gly
20 25 30
Gly Gly Gly Xaa Thr Ala Ala Ser His Gly Arg Arg Arg Pro Gln Gln
35 40 45
Val Arg Ala Val Gly Ser Ser Arg Arg Gly Xaa Xaa Gly Arg Pro Arg
50 55 60
Val Val Leu Leu Gln Pro Ala Arg Pro Gln Val Arg His Gly Ala
65 70 75

(2) INFORMATION FOR SEQ ID NO:1132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1156 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1156
(D) OTHER INFORMATION: / Ceres Seq. ID 1499720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1132:
attttttgctc aaaagaatca gtaaaaaacta aacattttga ctatataccta cttgaatcaa 60
ttcttgcgct gattttgaag tttttgtaca ttcagatatt ctagggtttt gtggtaaagt 120
gaatcgaaatc acgaaggcaa cgcgatacaa gtgattgacc aagtaacaac catgacccat 180
ctgtctgacc cgaatccgaa aaccaaaccg ggtatgatgc tcatgaaaca agaagacggg 240
tatttgcagc cggatgaagac taaaccggct ccgaagagac cgacttctaa agaccgtcac 300
acgaaagtag aaggacgagg tcggaggatc cgaatgccgg cgggttgcgc tgcctggggtc 360
ttccaattga ccgctgaact tggtcacaaa tccgacggag aaacgatacg gtggttattg 420
gaacgagctg aaccggcgat aattgaagca accggaaccc gaactgtacc ggctatttgc 480
gtatcgggta acggaaacttt aaaaaatccc acgagctctc cagtgttgaa tgacggcgcc 540
cgtgacgggt acggtgacct aatgaagaaa cggaggaaga gaaactgtac gacgcatttc 600
gtagacggtta atgacagctg tcatagctcc gttacttctg gggttagctcc gataacggcg 660

tcaaactacg	gcgttaatat	cctgaacggt	aatacacagg	ggtttgtgcc	gttttggcct	720
atgggtatgg	gtactgcgta	tggtactggt	gggcgggac	aaatgggcca	aatgtgggct	780
attctacacg	ttgctacagc	tccgtttctc	aatgttggtg	ctagaccggg	gtctagttat	840
gtctcaaacg	cttcagacgc	tgagcgagg	atggaaacga	gcggtggcgg	aacgacgcaa	900
ccgctgaggg	atttttcggt	ggagatttat	gataagagag	agcttcagtt	tttgggtggc	960
tcagggaact	catctccgct	ttcatgtcat	gagacttaag	gaattttaac	tcttagttct	1020
agtttttttt	tagtttttag	taagtttgat	tcttgattta	ggtaagtaa	gatttgaata	1080
agaattggga	gcacaatttc	aattttatgt	ttctgtcaaa	cattttggta	attaatgaaa	1140
ctatcctatc	attttt					

(2) INFORMATION FOR SEQ ID NO:1133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..293
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1133:

Met	Glu	Ser	Asn	His	Glu	Gly	Asn	Ala	Ile	Gln	Val	Ile	Asp	Gln	Val
1			5					10						15	
Thr	Thr	Met	Thr	His	Leu	Ser	Asp	Pro	Asn	Pro	Lys	Thr	Lys	Pro	Gly
			20					25					30		
Met	Met	Leu	Met	Lys	Gln	Glu	Asp	Gly	Tyr	Leu	Gln	Pro	Val	Lys	Thr
			35					40					45		
Lys	Pro	Ala	Pro	Lys	Arg	Pro	Thr	Ser	Lys	Asp	Arg	His	Thr	Lys	Val
			50					55					60		
Glu	Gly	Arg	Gly	Arg	Arg	Ile	Arg	Met	Pro	Ala	Gly	Cys	Ala	Ala	Arg
65						70					75			80	
Val	Phe	Gln	Leu	Thr	Arg	Glu	Leu	Gly	His	Lys	Ser	Asp	Gly	Glu	Thr
			85					90					95		
Ile	Arg	Trp	Leu	Leu	Glu	Arg	Ala	Glu	Pro	Ala	Ile	Ile	Glu	Ala	Thr
			100					105					110		
Gly	Thr	Gly	Thr	Val	Pro	Ala	Ile	Ala	Val	Ser	Val	Asn	Gly	Thr	Leu
			115					120					125		
Lys	Ile	Pro	Thr	Ser	Ser	Pro	Val	Leu	Asn	Asp	Gly	Gly	Arg	Asp	Gly
			130					135					140		
Asp	Gly	Asp	Leu	Met	Lys	Lys	Arg	Arg	Lys	Arg	Asn	Cys	Thr	Ser	Asp
145						150					155			160	
Phe	Val	Asp	Val	Asn	Asp	Ser	Cys	His	Ser	Ser	Val	Thr	Ser	Gly	Leu
						165					170			175	
Ala	Pro	Ile	Thr	Ala	Ser	Asn	Tyr	Gly	Val	Asn	Ile	Leu	Asn	Val	Asn
			180					185					190		
Thr	Gln	Gly	Phe	Val	Pro	Phe	Trp	Pro	Met	Gly	Met	Gly	Thr	Ala	Tyr
			195					200					205		
Val	Thr	Gly	Gly	Pro	Asp	Gln	Met	Gly	Gln	Met	Trp	Ala	Ile	Pro	Thr
			210					215					220		
Val	Ala	Thr	Ala	Pro	Phe	Leu	Asn	Val	Gly	Ala	Arg	Pro	Val	Ser	Ser
225						230					235			240	
Tyr	Val	Ser	Asn	Ala	Ser	Asp	Ala	Glu	Ala	Glu	Met	Glu	Thr	Ser	Gly
			245					250					255		
Gly	Gly	Thr	Thr	Gln	Pro	Leu	Arg	Asp	Phe	Ser	Leu	Glu	Ile	Tyr	Asp
			260					265					270		
Lys	Arg	Glu	Leu	Gln	Phe	Leu	Gly	Gly	Ser	Gly	Asn	Ser	Ser	Pro	Ser
			275					280					285		
Ser	Cys	His	Glu	Thr											
			290												

(2) INFORMATION FOR SEQ ID NO:1134:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 275 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..275
(D) OTHER INFORMATION: / Ceres Seq. ID 1499722
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1134:

Met	Thr	His	Leu	Ser	Asp	Pro	Asn	Pro	Lys	Thr	Lys	Pro	Gly	Met	Met
1			5					10					15		
Leu	Met	Lys	Gln	Glu	Asp	Gly	Tyr	Leu	Gln	Pro	Val	Lys	Thr	Lys	Pro
			20					25					30		
Ala	Pro	Lys	Arg	Pro	Thr	Ser	Lys	Asp	Arg	His	Thr	Lys	Val	Glu	Gly
			35				40					45			
Arg	Gly	Arg	Arg	Ile	Arg	Met	Pro	Ala	Gly	Cys	Ala	Ala	Arg	Val	Phe
			50			55				60					
Gln	Leu	Thr	Arg	Glu	Leu	Gly	His	Lys	Ser	Asp	Gly	Glu	Thr	Ile	Arg
65				70				75						80	
Trp	Leu	Leu	Glu	Arg	Ala	Glu	Pro	Ala	Ile	Glu	Ala	Thr	Gly	Thr	
			85					90					95		
Gly	Thr	Val	Pro	Ala	Ile	Ala	Val	Ser	Val	Asn	Gly	Thr	Leu	Lys	Ile
			100				105						110		
Pro	Thr	Ser	Ser	Pro	Val	Leu	Asn	Asp	Gly	Gly	Arg	Asp	Gly	Asp	Gly
			115				120					125			
Asp	Leu	Met	Lys	Lys	Arg	Arg	Lys	Arg	Asn	Cys	Thr	Ser	Asp	Phe	Val
			130				135					140			
Asp	Val	Asn	Asp	Ser	Cys	His	Ser	Ser	Val	Thr	Ser	Gly	Leu	Ala	Pro
145				150						155				160	
Ile	Thr	Ala	Ser	Asn	Tyr	Gly	Val	Asn	Ile	Leu	Asn	Val	Asn	Thr	Gln
			165						170					175	
Gly	Phe	Val	Pro	Phe	Trp	Pro	Met	Gly	Met	Gly	Thr	Ala	Tyr	Val	Thr
			180					185					190		
Gly	Gly	Pro	Asp	Gln	Met	Gly	Gln	Met	Trp	Ala	Ile	Pro	Thr	Val	Ala
			195				200					205			
Thr	Ala	Pro	Phe	Leu	Asn	Val	Gly	Ala	Arg	Pro	Val	Ser	Ser	Tyr	Val
			210			215					220				
Ser	Asn	Ala	Ser	Asp	Ala	Glu	Ala	Glu	Met	Glu	Thr	Ser	Gly	Gly	Gly
225				230						235				240	
Thr	Thr	Gln	Pro	Leu	Arg	Asp	Phe	Ser	Leu	Glu	Ile	Tyr	Asp	Lys	Arg
			245						250					255	
Glu	Leu	Gln	Phe	Leu	Gly	Gly	Ser	Gly	Asn	Ser	Ser	Pro	Ser	Ser	Cys
			260				265						270		
His	Glu	Thr													
			275												

(2) INFORMATION FOR SEQ ID NO:1135:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 261 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..261
(D) OTHER INFORMATION: / Ceres Seq. ID 1499723
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1135:

Met	Met	Leu	Met	Lys	Gln	Glu	Asp	Gly	Tyr	Leu	Gln	Pro	Val	Lys	Thr
1				5					10					15	
Lys	Pro	Ala	Pro	Lys	Arg	Pro	Thr	Ser	Lys	Asp	Arg	His	Thr	Lys	Val

(X17) Sequence Z-score						
cattaaagctg	gtgtgcagag	aaagctggaa	aatagagagt	tcgatgaact	ctgtgtacta	60
taaatgagagc	tcaggaggtt	gaaaacatcg	agattttccc	cgggtcgagg	ttcctgattg	120
aaatgaagac	cagaagatgc	tcataatgtg	gacaaactacc	tcaggatgag	aaatagactt	180
gtctcgcgac	ggaggtgtca	cggagcctca	aaaaagttgt	ataactctcg	cgttttgtgg	240
ttgtaggata	caaggaatgc	aaaagaatga	cggcgcgaaa	accatgtgaag	cgagatcgta	300
agaaagtttt	tttcatccgc	gagctgtacc	ggagtcocat	agagggcaagc	caaaactata	360
cagcttcgca	cgatctgcac	gagacagata	aggagttagt	gtctgtggac	agaagtgttg	420
aggtctcgat	atctctgata	caactggatt	cgtgaatcgt	tttaactcaa	atctccctaa	480
tcagattaga	atctctcggtt	acaagccgtg	cttagccctg	cttagtccca	agaagttttg	540
cgatcgaaga	aggatatgtg	atctctcttc	atgttttgtc	cttgatccaa	tctgcgatcg	600
tgatatgaga	acagtaatgg	ctagttttgg	tcctgggaag	gaatattgta	tctgtcttga	660
gtgtcctaga	agaggtctga	agattctctc	aggctttgtg	ggtaaatgga	aagtagacca	720
ctttgggact	aaacatcttg	attttcaagt	agacattctg	tcgaaacttg	ctagtgcatt	780
acaaggtgac	atacagattg	agaattcttg	ttctaattta	gtcggtctat	gctcagatga	840
tgttgaagta	ggtaggatcat	agaagaagac	ttgtaaattg	aatacaattc	catcagagac	900
taagtgtaag	acaaggtttt	gttatgttga	aaaggaaaag	gaagaagttc	tgaagaatat	960
atgttgttat	gttgatcatc	ataatttcca	taacttcta	acaaagacaa	aagcatgatg	1020
tcctgaactc	gtgtctcaaa	ctatcctctc	caactgtca	actgtgtata	atcttgatgg	1080

gattgacttt	atcaagtgtg	aagtcttagg	caaaagcttt	atgcttcac	agattcgga	1140
gatgatgggt	cttgctgttg	caatcatg	gaattgtgct	tctgaatcac	ttatccaaag	1200
tgctttcagc	aaggatgtga	ataatactgt	accaatggcg	ccagaagtgtg	gactttatct	1260
ggacgaatgc	ttcttcacat	cttaatacag	aaactttgaa	gacagtcacg	aagaagtgtc	1320
catggaagca	tacaagaag	aagctgaagc	attcaaatg	aagcatatct	attctcatat	1380
cggcgctaca	gagcgaaaat	acggaaatat	ggctcttttg	ttacattcct	tgaactatag	1440
aaactatcca	gacctaaact	ttggcagctg	tggacaaaaa	acagaccaag	ttctttgtca	1500
taagaaaatt	gatgaaagag	caagtcacatg	tccttaagca	aaatgatgga	agctttagtt	1560
gaagattttg	acattgtttt	tggtattggt	ggttaatccc	accatttttg	taacttttta	1620
atcaaatg	tatatatttg	tggtgtaagg	tgacactaat	gaattgattt	gttatcctcc	1680

(2) INFORMATION FOR SEQ ID NO:1137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..463
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1137:

Met	Leu	Thr	Thr	Thr	Thr	Asp	Glu	Glu	Ile	Asp	Leu	Ser	Cys	Asp	Gly
1				5					10					15	
Gly	Val	Thr	Glu	Pro	Gln	Lys	Val	Ala	Ile	Ile	Phe	Ala	Phe	Cys	Gly
			20					25					30		
Val	Gly	Tyr	Gln	Gly	Met	Gln	Lys	Asn	Pro	Gly	Ala	Lys	Thr	Ile	Glu
		35				40					45				
Gly	Glu	Leu	Glu	Glu	Ala	Leu	Phe	His	Ala	Gly	Ala	Val	Pro	Glu	Ser
	50				55					60					
Ile	Arg	Gly	Lys	Pro	Lys	Leu	Tyr	Asp	Phe	Ala	Arg	Ser	Ala	Arg	Thr
	65				70				75					80	
Asp	Lys	Gly	Val	Ser	Ala	Val	Gly	Gln	Val	Val	Ser	Gly	Arg	Phe	Ile
			85					90						95	
Val	Asp	Pro	Leu	Gly	Phe	Val	Asn	Arg	Leu	Asn	Ser	Asn	Leu	Pro	Asn
			100				105						110		
Gln	Ile	Arg	Ile	Phe	Gly	Tyr	Lys	His	Val	Thr	Pro	Ser	Phe	Ser	Ser
			115				120						125		
Lys	Lys	Phe	Cys	Asp	Arg	Arg	Arg	Tyr	Val	Tyr	Leu	Leu	Pro	Val	Phe
	130				135						140				
Ala	Leu	Asp	Pro	Ile	Ser	His	Arg	Asp	Arg	Glu	Thr	Val	Met	Ala	Ser
	145				150					155					160
Leu	Gly	Pro	Gly	Glu	Glu	Tyr	Val	Lys	Cys	Phe	Glu	Cys	Ser	Glu	Arg
			165						170					175	
Gly	Arg	Lys	Ile	Pro	Pro	Gly	Leu	Val	Gly	Lys	Trp	Lys	Gly	Thr	Asn
			180				185						190		
Phe	Gly	Thr	Lys	Ser	Leu	Asp	Phe	Gln	Ser	Asp	Ile	Ser	Ser	Asn	Asn
			195				200					205			
Ser	Ser	Ala	Leu	Arg	Ser	Asp	Ile	Lys	Ile	Glu	Ala	Leu	Ser	Ser	Asn
	210				215					220					
Leu	Ala	Gly	Leu	Cys	Ser	Val	Asp	Val	Glu	Val	Gly	Arg	Ile	Gln	Glu
	225				230				235					240	
Asp	Ser	Cys	Lys	Leu	Asn	Thr	Asn	Ser	Ser	Glu	Thr	Lys	Val	Lys	Ser
			245					250						255	
Lys	Phe	Cys	Tyr	Gly	Glu	Lys	Glu	Lys	Glu	Arg	Phe	Ser	Arg	Ile	Leu
			260				265						270		
Ser	Cys	Tyr	Val	Gly	Ser	Tyr	Asn	Phe	His	Asn	Phe	Thr	Thr	Arg	Thr
			275				280						285		
Lys	Ala	Asp	Asp	Pro	Thr	Ala	Asn	Arg	Gln	Ile	Ile	Ser	Phe	Thr	Ala
	290					295					300				

Asn Thr Val Ile Asn Leu Asp Gly Ile Asp Phe Ile Lys Cys Glu Val
305 310 315 320
Leu Gly Lys Ser Phe Met Leu His Gln Ile Arg Lys Met Met Gly Leu
325 330 335
Ala Val Ala Ile Met Arg Asn Cys Ala Ser Glu Ser Leu Ile Gln Ser
340 345 350
Ala Phe Ser Lys Asp Val Asn Ile Thr Val Pro Met Ala Pro Glu Val
355 360 365
Gly Leu Tyr Leu Asp Glu Cys Phe Phe Thr Ser Tyr Asn Arg Asn Phe
370 375 380
Glu Asp Ser His Glu Glu Val Ser Met Glu Ala Tyr Lys Glu Glu Ala
385 390 395 400
Glu Ala Phe Lys Leu Lys His Ile Tyr Ser His Ile Gly Ala Thr Glu
405 410 415
Arg Lys Tyr Gly Asn Met Ala Leu Trp Leu His Ser Leu Asn Tyr Arg
420 425 430
Asn Tyr Pro Asp Leu Asn Phe Gly Ser Cys Gly Gln Asn Thr Asp Gln
435 440 445
Val Leu Val His Lys Lys Ile Asp Glu Arg Ala Ser His Ser Leu
450 455 460

(2) INFORMATION FOR SEQ ID NO:1138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..426
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499730

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1138:

Met Gln Lys Asn Pro Gly Ala Lys Thr Ile Glu Gly Glu Leu Glu Glu
1 5 10 15
Ala Leu Phe His Ala Gly Ala Val Pro Glu Ser Ile Arg Gly Lys Pro
20 25 30
Lys Leu Tyr Asp Phe Ala Arg Ser Ala Arg Thr Asp Lys Gly Val Ser
35 40 45
Ala Val Gly Gln Val Val Ser Gly Arg Phe Ile Val Asp Pro Leu Gly
50 55 60
Phe Val Asn Arg Leu Asn Ser Asn Leu Pro Asn Gln Ile Arg Ile Phe
65 70 75 80
Gly Tyr Lys His Val Thr Pro Ser Phe Ser Ser Lys Lys Phe Cys Asp
85 90 95
Arg Arg Arg Tyr Val Tyr Leu Leu Pro Val Phe Ala Leu Asp Pro Ile
100 105 110
Ser His Arg Asp Arg Glu Thr Val Met Ala Ser Leu Gly Pro Gly Glu
115 120 125
Glu Tyr Val Lys Cys Phe Glu Cys Ser Glu Arg Gly Arg Lys Ile Pro
130 135 140
Pro Gly Leu Val Gly Lys Trp Lys Gly Thr Asn Phe Gly Thr Lys Ser
145 150 155 160
Leu Asp Phe Gln Ser Asp Ile Ser Ser Asn Asn Ser Ser Ala Leu Arg
165 170 175
Ser Asp Ile Lys Ile Glu Ala Leu Ser Ser Asn Leu Ala Gly Leu Cys
180 185 190
Ser Val Asp Val Glu Val Gly Arg Ile Gln Glu Asp Ser Cys Lys Leu
195 200 205
Asn Thr Asn Ser Ser Glu Thr Lys Val Lys Ser Lys Phe Cys Tyr Gly
210 215 220
Glu Lys Glu Lys Glu Arg Phe Ser Arg Ile Leu Ser Cys Tyr Val Gly

(2) INFORMATION FOR SEQ ID NO:1139:

(A) LENGTH: 306 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..306

(D) OTHER INFORMATION: / Ceres Seq. ID 1499731

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1139:

Met	Ala	Ser	Leu	Gly	Pro	Gly	Glu	Glu	Tyr	Val	Lys	Cys	Phe	Glu	Cys
1				5				10						15	
Ser	Glu	Arg	Gly	Arg	Lys	Ile	Pro	Pro	Gly	Leu	Val	Gly	Lys	Trp	Lys
			20					25					30		
Gly	Thr	Asn	Phe	Gly	Thr	Lys	Ser	Leu	Asp	Phe	Gln	Ser	Asp	Ile	Ser
		35					40					45			
Ser	Asn	Asn	Ser	Ser	Ala	Leu	Arg	Ser	Asp	Ile	Lys	Ile	Glu	Ala	Leu
	50					55					60				
Ser	Ser	Asn	Leu	Ala	Gly	Leu	Cys	Ser	Val	Asp	Val	Glu	Val	Gly	Arg
65				70					75					80	
Ile	Gln	Glu	Asp	Ser	Cys	Lys	Leu	Asn	Thr	Asn	Ser	Ser	Glu	Thr	Lys
			85					90					95		
Val	Lys	Ser	Lys	Phe	Cys	Tyr	Gly	Glu	Lys	Glu	Lys	Glu	Arg	Phe	Ser
			100					105					110		
Arg	Ile	Leu	Ser	Cys	Tyr	Val	Gly	Ser	Tyr	Asn	Phe	His	Asn	Phe	Thr
		115					120					125			
Thr	Arg	Thr	Lys	Ala	Asp	Asp	Pro	Thr	Ala	Asn	Arg	Gln	Ile	Ile	Ser
	130				135						140				
Phe	Thr	Ala	Asn	Thr	Val	Ile	Asn	Leu	Asp	Gly	Ile	Asp	Phe	Ile	Lys
145				150					155					160	
Cys	Glu	Val	Leu	Gly	Lys	Ser	Phe	Met	Leu	His	Gln	Ile	Arg	Lys	Met
			165					170					175		
Met	Gly	Leu	Ala	Val	Ala	Ile	Met	Arg	Asn	Cys	Ala	Ser	Glu	Ser	Leu
		180						185					190		

Ile	Gln	Ser	Ala	Phe	Ser	Lys	Asp	Val	Asn	Ile	Thr	Val	Pro	Met	Ala	
	195						200					205				
Pro	Glu	Val	Gly	Leu	Tyr	Leu	Asp	Glu	Cys	Phe	Phe	Thr	Ser	Tyr	Asn	
	210					215					220					
Arg	Asn	Phe	Glu	Asp	Ser	His	Glu	Glu	Val	Ser	Met	Glu	Ala	Tyr	Lys	
	225					230				235					240	
Glu	Glu	Ala	Glu	Ala	Phe	Lys	Leu	Lys	His	Ile	Tyr	Ser	His	Ile	Gly	
			245					250						255		
Ala	Thr	Glu	Arg	Lys	Tyr	Gly	Asn	Met	Ala	Leu	Trp	Leu	His	Ser	Leu	
			260				265							270		
Asn	Tyr	Arg	Asn	Tyr	Pro	Asp	Leu	Asn	Phe	Gly	Ser	Cys	Gly	Gln	Asn	
		275				280						285				
Thr	Asp	Gln	Val	Leu	Val	His	Lys	Lys	Ile	Asp	Glu	Arg	Ala	Ser	His	
		290				295				300						
Ser	Leu															
305																

(2) INFORMATION FOR SEQ ID NO:1140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1402
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499732

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1140:

gggatgtttg	tgaccttttg	tctcttcttc	tctaaaaatto	tctttctccc	aaaaactaaa	60
aaaaacaaaa	aaacaaaaaa	gtgacgcaat	gaaagaagaa	gactgtcttc	aaacatttca	120
caactatcaa	gactatacaag	accagtttca	tcttcatcat	catcacaaaa	ttctcccctg	180
gtcgtcgaca	tctttaccctt	cttttgacc	actccatttc	ccatctaaac	cgaccggtta	240
ttctgacccc	gttccactact	tcaacagaag	agcttcttct	tccttcttct	cttttgacta	300
taacagcggg	tttgtctctc	ctctctcttc	catggatcat	cctcagaacc	atctaaggat	360
tttatccgaa	gctcttggac	ccatcatgcg	tcgtggctcg	tcctttgggt	tcgatgttga	420
gatcatggga	aaattgagtg	cacaagaagt	catggatgct	aaggctttag	ctgcttcaaa	480
gagtcatagt	gaagctgaga	gaagaagacg	agagagaaac	aacactcctc	ttgctaaggct	540
cgctagtata	ttaccaaaaa	caacccaaaa	ggacaaaagt	tctttgtctg	cgggaagtgt	600
ccaacacatg	aaggagctaa	aacgacaaa	atcacagatc	accgacacgt	atcaagtccc	660
aacagagatg	gatgatctga	cgttagattc	gtctttacaac	gacgaggaag	gaaactttgt	720
gataagagca	tccttttctg	gccaaagacg	gactgacctc	atgcattgac	tcataatcgc	780
cttaaaagtct	cttcgtcttc	gaactctcaa	agctgagatc	gcaaccgtag	ttggttagagt	840
caagaacatc	ttgttcttga	gccgagaata	cgatgatgaa	gaagatcatg	atcatatctg	900
tagaaaacttc	gatgggtgatg	acgtggagga	ttatgatgaa	gagaggatga	tgaataatcg	960
tgtgagttcg	atagaagaag	cgttaaaagg	gggtatagag	aagtgtgttc	ataataatga	1020
tgaagatgac	gataacaata	acttggagaa	atcatcttca	gggggtatta	agaggcaaa	1080
gactagtaga	atggtggaatc	gatgttataa	ttagttaatt	aagtccaagt	tttatctaact	1140
aggggttagt	aattagactt	gcacaaatgg	atttgatttc	gggttgggtg	tattagtatt	1200
attttcggtg	tttttagtag	ttggggtatg	gtttattctt	ctatgttttt	ttaattctatg	1260
aagaaccttt	tgtttagggt	tttatagtga	tgagttttgt	ttatatatgg	tagttaagac	1320
attttatcgt	cttaattaat	ataggaaatg	tatagagctt	gggtttgtat	taatttatca	1380
agaagttttt	tttatcatat	tc				

(2) INFORMATION FOR SEQ ID NO:1141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..344

(D) OTHER INFORMATION: / Ceres Seq. ID 1499733

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1141:

Met Tyr Ala Met Lys Glu Glu Asp Cys Leu Gln Thr Phe His Asn Leu
1 5 10 15
Gln Asp Tyr Gln Asp Gln Phe His Leu His His His Pro Gln Ile Leu
20 25 30
Pro Trp Ser Ser Thr Ser Leu Pro Ser Phe Asp Pro Leu His Phe Pro
35 40 45
Ser Asn Pro Thr Arg Tyr Ser Asp Pro Val His Tyr Phe Asn Arg Arg
50 55 60
Ala Ser Ser Ser Ser Ser Phe Asp Tyr Asn Asp Gly Phe Val Ser
65 70 75 80
Pro Pro Pro Ser Met Asp His Pro Gln Asn His Leu Arg Ile Leu Ser
85 90 95
Glu Ala Leu Gly Pro Ile Met Arg Arg Gly Ser Ser Phe Gly Phe Asp
100 105 110
Gly Glu Ile Met Gly Lys Leu Ser Ala Gln Glu Val Met Asp Ala Lys
115 120 125
Ala Leu Ala Ala Ser Lys Ser His Ser Glu Ala Glu Arg Arg Arg Arg
130 135 140
Glu Arg Ile Asn Thr His Leu Ala Lys Leu Arg Ser Ile Leu Pro Asn
145 150 155
Thr Thr Lys Thr Asp Lys Ala Ser Leu Leu Ala Glu Val Ile Gln His
160 165 170 175
Met Lys Glu Leu Lys Arg Gln Thr Ser Gln Ile Thr Asp Thr Tyr Gln
180 185 190
Val Pro Thr Glu Cys Asp Asp Leu Thr Val Asp Ser Ser Tyr Asn Asp
195 200 205
Glu Glu Gly Asn Leu Val Ile Arg Ala Ser Phe Cys Cys Gln Asp Arg
210 215 220
Thr Asp Leu Met His Asp Val Ile Asn Ala Leu Lys Ser Leu Arg Leu
225 230 235 240
Arg Thr Leu Lys Ala Glu Ile Ala Thr Val Gly Gly Arg Val Lys Asn
245 250 255
Ile Leu Phe Leu Ser Arg Glu Tyr Asp Asp Glu Glu Asp His Asp Ser
260 265 270
Tyr Arg Arg Asn Phe Asp Gly Asp Asp Val Glu Asp Tyr Asp Glu Glu
275 280 285
Arg Met Met Asn Asn Arg Val Ser Ser Ile Glu Glu Ala Leu Lys Ala
290 295 300
Val Ile Glu Lys Cys Val His Asn Asn Asp Glu Ser Asn Asp Asn Asn
305 310 315 320
Asn Leu Glu Lys Ser Ser Ser Gly Gly Ile Lys Arg Gln Arg Thr Ser
325 330 335
Lys Met Val Asn Arg Cys Tyr Asn
340

(2) INFORMATION FOR SEQ ID NO:1142:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 341 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..341

(D) OTHER INFORMATION: / Ceres Seq. ID 1499734

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1142:

Met Lys Glu Glu Asp Cys Leu Gln Thr Phe His Asn Leu Gln Asp Tyr
1 5 10 15

Gln Asp Gln Phe His Leu His His His Pro Gln Ile Leu Pro Trp Ser
20 25 30
Ser Thr Ser Ser Leu Pro Ser Phe Asp Pro Leu His Phe Pro Ser Asn Pro
35 40 45
Thr Arg Tyr Ser Asp Pro Val His Tyr Phe Asn Arg Arg Ala Ser Ser
50 55 60
Ser Ser Ser Ser Phe Asp Tyr Asn Asp Gly Phe Val Ser Pro Pro Pro
65 70 75 80
Ser Met Asp His Pro Gln Asn His Leu Arg Ile Leu Ser Glu Ala Leu
85 90 95
Gly Pro Ile Met Arg Arg Gly Ser Ser Phe Gly Phe Asp Gly Glu Ile
100 105 110
Met Gly Lys Leu Ser Ala Gln Glu Val Met Asp Ala Lys Ala Leu Ala
115 120 125
Ala Ser Lys Ser His Ser Glu Ala Glu Arg Arg Arg Arg Glu Arg Ile
130 135 140
Asn Thr His Leu Ala Lys Leu Arg Ser Ile Leu Pro Asn Thr Thr Lys
145 150 155 160
Thr Asp Lys Ala Ser Leu Leu Ala Glu Val Ile Gln His Met Lys Glu
165 170 175
Leu Lys Arg Gln Thr Ser Gln Ile Thr Asp Thr Tyr Gln Val Pro Thr
180 185 190
Glu Cys Asp Asp Leu Thr Val Asp Ser Ser Tyr Asn Asp Glu Glu Gly
195 200 205
Asn Leu Val Ile Arg Ala Ser Phe Cys Cys Gln Asp Arg Thr Asp Leu
210 215 220
Met His Asp Val Ile Asn Ala Leu Lys Ser Leu Arg Leu Arg Thr Leu
225 230 235 240
Lys Ala Glu Ile Ala Thr Val Gly Gly Arg Val Lys Asn Ile Leu Phe
245 250 255
Leu Ser Arg Glu Tyr Asp Asp Glu Glu Asp His Asp Ser Tyr Arg Arg
260 265 270
Asn Phe Asp Gly Asp Asp Val Glu Asp Tyr Asp Glu Arg Met Met
275 280 285
Asn Asn Arg Val Ser Ser Ile Glu Glu Ala Leu Lys Ala Val Ile Glu
290 295 300
Lys Cys Val His Asn Asn Asp Glu Ser Asn Asp Asn Asn Asn Leu Glu
305 310 315 320
Lys Ser Ser Ser Gly Gly Ile Lys Arg Gln Arg Thr Ser Lys Met Val
325 330 335
Asn Arg Cys Tyr Asn
340

(2) INFORMATION FOR SEQ ID NO:1143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..260
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1143:

Met Asp His Pro Gln Asn His Leu Arg Ile Leu Ser Glu Ala Leu Gly
1 5 10 15
Pro Ile Met Arg Arg Gly Ser Ser Phe Gly Phe Asp Gly Glu Ile Met
20 25 30
Gly Lys Leu Ser Ala Gln Glu Val Met Asp Ala Lys Ala Leu Ala Ala
35 40 45
Ser Lys Ser His Ser Glu Ala Glu Arg Arg Arg Arg Glu Arg Ile Asn

aaatttcxg	acgtggtgga	gtgaacaac	aaaaaaaaca	catgattgat	tgattctgaa	60
attccattcat	atttttaaca	gagagatttct	gaggattctg	atatacagat	ctgcatcagag	120
agaagacagga	gaagagaaa	tggcgtggaa	tgaacttttc	agagatgttg	tgccgtttgc	180
tgcgattgttt	cggtgtgagt	gtgcacctgt	tgggtcaaac	acgcgtgtta	aggctgtctac	240
tttaagagata	ttagacttct	atgtctttgt	cttctactct	tatatgtttt	caacactctct	300
ctctcttcaca	ctttctgtaa	tctttgggaag	gtcaagaaga	ttaccagcag	ctaagtctcc	360
ttctttcttc	aagattttct	tacttgggct	tgttggatgt	cttgtttgaa	aggattttcca	420
tacagttccc	caactcttgc	atctgctatc	agcaatttgc	acacgggtctt	caacttcaca	480
ctcgtctgta	tcttcaggat	ggagcagaag	agggttaaga	gctctgcgac	ycagctctaaa	540
atcatttggtg	caataactat	tatatcttgt	gctctgctga	tgtgtctgta	taaaagcccca	600
caagtgctcg	cctctgcctc	ttttacaact	gtattaccat	ccggttaact	ctcacagact	660
ttgacctcaa	tagagtcaag	ctggaataac	ggaggcgctc	tgcgtgtctc	acagattatt	720
cttatatccg	tctgaactcg	gtcatggagg	tttaacctga	agagataacc	gtagtctctc	780
tctacaattt	atttgcaaca	ctaactctag	taccagtgat	tcttttttgc	gagagacact	840
tgactctctg	gggtgcctaa	ccagacattt	cctgcgtctg	aatcatatcc	tgcggaagtc	900
tcgttttact	atttcagccc	cttaccocaa	catggggctc	gcactgtag	ggtcgggtat	960
acatatccct	tctcaggcca	tgtcttatgt	cgattgcagt	cgcaatgggt	gcttatccgc	1020
tcggcgatgc	acttcacctt	gggagtgtca	tgtgattgat	gaatattgtc	mttgattctt	1080
acactgtgat	tgtggggcaa	ccaagagag	atacatcaat	aactgtagct	ggctctgagc	1140
agtcaccttt	gctcgttaca	catatcatag	aagatggagc	ctttccatca	agctaggattt	1200
gctgcaagtg	aaatctattt	actattttat	ataaataatg	gatccctaaa	agaggtgtac	1260
catatattgt	tatatattgc	tatatgtaca	taataagatt	ctgtctctct	ttctctgttt	1320

tattttgatg ttacatatga atgagaatta tgaatctata agaaatattt ggtcctttt
(2) INFORMATION FOR SEQ ID NO:1145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..131
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499741

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1145:

Met	Arg	Glu	Ala	Gly	Glu	Glu	Lys	Val	Ala	Trp	Lys	Tyr	Phe	Thr	Arg	
1				5					10					15		
Asp	Val	Val	Pro	Phe	Ala	Ala	Met	Phe	Ala	Val	Glu	Cys	Ala	Thr	Val	
			20					25					30			
Gly	Ser	Asn	Thr	Leu	Phe	Lys	Ala	Ala	Thr	Leu	Arg	Gly	Leu	Ser	Phe	
		35					40					45				
Tyr	Val	Phe	Val	Phe	Tyr	Ser	Tyr	Ile	Val	Ser	Thr	Leu	Leu	Leu	Leu	
		50				55					60					
Pro	Leu	Ser	Val	Ile	Phe	Gly	Arg	Ser	Arg	Arg	Leu	Pro	Ala	Ala	Lys	
65				70					75						80	
Ser	Pro	Leu	Phe	Phe	Lys	Ile	Phe	Leu	Leu	Gly	Leu	Val	Gly	Leu	Leu	
				85					90					95		
Val	Val	Lys	Val	Leu	His	Thr	Val	Pro	Gln	Leu	Leu	His	Leu	Leu	Ser	
			100					105					110			
Ala	Ile	Ser	His	Arg	Leu	Ser	His	Ser	His	Ser	Leu	Leu	Ser	Ser	Gly	
		115				120						125				
Trp	Ser	Lys														
		130														

(2) INFORMATION FOR SEQ ID NO:1146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..108
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499742

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1146:

Met	Phe	Ala	Val	Glu	Cys	Ala	Thr	Val	Gly	Ser	Asn	Thr	Leu	Phe	Lys	
1				5					10					15		
Ala	Ala	Thr	Leu	Arg	Gly	Leu	Ser	Phe	Tyr	Val	Phe	Val	Phe	Tyr	Ser	
			20					25					30			
Tyr	Ile	Val	Ser	Thr	Leu	Leu	Leu	Leu	Pro	Leu	Ser	Val	Ile	Phe	Gly	
		35				40					45					
Arg	Ser	Arg	Arg	Leu	Pro	Ala	Ala	Lys	Ser	Pro	Leu	Phe	Phe	Lys	Ile	
		50				55				60						
Phe	Leu	Leu	Gly	Leu	Val	Gly	Leu	Leu	Val	Val	Lys	Val	Leu	His	Thr	
65				70					75					80		
Val	Pro	Gln	Leu	Leu	His	Leu	Leu	Ser	Ala	Ile	Ser	His	Arg	Leu	Ser	
			85					90						95		
His	Ser	His	Ser	Leu	Leu	Ser	Ser	Gly	Trp	Ser	Lys					
		100						105								

(2) INFORMATION FOR SEQ ID NO:1147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..150
(D) OTHER INFORMATION: / Ceres Seq. ID 1499743
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1147:
Met Glu Val Tyr Pro Glu Glu Ile Thr Val Val Phe Phe Tyr Asn Leu
1 5 10 15
Phe Ala Thr Leu Ile Ser Val Pro Val Cys Leu Phe Ala Glu Ser Asn
20 25 30
Leu Thr Ser Trp Val Leu Lys Pro Asp Ile Ser Leu Ala Ala Ile Ile
35 40 45
Tyr Ser Gly Val Phe Val Ser Leu Phe Ser Ala Leu Thr His Thr Trp
50 55 60
Gly Leu His Leu Lys Gly Pro Val Tyr Ile Ser Leu Phe Arg Pro Leu
65 70 75 80
Ser Ile Ala Ile Ala Val Ala Met Gly Ala Ile Phe Leu Gly Asp Ala
85 90 95
Leu His Leu Gly Ser Val Ile Gly Ser Xaa Ile Leu Cys Xaa Gly Phe
100 105 110
Tyr Thr Val Ile Trp Gly Lys Ala Arg Glu Asp Thr Ile Lys Thr Val
115 120 125
Ala Gly Ser Glu Gln Ser Pro Leu Leu Leu Thr His Ile Ile Glu Asp
130 135 140
Gly Ala Phe Pro Leu Ser
145 150

(2) INFORMATION FOR SEQ ID NO:1148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..685

(D) OTHER INFORMATION: / Ceres Seq. ID 1499748

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148:

attcaaatctc acaacaacca atctacacac aaaacaataa caacaacaac aacaacaaca 60
acaacaaca acaacaaca acaacaaaat gttacaaaaa tcaatccttt tacctttctt 120
tctggtaatc atcttcgtct cagcatctca agctagtcgt caactctggg atagtggaaat 180
cagcgagatg tttggttcca aatccggggt tcatcatgga ttttcggggt ttccggggtc 240
ctctggagggt gctggagggtg ctggaggatg attcggagat atgatgaatg ctggagggtgc 300
acatacatgc tcggcgcaag gagctttagt cggtaagaag ctgacatgtc ccgaggagtg 360
ctacaatcca accaacgtta acaaggatgg ttataaaaagc accagcgcca gtggagggatg 420
ttcatttgac tgtacgacca agtgtgccgc gacttgttca aattaacatg ttaatttgca 480
catatatatt atatgttgt atagtatggt gttatgttat gttatagcat tatatagttc 540
atatatatgt caatataata aaaccggcaa ggtatatggg aggtttgtgt tcccttttgt 600
aattttgtat ggaatcttgat tagaagcttt ctatgaatct atgtacataa tatgattttg 660
aataaaagaa aatttagtgt ttctc

(2) INFORMATION FOR SEQ ID NO:1149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1499749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1149:

```
Met Phe Thr Lys Ser Ile Leu Leu Pro Phe Leu Leu Val Ile Ile Phe
1      5      10      15
Val Ser Ala Ser Gln Ala Ser Arg Gln Leu Trp Asp Ser Gly Ile Ser
      20      25      30
Glu Met Phe Gly Ser Lys Ser Gly Phe His His Gly Phe Ser Gly Phe
      35      40      45
Ser Gly Ser Ser Gly Gly Ala Gly Gly Ala Gly Ser Phe Gly Asp
      50      55      60
Met Met Asn Ala Gly Gly Ala His Thr Cys Ser Ala Gln Gly Ala Cys
65      70      75      80
Ser Gly Lys Lys Leu Thr Cys Pro Glu Glu Cys Tyr Lys Ser Thr Asn
      85      90      95
Val Asn Lys Asp Gly Tyr Lys Ser Thr Ser Arg Ser Gly Gly Cys Ser
      100      105      110
Phe Asp Cys Thr Thr Lys Cys Ala Ala Thr Cys Ser Asn
      115      120      125
```

(2) INFORMATION FOR SEQ ID NO:1150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92

(D) OTHER INFORMATION: / Ceres Seq. ID 1499750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1150:

```
Met Phe Gly Ser Lys Ser Gly Phe His His Gly Phe Ser Gly Phe Ser
1      5      10      15
Gly Ser Ser Gly Gly Ala Gly Gly Ala Gly Gly Ser Phe Gly Asp Met
      20      25      30
Met Asn Ala Gly Gly Ala His Thr Cys Ser Ala Gln Gly Ala Cys Ser
      35      40      45
Gly Lys Lys Leu Thr Cys Pro Glu Glu Cys Tyr Lys Ser Thr Asn Val
      50      55      60
Asn Lys Asp Gly Tyr Lys Ser Thr Ser Arg Ser Gly Gly Cys Ser Phe
65      70      75      80
Asp Cys Thr Thr Lys Cys Ala Ala Thr Cys Ser Asn
      85      90
```

(2) INFORMATION FOR SEQ ID NO:1151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 741 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..741

(D) OTHER INFORMATION: / Ceres Seq. ID 1499751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1151:

```
accttctctt gatcactcac tgcatacaaca atggccagag agaagattgt ggtggctggt 60
ggtaccacaa agagctggaa actactcttg gggctgagaa tatttgcatt catggctact 120
ttagctgcag ccattgtaat gtcactaaac aaagagacaa agaccttggt tgtggccacc 180
attgtactgt ttccatttaa agccacttta accgctaagt ttcagcacac accggttttt 240
gtgttctttg ttaatagctaa tgtaatgggt agcttccaca atttgttgat gattgtcttt 300
cagattttca gcccgaaact ggagtaacaaa ggtctccgctc tctctctat cgctatttct 360
```

gacatgctaa acgcaacact agtatctgcg gctgcaaacg cggcgggtgtt cgtggcagag 420
ctaggggaaga acgggaacaa gcacgcgaag tggaacaaag tctgcgacag gtttgccact 480
tactgtgatc acgggcgacg agcaatcatc gcagcattcg scggagtcac tctaagtctc 540
ctgggtgctcg ccgtctccat ttcccgccctc ttaatcaatt ctaaaaactt ctccaccacc 600
gccaccacaa cctccgtcgt ctaaaacatc gtggccaaaa attcagcaac atgtgtgtga 660
ccattttata gatgtgtggt ctactttgt gtgtttgtct ctcaagtcac tagcaaattg 720
tgtaatgcac tctttgttc t

(2) INFORMATION FOR SEQ ID NO:1152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..197
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1152:

Met Ala Arg Glu Lys Ile Val Val Ala Gly Gly Thr Thr Lys Ser Trp
1 5 10 15
Lys Leu Leu Leu Gly Leu Arg Ile Phe Ala Phe Met Ala Thr Leu Ala
20 25 30
Ala Ala Ile Val Met Ser Leu Asn Lys Glu Thr Lys Thr Leu Val Val
35 40 45
Ala Thr Ile Gly Thr Val Pro Ile Lys Ala Thr Leu Thr Ala Lys Phe
50 55 60
Gln His Thr Pro Ala Phe Val Phe Phe Val Ile Ala Asn Val Met Val
65 70 75 80
Ser Phe His Asn Leu Leu Met Ile Ala Leu Gln Ile Phe Ser Pro Lys
85 90 95
Leu Glu Tyr Lys Gly Leu Arg Leu Leu Ser Ile Ala Ile Leu Asp Met
100 105 110
Leu Asn Ala Thr Leu Val Ser Ala Ala Ala Asn Ala Ala Val Phe Val
115 120 125
Ala Glu Leu Gly Lys Asn Gly Asn Lys His Ala Lys Trp Asn Lys Val
130 135 140
Cys Asp Arg Phe Ala Thr Tyr Cys Asp His Gly Ala Gly Ala Ile Ile
145 150 155 160
Ala Ala Phe Xaa Gly Val Ile Leu Met Leu Leu Val Ser Ala Val Ser
165 170 175
Ile Ser Arg Leu Leu Ile Asn Ser Lys Asn Phe Ser Thr Thr Ala Thr
180 185 190
Thr Thr Ser Val Val
195

(2) INFORMATION FOR SEQ ID NO:1153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..170
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1153:

Met Ala Thr Leu Ala Ala Ala Ile Val Met Ser Leu Asn Lys Glu Thr
1 5 10 15
Lys Thr Leu Val Val Ala Thr Ile Gly Thr Val Pro Ile Lys Ala Thr
20 25 30

Leu Thr Ala Lys Phe Gln His Thr Pro Ala Phe Val Phe Phe Val Ile
35 40 45
Ala Asn Val Met Val Ser Phe His Asn Leu Leu Met Ile Ala Leu Gln
50 55 60
Ile Phe Ser Pro Lys Leu Glu Tyr Lys Gly Leu Arg Leu Leu Ser Ile
65 70 75 80
Ala Ile Leu Asp Met Leu Asn Ala Thr Leu Val Ser Ala Ala Ala Asn
85 90 95
Ala Ala Val Phe Val Ala Glu Leu Gly Lys Asn Gly Asn Lys His Ala
100 105 110
Lys Trp Asn Lys Val Cys Asp Arg Phe Ala Thr Tyr Cys Asp His Gly
115 120 125
Ala Gly Ala Ile Ile Ala Ala Phe Xaa Gly Val Ile Leu Met Leu Leu
130 135 140
Val Ser Ala Val Ser Ile Ser Arg Leu Leu Ile Asn Ser Lys Asn Phe
145 150 155 160
Ser Thr Thr Ala Thr Thr Thr Ser Val Val
165 170

(2) INFORMATION FOR SEQ ID NO:1154:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..161

(D) OTHER INFORMATION: / Ceres Seq. ID 1499754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1154:

Met Ser Leu Asn Lys Glu Thr Lys Thr Leu Val Val Ala Thr Ile Gly
1 5 10 15
Thr Val Pro Ile Lys Ala Thr Leu Thr Ala Lys Phe Gln His Thr Pro
20 25 30
Ala Phe Val Phe Phe Val Ile Ala Asn Val Met Val Ser Phe His Asn
35 40 45
Leu Leu Met Ile Ala Leu Gln Ile Phe Ser Pro Lys Leu Glu Tyr Lys
50 55 60
Gly Leu Arg Leu Leu Ser Ile Ala Ile Leu Asp Met Leu Asn Ala Thr
65 70 75 80
Leu Val Ser Ala Ala Ala Asn Ala Ala Val Phe Val Ala Glu Leu Gly
85 90 95
Lys Asn Gly Asn Lys His Ala Lys Trp Asn Lys Val Cys Asp Arg Phe
100 105 110
Ala Thr Tyr Cys Asp His Gly Ala Ile Ile Ala Ala Phe Xaa
115 120 125
Gly Val Ile Leu Met Leu Leu Val Ser Ala Val Ser Ile Ser Arg Leu
130 135 140
Leu Ile Asn Ser Lys Asn Phe Ser Thr Thr Ala Thr Thr Thr Ser Val
145 150 155 160
Val

(2) INFORMATION FOR SEQ ID NO:1155:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 667 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..667

(D) OTHER INFORMATION: / Ceres Seq. ID 1499755

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1155:

acaacttccc	cattttctgc	tcttttttgt	tcaactccaa	tcacacaatt	cacaacccat	60
tgagaaacca	ataaaataac	ctcaatcaaa	aaaaaaaaa	aaaaaagatg	aaattctcaa	120
tttagtaaa	gagaaaaaag	ccatttcgaa	taacttgaaa	aggttttgtt	tttgcaaga	180
aaaatgaag	agaagggcga	gagtggtgga	ggagtaggat	acgtgagagc	agatcagata	240
gatttaaga	gtctggacga	gcaattgcag	agacacttaa	gtaaagcatg	gacgatggag	300
aagaggaaga	gtttgagtga	tgggtgaagt	aacgtcaata	acaccgcaca	taaccagaa	360
aacttcggac	atgcacagct	tgtgtttcag	agggcgcttc	cttggtgtgtg	gatatagcaa	420
caacaacaac	agcagcaaga	acgacataat	taggtcgacc	gagggtgaga	agtcgagagc	480
agagtgggag	attgatcctt	ctaagcttat	aatcaaaagt	gtgattgcta	gaggtacttt	540
tggtaacggt	caccgtggaa	tctacgatgg	tcaagatgtc	gccgtaaaac	tactagactg	600
gggagaagag	gggcacaggt	cagacgcaga	gatagcttcg	cttagagctg	cttttactca	660
agaagtt						

(2) INFORMATION FOR SEQ ID NO:1156:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1499756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1156:

Met	Val	Glu	Lys	Ala	Glu	Ser	Gly	Gly	Val	Gly	Tyr	Val	Arg	Ala
1			5					10					15	
Asp	Gln	Ile	Asp	Leu	Lys	Ser	Leu	Asp	Glu	Gln	Leu	Gln	Arg	His
			20					25					30	
Ser	Lys	Ala	Trp	Thr	Met	Glu	Lys	Arg	Lys	Ser	Leu	Ser	Asp	Gly
			35					40					45	
Asp	Asn	Val	Asn	Asn	Thr	Arg	His	Asn	Gln	Asn	Asn	Phe	Gly	His
			50					55					60	
Gln	Leu	Val	Phe	Gln	Arg	Pro	Leu	Pro	Trp	Trp	Trp	Trp	Ile	
			65					70					75	

(2) INFORMATION FOR SEQ ID NO:1157:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..116

(D) OTHER INFORMATION: / Ceres Seq. ID 1499757

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1157:

Met	Val	Lys	Ile	Thr	Ser	Ile	Thr	Pro	Asp	Ile	Thr	Arg	Thr	Thr	Ser
1			5					10						15	
Asp	Ile	Asp	Ser	Leu	Cys	Phe	Arg	Gly	Arg	Phe	Leu	Gly	Gly	Gly	Tyr
			20					25						30	
Ser	Asn	Asn	Asn	Asn	Ser	Ser	Lys	Asn	Asp	Ile	Ile	Arg	Ser	Thr	Glu
			35					40					45		
Val	Glu	Lys	Ser	Arg	Arg	Glu	Trp	Glu	Ile	Asp	Pro	Ser	Lys	Leu	Ile
			50					55					60		
Ile	Lys	Ser	Val	Ile	Ala	Arg	Gly	Thr	Phe	Gly	Thr	Val	His	Arg	Gly
			65					70					75		80
Ile	Tyr	Asp	Gly	Gln	Asp	Val	Ala	Val	Lys	Leu	Leu	Asp	Trp	Gly	Glu
			85					90					95		

Glu Gly His Arg Ser Asp Ala Glu Ile Ala Ser Leu Arg Ala Ala Phe
100 105 110
Thr Gln Glu Val
115

(2) INFORMATION FOR SEQ ID NO:1158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..224
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499758

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1158:

tttttttcgt cgagcagcgc cgctttttgg ccgaggaagg ataaagagag acgccatggg 60
aagaagacct gcgaggtgtt accgtcagat caagggtaag ccatacccaa agtctcgcta 120
ctgtcgtggt gtgccagatc caaaaatcag gatctacgat gttggtatga agaggaaggg 180
tgttgatgag ttccatggc gtctctcttt atctctctc ggcc

(2) INFORMATION FOR SEQ ID NO:1159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1159:

Phe Phe Arg Arg Ala Ala Leu Phe Gly Arg Gly Ile Lys Arg
1 5 10 15
Asp Ala Met Gly Arg Arg Pro Ala Arg Cys Tyr Arg Gln Ile Lys Gly
20 25 30
Lys Pro Tyr Pro Lys Ser Arg Tyr Cys Arg Gly Val Pro Asp Pro Lys
35 40 45
Ile Arg Ile Tyr Asp Val Gly Met Lys Arg Lys Gly Val Asp Glu Phe
50 55 60
Pro Trp Arg Leu Ser Leu Ser Phe Leu Gly
65 70

(2) INFORMATION FOR SEQ ID NO:1160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..56
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499760

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1160:

Met Gly Arg Arg Pro Ala Arg Cys Tyr Arg Gln Ile Lys Gly Lys Pro
1 5 10 15
Tyr Pro Lys Ser Arg Tyr Cys Arg Gly Val Pro Asp Pro Lys Ile Arg
20 25 30
Ile Tyr Asp Val Gly Met Lys Arg Lys Gly Val Asp Glu Phe Pro Trp
35 40 45
Arg Leu Ser Leu Ser Phe Leu Gly

50 55
(2) INFORMATION FOR SEQ ID NO:1161:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1331 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1331
(D) OTHER INFORMATION: / Ceres Seq. ID 1499765
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1161:
attttttctt tcttcttcat ttttctatct acattctctg aaactcatat catattttca 60
aagctcttaa cccaaaaaac ctaagtcttt tttttcttca aattattggt tatattaatg 120
ttttaagcta tgatggatat gactcctaca ataacaacaa caacaacacc aactcctaaa 180
tcaccgcgac ccgaatccga aactccgacc cggatccaac cggcgaaaacc catttctttt 240
agcaacggca tcatcaaacg ccaccaccac caccaccatc ctctcctctt tacttacaaa 300
gaatgtctca aaaaaccacg ggcggttita ggtggtcacg ctctcgacgg ttgcggcgaa 360
ttcatgcggt ctccgtcgtc aatctcctcc gatccaactt ctctcaaatg tgcgtgcctg 420
tggtctccac cgtaatttcc accgcggtga tccagataac aacaacgact cttcccaaat 480
ccctctctct ccttccactg bcgtagagaa tcaactctac caccgtcact atccaccacc 540
accaccactt cctccaccac cacgtagctc taactcagct tctctctcac caattcttct 600
ctctttacatg ctctttatct tctcgggtac taataacaac aacaacaact tagcttcttt 660
ctcgcgatct aaacttctcg ccggaacaaa ccaccaccac caccaccaac atactcttca 720
cggatctctg aaaaagattc gaacaaaatt cagccagttt cagaaaagaga agatgatga 780
attcgcgcaa cgtgtgtggt ggaagatgca aaaacgtgac saagacgatg ttcgtgatgt 840
ttgcggcgag atcggagttg ataaaagtgt tctcaaatgt tggatgcata acaacaaaaa 900
cacctttaa cgcggtgata tcgcgggaaa cgagatccgg caaatcgata acggcggagg 960
aaaccacact ccgattctcg ccggcgagat taataaccat acaatggac accacgtgat 1020
cggagagaga ggagagcttc accagagtgt tagtagcgcg ggtggtggcg gaggatttga 1080
tagttagatc gcggagacta accgttggtaa cgttaacgga tcatcgctgt cgttgagtta 1140
aagatgagag tgcaggttta ataagaagct tagagtaagc ttattcgtat tatcatcggt 1200
aataactttc tattaatat taattaagat ctttagcttt gttgttttt gcattattat 1260
tagttttgat ttaatgttct ttaccacgct ggtgtctcgc tcgatgagga ataataccat 1320
aacaatgttc g
(2) INFORMATION FOR SEQ ID NO:1162:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..175
(D) OTHER INFORMATION: / Ceres Seq. ID 1499766
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1162:
Met Leu Leu Ser Leu Ser Gly Thr Asn Asn Asn Asn Asn Asn Leu Ala
1 5 10 15
Ser Phe Ser Asp Leu Asn Phe Ser Ala Gly Asn Asn His His His His
20 25 30
His Gln His Thr Leu His Gly Ser Arg Lys Arg Phe Arg Thr Lys Phe
35 40 45
Ser Gln Phe Gln Lys Glu Lys Met His Glu Phe Ala Glu Arg Val Gly
50 55 60
Trp Lys Met Gln Lys Arg Asp Xaa Asp Asp Val Arg Asp Phe Cys Arg
65 70 75 80
Gln Ile Gly Val Asp Lys Ser Val Leu Lys Val Trp Met His Asn Asn
85 90 95
Lys Asn Thr Phe Asn Arg Arg Asp Ile Ala Gly Asn Glu Ile Arg Gln

Met	Asn	Ser	Pro	Asn	Val	Leu	Val	Gly	Arg	Cys	Lys	Asn	Val	Xaa	Lys
1			5					10						15	
Thr	Met	Phe	Val	Ile	Phe	Ala	Gly	Arg	Ser	Glu	Leu	Ile	Lys	Val	Phe
			20					25					30		
Ser	Lys	Phe	Gly	Cys	Ile	Thr	Thr	Lys	Thr	Pro	Leu	Thr	Ala	Val	Ile
			35				40					45			
Ser	Pro	Glu	Thr	Arg	Ser	Gly	Lys	Ser	Ile	Thr	Ala	Glu	Glu	Thr	Thr
			50			55					60				
Leu	Arg	Phe	Ser	Pro	Ala	Arg	Leu	Ile	Thr	Ile	Thr	Met	Asp	Thr	Thr
65					70				75					80	
Val	Ser	Glu	Glu	Glu	Glu	Ser	Phe	Thr	Arg	Val	Leu	Val	Ala	Ala	Val
				85					90					95	

Val Ala Glu Asp Leu Ile Val Ile Ala Ala Glu Leu Thr Val Val Thr
100 105 110
Leu Thr Asp His Arg Arg Arg Glu Val Lys Asp Glu Ser Val Arg Leu
115 120 125
Ile Arg Ser Leu Glu
130

(2) INFORMATION FOR SEQ ID NO:1165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..491
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499769

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1165:

aatttgctaa	ggaaaaaaa	aacgaaaacg	tgtgtctgtc	tcttctcgta	gcgtctctca	60
agctcagatg	aattttgggt	tgccaagtat	atcttggttt	ggtagcatca	gcacaaagaa	120
agatgtagct	atgattgatt	ccgtgacacc	aacaacaact	tctotattgg	aacagccaga	180
gcaagagaaa	gcaacaacct	tctttctcaa	acagccagag	aaagagaaa	gcttatttga	240
tataaagata	tggacttggt	cctccttcag	ttcagttctt	ccttggtctg	caaattgcctc	300
tgatggtaag	cagaaaccca	ctactatcaa	cagaggggta	aaaaggcatg	ctctttctct	360
gaggtcatca	aggatcaaat	gggtgtaata	ctgtttatcg	gtttagacct	tatgggtgtct	420
aagggttcgt	ggcatacagg	gacgarggcg	tttckgtcac	agcttttccc	gagatatgga	480
cattatttgt	g					

(2) INFORMATION FOR SEQ ID NO:1166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..112
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499770

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1166:

Met	Asn	Phe	Gly	Leu	Pro	Ser	Ile	Ser	Trp	Phe	Gly	Ser	Ile	Ser	Thr	
1			5					10					15			
Lys	Lys	Asp	Val	Ala	Met	Ile	Asp	Ser	Val	Thr	Pro	Thr	Thr	Thr	Ser	
			20					25					30			
Leu	Leu	Glu	Gln	Pro	Glu	Gln	Glu	Lys	Ala	Thr	Thr	Phe	Leu	Leu	Lys	
			35					40					45			
Gln	Pro	Glu	Lys	Glu	Lys	Gly	Leu	Phe	Asp	Ile	Lys	Ile	Trp	Thr	Trp	
			50				55					60				
Ser	Ser	Phe	Ser	Ser	Val	Leu	Pro	Trp	Ser	Ala	Asn	Ala	Ser	Asp	Gly	
							70					75			80	
Lys	Gln	Lys	Pro	Thr	Thr	Ile	Asn	Arg	Gly	Leu	Lys	Arg	His	Ala	Leu	
							85					90			95	
Ser	Arg	Arg	Ser	Ser	Arg	Ile	Lys	Trp	Cys	Glu	Tyr	Cys	Leu	Ser	Val	
							100			105			110			

(2) INFORMATION FOR SEQ ID NO:1167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..91

(D) OTHER INFORMATION: / Ceres Seq. ID 1499771

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1167:

Met	Ile	Asp	Ser	Val	Thr	Pro	Thr	Thr	Thr	Ser	Leu	Leu	Glu	Gln	Pro
1			5						10					15	
Glu	Gln	Glu	Lys	Ala	Thr	Thr	Phe	Leu	Leu	Lys	Gln	Pro	Glu	Lys	Glu
			20					25				30			
Lys	Gly	Leu	Phe	Asp	Ile	Lys	Ile	Trp	Thr	Trp	Ser	Ser	Phe	Ser	Ser
		35					40				45				
Val	Leu	Pro	Trp	Ser	Ala	Asn	Ala	Ser	Asp	Gly	Lys	Gln	Lys	Pro	Thr
	50					55					60				
Thr	Ile	Asn	Arg	Gly	Leu	Lys	Arg	His	Ala	Leu	Ser	Arg	Arg	Ser	Ser
	65				70					75				80	
Arg	Ile	Lys	Trp	Cys	Glu	Tyr	Cys	Leu	Ser	Val					
			85					90							

(2) INFORMATION FOR SEQ ID NO:1168:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1277 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1277

(D) OTHER INFORMATION: / Ceres Seq. ID 1499772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1168:

attttcttctt	cacggttaga	tttttctcgc	cttaattttc	caataacgct	ctcagagaga	60
ccatttgatg	aagctttctgc	cttctggaat	ttgaaaagga	tttgataaga	cgaattcata	120
gaagattacc	gcaagttcat	caactttttg	aacttggtat	ggagataatc	tcactgaaac	180
ttgtgcccc	gtgetctgtg	gttacttgga	gtagtaaat	agcaacgata	agattggtcc	240
caaatcggtc	aagtttggtta	ttctcagggg	tcaaaaaatc	cagacttggt	attcgaagtg	300
gaaattccga	tggttatggt	gttggtgaga	atgatgactt	gggtcgtata	gccagaagag	360
gagaatcaac	gtcaaaaggt	ttgattcctg	gtttgcctga	tgaatcaaat	gggtgaaattg	420
ctgctcgaa	cagtcattct	cactgcgagt	ggaagcccaa	gcttagagta	cattatgaga	480
aagccggttg	tgacaatctc	gatgctcctg	cgggtgtggt	tcttccctggc	ttggcggttg	540
gttcatttca	ctatgagaag	cagcttaccg	atttgggaag	ggattatcga	gtatgggcta	600
ttgattttct	tggacagggt	ttatctctcc	ctactgaaga	tcctactacc	atgactgaag	660
aaacagcttc	ctcggaaagt	aaggaaccat	tttggggatt	tggtgacaaa	actgaaccgt	720
gggctgatca	actttgtatt	ctctctggtc	tctggaggga	tcaaagttac	tattttgtag	780
aagagggttat	cggtgagcct	gtgtacattg	ctgggaactc	acttggaggg	tatgtagctc	840
tctactttgc	agcaaccatc	ctctacactg	ttaagggtgt	taccttgctt	aatgcaaac	900
ctttctgggg	ttttctccct	aatccagtaa	gatccccaaa	gctagcacgt	ctctttccat	960
ggccccggagc	attccctctg	ccggaagag	tgaaaaaaaaa	tcacagaatt	gggtgtggcaa	1020
aagataagtg	atcctgaaa	catagctgag	atacttaaac	aggtctacac	agaccattct	1080
accaatgtgg	ataaagtatt	ctcacgtatt	gtggagggtca	cacagcatcc	ggctgtgtca	1140
gcatacgtttg	cttcaattat	gcttgcctct	ggtggagagc	tatctttctc	cgaagcttta	1200
tctagtgata	aggaatacaa	gttgcagata	tgtctcatgt	atggaagaga	agatccatgg	1260
gtgagaccgt	tatgggg					

(2) INFORMATION FOR SEQ ID NO:1169:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 290 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..290

(D) OTHER INFORMATION: / Ceres Seq. ID 1499773

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1169:

Met Glu Ile Ile Ser Leu Asn Val Val Pro Gln Cys Ser Val Val Thr
1 5 10 15
Trp Ser Ser Lys Leu Ala Thr Ile Arg Leu Val Pro Asn Arg Ser Ser
20 25 30
Leu Leu Phe Ser Gly Val Lys Lys Ser Arg Leu Val Ile Arg Ser Gly
35 40 45
Asn Ser Asp Gly Tyr Val Val Gly Glu Asn Asp Asp Leu Gly Arg Ile
50 55 60
Ala Arg Arg Gly Glu Ser Thr Ser Lys Val Leu Ile Pro Gly Leu Pro
65 70 75 80
Asp Glu Ser Asn Gly Glu Ile Ala Ala Arg Ile Ser His Ser His Cys
85 90 95
Glu Trp Lys Pro Lys Leu Arg Val His Tyr Glu Lys Ala Gly Cys Asp
100 105 110
Asn Leu Asp Ala Pro Ala Val Leu Phe Leu Pro Gly Phe Gly Val Gly
115 120 125
Ser Phe His Tyr Glu Lys Gln Leu Thr Asp Leu Gly Arg Asp Tyr Arg
130 135 140
Val Trp Ala Ile Asp Phe Leu Gly Gln Gly Leu Ser Leu Pro Thr Glu
145 150 155 160
Asp Pro Thr Thr Met Thr Glu Glu Thr Ser Ser Ser Glu Asp Lys Glu
165 170 175
Pro Phe Trp Gly Phe Gly Asp Lys Thr Glu Pro Trp Ala Asp Gln Leu
180 185 190
Val Phe Ser Leu Asp Leu Trp Arg Asp Gln Val Gln Tyr Phe Val Glu
195 200 205
Glu Val Ile Gly Glu Pro Val Tyr Ile Ala Gly Asn Ser Leu Gly Gly
210 215 220
Tyr Val Ala Leu Tyr Phe Ala Ala Thr His Pro His Leu Val Lys Gly
225 230 235 240
Val Thr Leu Leu Asn Ala Thr Pro Phe Trp Gly Phe Phe Pro Asn Pro
245 250 255
Val Arg Ser Pro Lys Leu Ala Arg Leu Phe Pro Trp Gly Ala Phe
260 265 270
Pro Leu Pro Glu Arg Val Lys Lys Asn His Arg Ile Gly Val Ala Lys
275 280 285
Asp Lys
290

(2) INFORMATION FOR SEQ ID NO:1170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1843 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1843

(D) OTHER INFORMATION: / Ceres Seq. ID 1499777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1170:

acacacaccaa	agcggttaga	aaaaaaaaacag	cgataaaacc	gaaacatcaa	gcaaacaaaa	60
aaaaagagga	gaattttttt	ttttgttttt	cgttttcaaa	acaaaaatct	ttgaatttta	120
tggcaaccgc	tcttctccga	acaaacttta	tccggcgatc	ttaccgttta	cccgctttta	180
gcccggtggg	tctctccacc	gtgactgttt	ccacgcgcgt	cgtcccgagg	attctctcct	240
ttggacaaca	agcaccggaa	ccacctcttc	accacccaaa	accacactga	caatctcacg	300
atggtctcga	tctctccgat	caagcccgctc	ttttctcttc	tatcccaacc	tttgatctcc	360
tccggtccac	cgccggtgtg	catgcggcgg	cgataggtcc	tatggtcgac	ctagggacgt	420
gggtcatgag	ctctaaactt	atggacgctt	ccgtgacgcg	tggcatggtt	ttagggcttg	480

tgaaaagtac	gttttatgac	catttttgcg	cgggtgaaga	tgccgacgca	gcgcgtgagc	540
gcgtgagaag	cgtttatgaa	gctaccggtc	ttaaagggat	gcttgctctat	gcgcgtgaaac	600
acgcgcgatga	cgctgtatct	tgtgatgata	acatgcaaca	attcatcgca	accattgaag	660
ctgcacaaatc	tttaaccaac	tctcacttta	gctcagtggt	tgtagaagata	attgcacatt	720
gtcccaattag	tcttctgaaa	cgagttagcg	atctgcttcg	gtgggaatac	aaaagtccaa	780
acttcaaaact	ctcatgggaag	ctcaaatcgt	tcccggtttt	ctccgattcg	agtcctctct	840
accacacaaa	ctcagaaccg	gaaccggtta	cgcgggaaga	agaacgggag	ctcgaagcag	900
ctcatgggaag	gattcaagaa	atctgttagga	aatgccaaaag	agtcacaaat	accattgttg	960
attgatgcgg	aagacacaa	cctccaaccc	gcgatcgatt	acatggctta	ttcatcgggc	1020
atcatgttca	atgctgacaa	agaccgacca	atcgtttaca	acacgattca	ggcgtaactt	1080
agagacgcgg	gtgagagact	gcatttgcca	gtacaaaatc	ctgagaaaag	gaatgttctt	1140
atgggggttca	agttggtgag	aggggcttac	atgtctagcg	aagctagctt	ggcggattcc	1200
ctggggttcca	agtcgccagt	ccacgacaca	attcaggata	ctcactcttg	ttacaatgat	1260
tgtatgacat	tcttgatgga	gaagacatca	aacgggtctg	gttctgggtg	cgttctcgca	1320
acacataaacg	ctgatttcggg	gagacttgcg	tcgaggaaaag	cgagtgdhct	cggttatgat	1380
aaacagaacg	ggaagataga	gtttgcacag	ctatatggta	tgctggatgc	attgtctctg	1440
gtttaaagag	agccgggttc	aattgttaga	agtacatgcc	gtttggaccc	gtcgcaacgc	1500
ctataccgta	tcttctccga	cgcgcattat	agaaccgggg	aatgatggcc	accggagctc	1560
atgaccgtca	actcatgagg	atggaactta	agaggagatt	aatcgccggg	attgcgtaaa	1620
gagagagat	ggagccatta	aatgaatttg	ggaaatgtag	atgaataaat	ttcttctatg	1680
tagtttaaga	aattgaaaac	aaaaaattat	aatataagaa	atggagttag	taagaacatt	1740
tctctgggct	aaatatTTTT	catgagggac	tatgttttta	ctatcaatat	atcattcaca	1800
aatgtatatt	caccttatca	ataaaaatgt	ttttactttt	ttt		

(2) INFORMATION FOR SEQ ID NO:1171:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 320 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..320

(D) OTHER INFORMATION: / Ceres Seq. ID 1499778

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1171:

Thr	Thr	Lys	Ala	Phe	Arg	Lys	Lys	Thr	Ala	Ile	Lys	Pro	Lys	His	Gln
1			5					10						15	
Ala	Asn	Lys	Lys	Lys	Glu	Glu	Asn	Phe	Phe	Phe	Leu	Phe	Ser	Ser	Phe
			20				25					30			
Lys	Thr	Lys	Ser	Leu	Asn	Phe	Met	Ala	Thr	Arg	Leu	Leu	Arg	Thr	Asn
			35				40					45			
Phe	Ile	Arg	Arg	Ser	Tyr	Arg	Leu	Pro	Ala	Phe	Ser	Pro	Val	Gly	Pro
			50			55					60				
Pro	Thr	Val	Thr	Ala	Ser	Thr	Ala	Val	Val	Pro	Glu	Ile	Leu	Ser	Phe
			65			70				75				80	
Gly	Gln	Gln	Ala	Pro	Glu	Pro	Pro	Leu	His	His	Pro	Lys	Pro	Thr	Glu
			85				90					95			
Gln	Ser	His	Asp	Gly	Leu	Asp	Leu	Ser	Asp	Gln	Ala	Arg	Leu	Phe	Ser
			100				105					110			
Ser	Ile	Pro	Thr	Ser	Asp	Leu	Leu	Arg	Ser	Thr	Ala	Val	Leu	His	Ala
			115				120					125			
Ala	Ala	Ile	Gly	Pro	Met	Val	Asp	Leu	Gly	Thr	Trp	Val	Met	Ser	Ser
			130			135					140				
Lys	Leu	Met	Asp	Ala	Ser	Val	Thr	Arg	Gly	Met	Val	Leu	Gly	Leu	Val
			145			150				155				160	
Lys	Ser	Thr	Phe	Tyr	Asp	His	Phe	Cys	Ala	Gly	Glu	Asp	Ala	Asp	Ala
			165				170							175	
Ala	Ala	Glu	Arg	Val	Arg	Ser	Val	Tyr	Glu	Ala	Thr	Gly	Leu	Lys	Gly
			180				185						190		
Met	Leu	Val	Tyr	Gly	Val	Glu	His	Ala	Asp	Asp	Ala	Val	Ser	Cys	Asp
			195				200					205			

Asp	Asn	Met	Gln	Gln	Phe	Ile	Arg	Thr	Ile	Glu	Ala	Ala	Lys	Ser	Leu	
210						215				220						
Pro	Thr	Ser	His	Phe	Ser	Ser	Val	Val	Val	Lys	Ile	Thr	Ala	Ile	Cys	
225				230						235					240	
Pro	Ile	Ser	Leu	Leu	Lys	Arg	Val	Ser	Asp	Leu	Leu	Arg	Trp	Glu	Tyr	
			245						250					255		
Lys	Ser	Pro	Asn	Phe	Lys	Leu	Ser	Trp	Lys	Leu	Lys	Ser	Phe	Pro	Val	
			260					265					270			
Phe	Ser	Asp	Ser	Ser	Pro	Leu	Tyr	His	Thr	Asn	Ser	Glu	Pro	Glu	Pro	
		275					280					285				
Leu	Thr	Ala	Glu	Glu	Glu	Arg	Glu	Leu	Glu	Ala	Ala	His	Gly	Arg	Ile	
		290				295				300						
Gln	Glu	Ile	Cys	Arg	Lys	Cys	Gln	Arg	Val	Gln	Cys	Thr	Ile	Val	Asp	
305					310					315					320	

(2) INFORMATION FOR SEQ ID NO:1172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..281
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1172:

Met	Ala	Thr	Arg	Leu	Leu	Arg	Thr	Asn	Phe	Ile	Arg	Arg	Ser	Tyr	Arg	
1			5					10					15			
Leu	Pro	Ala	Phe	Ser	Pro	Val	Gly	Pro	Pro	Thr	Val	Thr	Ala	Ser	Thr	
		20					25						30			
Ala	Val	Val	Pro	Glu	Ile	Leu	Ser	Phe	Gly	Gln	Gln	Ala	Pro	Glu	Pro	
		35				40					45					
Pro	Leu	His	His	Pro	Lys	Pro	Thr	Glu	Gln	Ser	His	Asp	Gly	Leu	Asp	
	50				55					60						
Leu	Ser	Asp	Gln	Ala	Arg	Leu	Phe	Ser	Ser	Ile	Pro	Thr	Ser	Asp	Leu	
65				70						75				80		
Leu	Arg	Ser	Thr	Ala	Val	Leu	His	Ala	Ala	Ala	Ile	Gly	Pro	Met	Val	
			85					90					95			
Asp	Leu	Gly	Thr	Trp	Val	Met	Ser	Ser	Lys	Leu	Met	Asp	Ala	Ser	Val	
			100					105					110			
Thr	Arg	Gly	Met	Val	Leu	Gly	Leu	Val	Lys	Ser	Thr	Phe	Tyr	Asp	His	
		115				120						125				
Phe	Cys	Ala	Gly	Glu	Asp	Ala	Asp	Ala	Ala	Ala	Glu	Arg	Val	Arg	Ser	
		130				135					140					
Val	Tyr	Glu	Ala	Thr	Gly	Leu	Lys	Gly	Met	Leu	Val	Tyr	Gly	Val	Glu	
145				150					155					160		
His	Ala	Asp	Asp	Ala	Val	Ser	Cys	Asp	Asn	Met	Gln	Gln	Phe	Ile		
		165						170					175			
Arg	Thr	Ile	Glu	Ala	Ala	Lys	Ser	Leu	Pro	Thr	Ser	His	Phe	Ser	Ser	
		180						185					190			
Val	Val	Val	Lys	Ile	Thr	Ala	Ile	Cys	Pro	Ile	Ser	Leu	Leu	Lys	Arg	
		195					200					205				
Val	Ser	Asp	Leu	Leu	Arg	Trp	Glu	Tyr	Lys	Ser	Pro	Asn	Phe	Lys	Leu	
		210				215					220					
Ser	Trp	Lys	Leu	Lys	Ser	Phe	Pro	Val	Phe	Ser	Asp	Ser	Ser	Pro	Leu	
225				230						235					240	
Tyr	His	Thr	Asn	Ser	Glu	Pro	Glu	Pro	Leu	Thr	Ala	Glu	Glu	Glu	Arg	
			245						250				255			
Glu	Leu	Glu	Ala	Ala	His	Gly	Arg	Ile	Gln	Glu	Ile	Cys	Arg	Lys	Cys	

260 265 270
Gln Arg Val Gln Cys Thr Ile Val Asp
275 280
(2) INFORMATION FOR SEQ ID NO:1173:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 187 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..187
(D) OTHER INFORMATION: / Ceres Seq. ID 1499780
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1173:
Met Val Asp Leu Gly Thr Trp Val Met Ser Ser Lys Leu Met Asp Ala
1 5 10 15
Ser Val Thr Arg Gly Met Val Leu Gly Leu Val Lys Ser Thr Phe Tyr
20 25 30
Asp His Phe Cys Ala Gly Glu Asp Ala Asp Ala Ala Glu Arg Val
35 40 45
Arg Ser Val Tyr Glu Ala Thr Gly Leu Lys Gly Met Leu Val Tyr Gly
50 55 60
Val Glu His Ala Asp Asp Ala Val Ser Cys Asp Asp Asn Met Gln Gln
65 70 75 80
Phe Ile Arg Thr Ile Glu Ala Ala Lys Ser Leu Pro Thr Ser His Phe
85 90 95
Ser Ser Val Val Val Lys Ile Thr Ala Ile Cys Pro Ile Ser Leu Leu
100 105 110
Lys Arg Val Ser Asp Leu Leu Arg Trp Glu Tyr Lys Ser Pro Asn Phe
115 120 125
Lys Leu Ser Trp Lys Leu Lys Ser Phe Pro Val Phe Ser Asp Ser Ser
130 135 140
Pro Leu Tyr His Thr Asn Ser Glu Pro Glu Pro Leu Thr Ala Glu Glu
145 150 155 160
Glu Arg Glu Leu Glu Ala Ala His Gly Arg Ile Gln Glu Ile Cys Arg
165 170 175
Lys Cys Gln Arg Val Gln Cys Thr Ile Val Asp
180 185

(2) INFORMATION FOR SEQ ID NO:1174:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 553 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..553
(D) OTHER INFORMATION: / Ceres Seq. ID 1499785
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1174:
gacgttggttt cttatatcgt tgccagagag agtttgacgg cggagagata tggcggcggtt 60
gatggagatca gtctgctggcc gagctctaaa attctcatcg acggcgcaatt tcaggtcaat 120
ccgacgcggc gaaacaccaa cactctgtat caaatcattc tccaccatta tgtcaccacc 180
gtcaaaagcc atcgtcttacg aagaacacgg ctctcccgat tccgtcacca gattgggtgaa 240
tctcccgccg gtggaagtga aagaaaaacga cgtttgtgtt aaatgatcg ccgctccgat 300
caaccctcc gatatacaatc gaattgaagg tgtgtatccg gtgagggcac cggtagccagc 360
ggttgggtgt tatgaaggtg ttggtgaagt ttatgcagtt ggctccaatg ttaatggttt 420
ttctctgtgt gattgggtca ttccatctcc acottcttca gggacttggc agacttatgt 480
tgtgaaggaa gagagtgtgt ggcacaaaaa cgataaagag tgtccaatgg agtatgcagc 540
gacgattact gtt

(2) INFORMATION FOR SEQ ID NO:1175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..168
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499786

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1175:

Met Ala Ala Leu Met Glu Ser Val Val Gly Arg Ala Leu Lys Phe Ser
1 5 10 15
Ser Thr Ala Asn Phe Arg Ser Ile Arg Arg Gly Glu Thr Pro Thr Leu
20 25 30
Cys Ile Lys Ser Phe Ser Thr Ile Met Ser Pro Pro Ser Lys Ala Ile
35 40 45
Val Tyr Glu Glu His Gly Ser Pro Asp Ser Val Thr Arg Leu Val Asn
50 55 60
Leu Pro Pro Val Glu Val Lys Glu Asn Asp Val Cys Val Lys Met Ile
65 70 75 80
Ala Ala Pro Ile Asn Pro Ser Asp Ile Asn Arg Ile Glu Gly Val Tyr
85 90 95
Pro Val Arg Pro Pro Val Pro Ala Val Gly Gly Tyr Glu Gly Val Gly
100 105 110
Glu Val Tyr Ala Val Gly Ser Asn Val Asn Gly Phe Ser Pro Gly Asp
115 120 125
Trp Val Ile Pro Ser Pro Pro Ser Ser Gly Thr Trp Gln Thr Tyr Val
130 135 140
Val Lys Glu Glu Ser Val Trp His Lys Ile Asp Lys Glu Cys Pro Met
145 150 155 160
Glu Tyr Ala Ala Thr Ile Thr Val
165

(2) INFORMATION FOR SEQ ID NO:1176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..164
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499787

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1176:

Met Glu Ser Val Val Gly Arg Ala Leu Lys Phe Ser Ser Thr Ala Asn
1 5 10 15
Phe Arg Ser Ile Arg Arg Gly Glu Thr Pro Thr Leu Cys Ile Lys Ser
20 25 30
Phe Ser Thr Ile Met Ser Pro Pro Ser Lys Ala Ile Val Tyr Glu Glu
35 40 45
His Gly Ser Pro Asp Ser Val Thr Arg Leu Val Asn Leu Pro Pro Val
50 55 60
Glu Val Lys Glu Asn Asp Val Cys Val Lys Met Ile Ala Ala Pro Ile
65 70 75 80
Asn Pro Ser Asp Ile Asn Arg Ile Glu Gly Val Tyr Pro Val Arg Pro
85 90 95
Pro Val Pro Ala Val Gly Gly Tyr Glu Gly Val Gly Glu Val Tyr Ala
100 105 110
Val Gly Ser Asn Val Asn Gly Phe Ser Pro Gly Asp Trp Val Ile Pro

(2) INFORMATION FOR SEQ ID NO:1177:

(A) LENGTH: 128 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

```
(A) NAME/KEY: peptid
(B) LOCATION: 1..128
(D) OTHER INFORMATION
```

(2) INFORMATION FOR SEQ ID NO:1178:

(A) LENGTH: 1910 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) NAME/KEY: -
(B) LOCATION: 1..1910
(D) OTHER INFORMATION: / Ceres Seq. ID 1499789

(X1) SEQUENCE DESCRIPTION						
atttaaaaaa	gaaaaaaagaa	gaaaagagag	agagagactc	acaatacata	atatctctct	60
cattaaactca	taatcacttt	aaagaacatt	ggatcagatc	tcattacata	gggatgtgta	120
tgaaaaagct	aaacacaacca	gttctagtaa	ctctgtccga	ctatagaagc	gggatgaataa	180
aaatcgctga	tgctgaattt	tgtggtgatc	tcttgtagag	ctatagattt	ggtaaaagata	240
attgttcocg	ccgagaattt	cgatcaactc	cggcagcgac	ggctccggcg	ccggtacaaca	300
ccacgcagat	agagtgtgaa	gaggtataat	atggatctca	agctcaacac	aacaaattctg	360
ttagtgcaga	tacatcattg	ctattttcog	attcagatcc	ataagtactt	gagagatctg	420
tgacgcgaac	cggttcaaac	gaagaattctg	aaaccggctc	aaacgcaga	aatgtgtaata	480
atttggttaga	tgcgagctcc	acaaacttgc	caaatgtaga	gaacaaaaag	caacggaatg	540
gagagaattg	tgatagatgaa	gagaaagaa	aaataaaca	gagatcata	tcggattcag	600
aaagatagat	aaacctagag	aagtgtcttc	ggacacaa	aaactattg	cttggaaatg	660
aqagatgaqa	aaagaacag	cagatctcgt	cagatcaga	agaagaagta	aacctagaga	720

attttcttgc	gacacaagaa	aactacgagc	tttactgtcc	tagctgtagc	acatgtatca	780
ccagaaatgt	gggtctcaag	aaaaaaaac	gaggggaagca	cgtaaatcca	tctctggatc	840
tgaacccga	tataccgggt	gttgaaacgg	acgaaccaag	cgacattgag	gagatggaat	900
caccagttaa	gggttatgtc	cctgagactc	ggattgagga	tgatcaagaa	gataaagagg	960
gaactatctt	tacttggctt	gtttgtgac	taagtactt	catccgggta	ggaacaaaat	1020
tcttacaact	tgattatata	aggggaaaac	cggttgagaa	atcagttgaa	gaatatatat	1080
atgtgaggaa	gagtataaac	accacacaat	caccacacca	aattcaaccg	gacggagaaa	1140
gattcggcat	tgagttgtta	aagagcaccg	tctacggcgg	tctcactgag	accatcacca	1200
gcctcggcgt	tgtatcatct	gcttctgcct	ctggttctct	caccatgaat	atattgscct	1260
ttgctgtcgc	aaatttggcc	gggtgggtca	tcgtcctcgc	tcaaaacttt	caagatctaa	1320
gaacacgttt	agatcaagag	aaagataggt	acgaggaatt	gttaggggaga	cgtactataat	1380
cccggataca	tatcttagta	cggtcatgt	cttaccatttt	cttcggccta	attcctccgt	1440
tagtttaacg	attttctctt	tacgaaacgg	gaatcaagaa	ctacaagctc	atctcggttt	1500
tcttgggttc	cttgggtttgc	gtaattttgc	tcggttcgat	caaggtctat	gtccgaaaaac	1560
caaccaattc	atgtggatcg	actaaagctt	atctcaaatc	tcgcgcttat	tatacgtcta	1620
ttgttgttgc	ttcttgcgga	atctcatacg	ttgtcggaga	tattatggga	gagtatatcg	1680
agaagctcag	tttgggttgt	ttagaccaga	tcagataaac	ttcaccatgt	tatggaatta	1740
aacccgagga	gtgcgggttt	acttctcttt	aatatacagt	gggacataaga	accggtctga	1800
ccaacgttgt	ataatttctg	ttctaattac	ttactaaatc	tcgtatcttt	ttctagtaaa	1860
aaatcaaaac	taagtcttct	atagaataaa	tgtgttttga	ggtttttctc		

(2) INFORMATION FOR SEQ ID NO:1179:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 589 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..589

(D) OTHER INFORMATION: / Ceres Seq. ID 1499790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1179:

Leu	Lys	Lys	Lys	Lys	Glu	Glu	Lys	Arg	Glu	Arg	Asp	Ser	Gln	Ile	Ile	
1			5					10					15			
Ile	Ser	Pro	Ser	Leu	Thr	His	Asn	His	Phe	Lys	Glu	His	Trp	Asn	Gln	
			20					25					30			
Ile	His	Tyr	Ile	Gly	Ile	Asp	Met	Glu	Lys	Ser	Asn	Gln	Pro	Val	His	
			35				40					45				
Val	Thr	Leu	Ser	Glu	Leu	Lys	Asp	Gly	Asp	Lys	Glu	Ile	Val	Asp	Ala	
			50			55					60					
Glu	Phe	Leu	Val	Asp	Leu	Leu	Glu	Ser	Tyr	Arg	Phe	Gly	Lys	Asp	Asn	
65				70					75					80		
Val	Pro	Ala	Arg	Glu	Phe	Arg	Ser	Lys	Ala	Ala	Thr	Ala	Pro	Ala		
			85						90				95			
Pro	Val	Asn	Thr	Thr	Glu	Ile	Glu	Leu	Glu	Glu	Asp	Asn	Asp	Gly	Ser	
			100					105					110			
Gln	Ala	Gln	Gly	Asn	Asn	Ser	Val	Ser	Glu	Ser	Thr	Ser	Ser	Leu	Phe	
			115			120						125				
Ser	Asp	Ser	Asp	Pro	Ile	Val	Leu	Glu	Ser	Thr	Val	Ser	Glu	Thr	Gly	
			130			135					140					
Ser	Asn	Glu	Glu	Ser	Glu	Thr	Gly	Ser	Asn	Glu	Glu	Asn	Gly	Asn	Asn	
145				150					155					160		
Trp	Leu	Glu	Ser	Ser	Ser	Thr	Asn	Leu	Pro	Asn	Val	Glu	Asn	Lys	Arg	
				165					170					175		
Gln	Arg	Asn	Gly	Glu	Asp	Cys	Glu	Ile	Glu	Glu	Glu	Glu	Glu	Asn	Asn	
			180					185						190		
Glu	Arg	Ser	Leu	Ser	Asp	Ser	Glu	Glu	Lys	Ser	Asn	Leu	Glu	Lys	Leu	
			195				200					205				
Leu	Gly	Thr	Gln	Glu	Asn	Tyr	Glu	Leu	Gly	Asn	Glu	Asp	Glu	Glu	Lys	
			210			215					220					
Asn	Glu	Arg	Ser	Ser	Ser	Asp	Ser	Glu	Glu	Lys	Ser	Asn	Leu	Glu	Asn	

225 230 235 240
Phe Leu Ala Thr Gln Glu Asn Tyr Glu Leu Tyr Cys Pro Ser Cys Ser
245 250 255
Thr Cys Ile Thr Arg Asn Val Val Leu Lys Lys Arg Lys Arg Gly Lys
260 265 270
His Val Asn Ser Ser Leu Asp Leu Lys Pro Asp Ile Pro Val Val Glu
275 280 285
Pro Asp Glu Pro Ser Asp Ile Glu Glu Met Glu Ser Pro Val Lys Val
290 295 300
Tyr Val Pro Glu Thr Arg Ile Glu Asp Asp Gln Glu Asp Lys Glu Gly
305 310 315 320
Thr Ile Phe Thr Cys Leu Val Cys Asp Leu Lys Tyr Phe Ile Arg Leu
325 330 335
Gly Thr Lys Phe Leu Gln Leu Asp Tyr Ile Arg Gly Lys Pro Val Glu
340 345 350
Lys Ser Val Glu Glu Tyr Ile Asp Val Arg Lys Ser Ile Asn Thr Thr
355 360 365
Gln Ser Pro Pro Gln Ile Gln Pro Asp Gly Glu Arg Phe Ala Ile Glu
370 375 380
Leu Leu Lys Ser Thr Val Tyr Gly Gly Leu Thr Glu Thr Ile Thr Ser
385 390 395 400
Leu Gly Val Val Ser Ser Ala Ser Ala Ser Gly Ser Ser Thr Met Asn
405 410 415
Ile Leu Xaa Leu Ala Val Ala Asn Leu Ala Gly Gly Leu Ile Val Leu
420 425 430
Ala Gln Asn Phe Gln Asp Leu Arg Asn Ser Ser Asp Gln Glu Lys Asp
435 440 445
Arg Tyr Glu Glu Leu Leu Gly Arg Arg Thr Lys Ser Arg Ile His Ile
450 455 460
Leu Val Ala Val Met Ser Tyr Ile Phe Phe Gly Leu Ile Pro Pro Leu
465 470 475 480
Val Tyr Ala Phe Ser Phe Tyr Glu Thr Gly Ile Lys Asn Tyr Lys Leu
485 490 495
Ile Ser Val Phe Leu Gly Ser Leu Val Cys Val Ile Leu Leu Gly Ser
500 505 510
Ile Lys Val Tyr Val Arg Lys Pro Thr Asn Ser Cys Gly Ser Thr Lys
515 520 525
Ala Tyr Leu Lys Ser Ala Ala Tyr Tyr Thr Ser Ile Val Val Ala Ser
530 535 540
Cys Gly Ile Ser Tyr Val Val Gly Asp Ile Met Gly Glu Tyr Ile Glu
545 550 555 560
Lys Leu Ser Leu Val Gly Leu Asp Gln Ile Ser Ile Thr Ser Pro Cys
565 570 575
Tyr Gly Ile Lys Pro Glu Glu Cys Arg Phe Thr Ser Phe
580 585

(2) INFORMATION FOR SEQ ID NO:1180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 550 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..550
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499791

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1180:

Met Glu Lys Ser Asn Gln Pro Val His Val Thr Leu Ser Glu Leu Lys
1 5 10 15
Asp Gly Asp Lys Lys Glu Ile Val Asp Ala Glu Phe Leu Val Asp Leu Leu
20 25 30

Glu Ser Tyr Arg Phe Gly Lys Asp Asn Val Pro Ala Arg Glu Phe Arg
35 40 45
Ser Lys Ala Ala Ala Thr Ala Pro Ala Pro Val Asn Thr Thr Glu Ile
50 55 60
Glu Leu Glu Glu Asp Asn Asp Gly Ser Gln Ala Gln Gly Asn Asn Ser
65 70 75 80
Val Ser Glu Ser Thr Ser Ser Leu Phe Ser Asp Ser Asp Pro Ile Val
85 90 95
Leu Glu Ser Thr Val Ser Glu Thr Gly Ser Asn Glu Glu Ser Glu Thr
100 105 110
Gly Ser Asn Glu Glu Asn Gly Asn Asn Trp Leu Glu Ser Ser Ser Thr
115 120 125
Asn Leu Pro Asn Val Glu Asn Lys Arg Gln Arg Asn Gly Glu Asp Cys
130 135 140
Glu Ile Glu Glu Glu Glu Glu Asn Asn Glu Arg Ser Leu Ser Asp Ser
145 150 155 160
Glu Glu Lys Ser Asn Leu Glu Lys Leu Leu Gly Thr Gln Glu Asn Tyr
165 170 175
Glu Leu Gly Asn Glu Asp Glu Glu Lys Asn Glu Arg Ser Ser Ser Asp
180 185 190
Ser Glu Glu Lys Ser Asn Leu Glu Asn Phe Leu Ala Thr Gln Glu Asn
195 200 205
Tyr Glu Leu Tyr Cys Pro Ser Cys Ser Thr Cys Ile Thr Arg Asn Val
210 215 220
Val Leu Lys Lys Arg Lys Arg Gly Lys His Val Asn Ser Ser Leu Asp
225 230 235 240
Leu Lys Pro Asp Ile Pro Val Val Glu Pro Asp Glu Pro Ser Asp Ile
245 250 255
Glu Glu Met Glu Ser Pro Val Lys Val Tyr Val Pro Glu Thr Arg Ile
260 265 270
Glu Asp Asp Gln Glu Asp Lys Glu Gly Thr Ile Phe Thr Cys Leu Val
275 280 285
Cys Asp Leu Lys Tyr Phe Ile Arg Leu Gly Thr Lys Phe Leu Gln Leu
290 295 300
Asp Tyr Ile Arg Gly Lys Pro Val Glu Lys Ser Val Glu Glu Tyr Ile
305 310 315 320
Asp Val Arg Lys Ser Ile Asn Thr Thr Gln Ser Pro Pro Gln Ile Gln
325 330 335
Pro Asp Gly Glu Arg Phe Ala Ile Glu Leu Leu Lys Ser Thr Val Tyr
340 345 350
Gly Gly Leu Thr Glu Thr Ile Thr Ser Leu Gly Val Val Ser Ser Ala
355 360 365
Ser Ala Ser Gly Ser Ser Thr Met Asn Ile Leu Xaa Leu Ala Val Ala
370 375 380
Asn Leu Ala Gly Gly Leu Ile Val Leu Ala Gln Asn Phe Gln Asp Leu
385 390 395 400
Arg Asn Ser Ser Asp Gln Glu Lys Asp Arg Tyr Glu Glu Leu Glu Gly
405 410 415
Arg Arg Thr Lys Ser Arg Ile His Ile Leu Val Ala Val Met Ser Tyr
420 425 430
Ile Phe Phe Gly Leu Ile Pro Pro Leu Val Tyr Ala Phe Ser Phe Tyr
435 440 445
Glu Thr Gly Ile Lys Asn Tyr Lys Leu Ile Ser Val Phe Leu Gly Ser
450 455 460
Leu Val Cys Val Ile Leu Leu Gly Ser Ile Lys Val Tyr Val Arg Lys
465 470 475 480
Pro Thr Asn Ser Cys Gly Ser Thr Lys Ala Tyr Leu Lys Ser Ala Ala
485 490 495
Tyr Tyr Thr Ser Ile Val Val Ala Ser Cys Gly Ile Ser Tyr Val Val
500 505 510
Gly Asp Ile Met Gly Glu Tyr Ile Glu Lys Leu Ser Leu Val Gly Leu

Met	Asp	Pro	Met	Arg	Ile	Val	Ser	Cys	Ser	Arg	Ser	Asp	Trp	Leu	Leu
1				5					10					15	
Leu	Leu	Leu	Ser	Ser	Asp	Pro	Pro	Val	Pro	Ser	Pro	Phe	Ala	Asp	Ser
			20					25					30		
Ile	Thr	Pro	Thr	Pro	Pro	Val	Asp	Leu	Pro	Ser	Ser	Leu	Ser	Arg	Lys
		35					40					45			

Leu Val Lys Glu Lys Gln Ser Thr Asn Asn Thr Ser Leu Leu Ile Thr
50 55 60
Lys Glu Glu Gly Leu Glu Leu Tyr Glu Asp Met Ile Leu Gly Arg Ser
65 70 75 80
Phe Glu Asp Met Cys Ala Gln Met Tyr Tyr Arg Gly Lys Met Phe Gly
85 90 95
Phe Val His Leu Tyr Asn Gly Gln Glu Ala Val Ser Thr Gly Phe Ile
100 105 110
Lys Leu Leu Thr Lys Ser Asp Ser Val Val Ser Thr Tyr Arg Asp His
115 120 125
Val His Ala Leu Ser Lys Gly Val Ser Ala Arg Ala Val Met Ser Glu
130 135 140
Leu Phe Gly Lys Val Thr Gly Cys Cys Arg Gly Gln Gly Gly Ser Met
145 150 155 160
His Met Phe Ser Lys Glu His Asn Met Leu Gly Gly Phe Ala Phe Ile
165 170 175
Gly Glu Gly Ile Pro Val Ala Thr Gly Ala Ala Phe Ser Ser Lys Tyr
180 185 190
Arg Arg Glu Val Leu Lys Gln Asp Cys Asp Asp Val Thr Val Ala Phe
195 200 205
Phe Gly Asp Gly Thr Cys Asn Asn Gly Gln Phe Phe Glu Cys Leu Asn
210 215 220
Met Ala Ala Leu Tyr Lys Leu Pro Ile Ile Phe Val Val Glu Asn Asn
225 230 235 240
Leu Trp Ala Ile Gly Met Ser His Leu Arg Ala Thr Ser Asp Pro Glu
245 250 255
Ile Trp Lys Lys Gly Pro Ala Phe Gly Met Pro Gly Val His Val Asp
260 265 270
Gly Xaa Asp Val Leu Lys Val Arg Glu Val Ala Lys Glu Ala Val Thr
275 280 285
Arg Ala Arg Arg Gly Glu Gly Pro Thr Leu Val Glu Cys Glu Thr Tyr
290 295 300
Arg Phe Arg Gly His Ser Leu Ala Asp Pro Asp Glu Leu Arg Asp Ala
305 310 315 320
Ala Glu Lys Ala Lys Tyr Ala Ala Arg Asp Pro Ile Ala Ala Leu Lys
325 330 335
Lys Tyr Leu Ile Glu Asn Lys Leu Ala Lys Glu Ala Glu Leu Lys Ser
340 345 350
Ile Glu Lys Lys Ile Asp Glu Leu Val Glu Glu Ala Val Glu Phe Ala
355 360 365
Asp Ala Ser Pro Gln Pro Gly Arg Ser Gln Leu Leu Glu Asn Val Phe
370 375 380
Ala Asp Pro Lys Gly Phe Gly Ile Gly Pro Asp Gly Arg Tyr Arg Cys
385 390 395 400
Glu Asp Pro Lys Phe Thr Glu Gly Thr Ala Gln Val
405 410

(2) INFORMATION FOR SEQ ID NO:1183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..409
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499794

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1183:

Met Arg Ile Val Ser Cys Ser Arg Ser Asp Trp Leu Leu Leu Leu
1 5 10 15
Ser Ser Asp Pro Pro Val Pro Ser Pro Phe Ala Asp Ser Ile Thr Pro

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1184:

```

Met Ile Leu Gly Arg Ser Phe Glu Asp Met Cys Ala Gln Met Tyr Tyr
1           5           10           15
Arg Gly Lys Met Phe Gly Phe Val His Leu Tyr Asn Gly Gln Glu Ala
          20           25           30
Val Ser Thr Gly Phe Ile Lys Leu Thr Lys Ser Asp Ser Val Val
          35           40           45
Ser Thr Tyr Arg Asp His Val His Ala Leu Ser Lys Gly Val Ser Ala
          50           55           60
Arg Ala Val Met Ser Glu Leu Phe Gly Lys Val Thr Gly Cys Cys Arg
65          70          75          80
Gly Gln Gly Gly Ser Met His Met Phe Ser Lys Glu His Asn Met Leu
          85          90          95
Gly Gly Phe Ala Phe Ile Gly Glu Gly Ile Pro Val Ala Thr Gly Ala
          100         105         110
Ala Phe Ser Ser Lys Tyr Arg Arg Glu Val Leu Lys Gln Asp Cys Asp
          115         120         125
Asp Val Thr Val Ala Phe Phe Gly Asp Gly Thr Cys Asn Asn Gly Gln
          130         135         140
Phe Phe Glu Cys Leu Asn Met Ala Ala Leu Tyr Lys Leu Pro Ile Ile
145         150         155         160
Phe Val Val Glu Asn Asn Leu Trp Ala Ile Gly Met Ser His Leu Arg
          165         170         175
Ala Thr Ser Asp Pro Glu Ile Trp Lys Lys Gly Pro Ala Phe Gly Met
          180         185         190
Pro Gly Val His Val Asp Gly Xaa Asp Val Leu Lys Val Arg Glu Val
          195         200         205
Ala Lys Glu Ala Val Thr Arg Ala Arg Arg Gly Glu Gly Pro Thr Leu
          210         215         220
Val Glu Cys Glu Thr Tyr Arg Phe Arg Gly His Ser Leu Ala Asp Pro
225         230         235         240
Asp Glu Leu Arg Asp Ala Ala Glu Lys Ala Lys Tyr Ala Ala Arg Asp
          245         250         255
Pro Ile Ala Ala Leu Lys Lys Tyr Leu Ile Glu Asn Lys Leu Ala Lys
          260         265         270
Glu Ala Glu Leu Lys Ser Ile Glu Lys Lys Ile Asp Glu Leu Val Glu
          275         280         285
Glu Ala Val Glu Phe Ala Asp Ala Ser Pro Gln Pro Gly Arg Ser Gln
          290         295         300
Leu Leu Glu Asn Val Phe Ala Asp Pro Lys Gly Phe Gly Ile Gly Pro
305         310         315         320
Asp Gly Arg Tyr Arg Cys Glu Asp Pro Lys Phe Thr Glu Gly Thr Ala
          325         330         335
Gln Val

```

(2) INFORMATION FOR SEQ ID NO:1185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1319 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1319
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1185:

```

gggtttgaga gttatcgttt cgaagcttga tcctaatatt caacaatgac gataatgtca    60
gatcttcacac gggatttgtt agcggagatt ctccagttagg ttccgttgac atctcttaaga    120
gcagtcgcgat tgacttgcaa aaagtggaaac gatttatcca aagatcggag ctttctcaag    180
aagcaaatcg tcgaaacaaa gaagaagcaa ttggaatcga aggagattga ggtgatcatg    240
atgaggaatt ttagggttta tctaacaagc atcgatatcc acaacaatgt tgatctatca    300

```

tttacgccta	aaggtacact	tattagctta	agcgatgatg	caaaccatca	tcaagtcgat	360
aatgtatcta	gagctcttca	ctgcgatggt	ttactattat	gcatacccaa	agacctccac	420
tatagctctg	tbggtttgga	acccttattt	tggtaaaca	agatggatcc	aaccagaaaa	480
ttcttaccac	agaaaggaca	attacgctct	tgggtacgat	gagaagaaga	accacaaaaa	540
cctgagattg	aaggatgatt	attacgctcc	acgggaacgg	atttgtgagt	ttgaactcta	600
cagttttgag	tctaattcat	ggaaggttgt	acttgatgtc	agtcctgact	ggatatatac	660
ttcttataac	cgtggcttgt	ctctaaaggg	gaatacttac	tggtatgcaa	caagagaagca	720
tgctcaatgtt	gatttcttga	tttgttttga	tttcaacaac	gagaaaattg	gaaccgcgttt	780
gcctctgcct	tttaacgcta	cagagctctc	tacttatgaa	gatgtgtgta	ctctctctag	840
tgttggagaa	gagcagcttg	cggtgttgtt	tcagagtgag	tatacatgtg	tgatggagat	900
ttgggtttacg	agcaaggttg	agtcacacaga	ggtttgtgtg	aacaaattgt	tcttagaggt	960
tgatttgata	gcaatcacgt	ctcactttca	gtttctggca	gaggtctggga	gtttcttcat	1020
tgaccagaag	aagaattgtt	ttgtggtttt	tgataaagat	atggatgagg	ctaccgatcg	1080
cgacatggct	tacgttgttg	ggaagaacgg	atacttcaaa	aaagtggata	ttggggaaaga	1140
agcatcacag	agttgtttcc	cacttgatg	ttcttatgtt	ccaagctcag	agcaaatcac	1200
cgagctaac	tgattattac	gaactactgt	tttcttttcc	tgctcatctc	gattgtataa	1260
atctgacat	tgttatcagt	tatctggaat	ctcagagaca	tgccctctct	actatatgc	

(2) INFORMATION FOR SEQ ID NO:1186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..292
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1186:

Met	Met	Gln	Thr	Ile	Ile	Lys	Ser	Ile	Met	Tyr	Leu	Glu	Ser	Phe	Thr
1				5				10						15	
Ala	Met	Val	Tyr	Tyr	Ala	Ser	Pro	Lys	Thr	Ser	Thr	Ile	Gly	Leu	
				20				25					30		
Xaa	Val	Trp	Asn	Pro	Tyr	Phe	Gly	Gln	Thr	Arg	Trp	Ile	Gln	Pro	Arg
			35				40					45			
Asn	Ser	Tyr	His	Arg	Lys	Asp	Asn	Tyr	Ala	Leu	Gly	Tyr	Asp	Glu	Lys
			50			55					60				
Lys	Asn	His	Lys	Ile	Leu	Arg	Leu	Lys	Asp	Asp	Tyr	Tyr	Ala	Pro	Arg
65				70					75					80	
Glu	Arg	Ile	Cys	Glu	Phe	Glu	Leu	Tyr	Ser	Phe	Glu	Ser	Asn	Ser	Trp
			85					90					95		
Lys	Val	Val	Leu	Asp	Val	Ser	Pro	Asp	Trp	Tyr	Ile	Pro	Ser	Tyr	Asn
			100					105					110		
Arg	Gly	Leu	Ser	Leu	Lys	Gly	Asn	Thr	Tyr	Trp	Tyr	Ala	Thr	Glu	Lys
			115				120					125			
His	Val	Asn	Val	Asp	Phe	Leu	Ile	Cys	Phe	Asp	Phe	Thr	Thr	Glu	Lys
			130			135					140				
Phe	Gly	Pro	Arg	Leu	Pro	Leu	Pro	Phe	Asn	Ala	Thr	Glu	Ser	Pro	Thr
			145			150				155				160	
Tyr	Glu	Asp	Val	Val	Thr	Leu	Ser	Ser	Val	Gly	Glu	Glu	Gln	Leu	Ala
			165					170					175		
Val	Leu	Phe	Gln	Ser	Glu	Tyr	Thr	Leu	Met	Met	Glu	Ile	Trp	Val	Thr
			180					185					190		
Ser	Lys	Val	Glu	Ser	Thr	Glu	Val	Leu	Trp	Asn	Lys	Leu	Phe	Leu	Glu
			195					200				205			
Val	Asp	Leu	Ile	Ala	Ile	Ser	Ser	His	Phe	Gln	Phe	Leu	Ala	Glu	Ala
			210			215					220				
Gly	Ser	Phe	Phe	Ile	Asp	Gln	Lys	Lys	Asn	Val	Val	Val	Val	Phe	Asp
225				230					235					240	
Lys	Asp	Met	Asp	Glu	Ala	Thr	Asp	Arg	Asp	Met	Ala	Tyr	Val	Val	Gly
			245						250					255	

Lys Asn Gly Tyr Phe Lys Lys Val Asp Ile Gly Glu Glu Ala Tyr Thr
260 265 270
Ser Cys Phe Pro Leu Val Cys Ser Tyr Val Pro Ser Ser Glu Gln Ile
275 280 285
Arg Gln Leu Thr
290

(2) INFORMATION FOR SEQ ID NO:1187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..291

(D) OTHER INFORMATION: / Ceres Seq. ID 1499802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1187:

Met Gln Thr Ile Ile Lys Ser Ile Met Tyr Leu Glu Ser Phe Thr Ala
1 5 10 15
Met Val Tyr Tyr Tyr Ala Ser Pro Lys Thr Ser Thr Ile Gly Leu Xaa
20 25 30
Val Trp Asn Pro Tyr Phe Gly Gln Thr Arg Trp Ile Gln Pro Arg Asn
35 40 45
Ser Tyr His Arg Lys Asp Asn Tyr Ala Leu Gly Tyr Asp Glu Lys Lys
50 55 60
Asn His Lys Ile Leu Arg Leu Lys Asp Asp Tyr Tyr Ala Pro Arg Glu
65 70 75 80
Arg Ile Cys Glu Phe Glu Leu Tyr Ser Phe Glu Ser Asn Ser Trp Lys
85 90 95
Val Val Leu Asp Val Ser Pro Asp Trp Tyr Ile Pro Ser Tyr Asn Arg
100 105 110
Gly Leu Ser Leu Lys Gly Asn Thr Tyr Trp Tyr Ala Thr Glu Lys His
115 120 125
Val Asn Val Asp Phe Leu Ile Cys Phe Asp Phe Thr Thr Glu Lys Phe
130 135 140
Gly Pro Arg Leu Pro Leu Pro Phe Asn Ala Thr Glu Ser Pro Thr Tyr
145 150 155 160
Glu Asp Val Val Thr Leu Ser Ser Val Gly Glu Glu Gln Leu Ala Val
165 170 175
Leu Phe Gln Ser Glu Tyr Thr Leu Met Met Glu Ile Trp Val Thr Ser
180 185 190
Lys Val Glu Ser Thr Glu Val Leu Trp Asn Lys Leu Phe Leu Glu Val
195 200 205
Asp Leu Ile Ala Ile Ser Ser His Phe Gln Phe Leu Ala Glu Ala Gly
210 215 220
Ser Phe Phe Ile Asp Gln Lys Lys Asn Val Val Val Phe Asp Lys
225 230 235 240
Asp Met Asp Glu Ala Thr Asp Arg Asp Met Ala Tyr Val Val Gly Lys
245 250 255
Asn Gly Tyr Phe Lys Lys Val Asp Ile Gly Glu Glu Ala Tyr Thr Ser
260 265 270
Cys Phe Pro Leu Val Cys Ser Tyr Val Pro Ser Ser Glu Gln Ile Arg
275 280 285
Gln Leu Thr
290

(2) INFORMATION FOR SEQ ID NO:1188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..283
(D) OTHER INFORMATION: / Ceres Seq. ID 1499803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1188:

Met	Tyr	Leu	Glu	Ser	Phe	Thr	Ala	Met	Val	Tyr	Tyr	Ala	Ser	Pro
1			5						10				15	
Lys	Thr	Ser	Thr	Ile	Gly	Leu	Xaa	Val	Trp	Asn	Pro	Tyr	Phe	Gly
			20					25					30	
Thr	Arg	Trp	Ile	Gln	Pro	Arg	Asn	Ser	Tyr	His	Arg	Lys	Asp	Asn
			35				40					45		
Ala	Leu	Gly	Tyr	Asp	Glu	Lys	Asn	His	Lys	Ile	Leu	Arg	Leu	Lys
			50				55			60				
Asp	Asp	Tyr	Tyr	Ala	Pro	Arg	Glu	Arg	Ile	Cys	Glu	Phe	Glu	Tyr
65					70				75					80
Ser	Phe	Glu	Ser	Asn	Ser	Trp	Lys	Val	Val	Leu	Asp	Val	Ser	Pro
			85					90					95	
Trp	Tyr	Ile	Pro	Ser	Tyr	Asn	Arg	Gly	Leu	Ser	Leu	Lys	Gly	Asn
			100					105					110	
Tyr	Trp	Tyr	Ala	Thr	Glu	Lys	His	Val	Asn	Val	Asp	Phe	Leu	Ile
			115				120					125		
Phe	Asp	Phe	Thr	Thr	Glu	Lys	Phe	Gly	Pro	Arg	Leu	Pro	Leu	Pro
			130			135					140			
Asn	Ala	Thr	Glu	Ser	Pro	Thr	Tyr	Glu	Asp	Val	Val	Thr	Leu	Ser
			145			150				155				160
Val	Gly	Glu	Glu	Gln	Leu	Ala	Val	Leu	Phe	Gln	Ser	Glu	Tyr	Thr
			165					170					175	
Met	Met	Glu	Ile	Trp	Val	Thr	Ser	Lys	Val	Glu	Ser	Thr	Glu	Val
			180					185					190	
Trp	Asn	Lys	Leu	Phe	Leu	Glu	Val	Asp	Leu	Ile	Ala	Ile	Ser	His
			195			200					205			
Phe	Gln	Phe	Leu	Ala	Glu	Ala	Gly	Ser	Phe	Phe	Ile	Asp	Gln	Lys
			210			215					220			
Asn	Val	Val	Val	Val	Phe	Asp	Lys	Asp	Met	Asp	Glu	Ala	Thr	Asp
			225			230				235				240
Asp	Met	Ala	Tyr	Val	Val	Gly	Lys	Asn	Gly	Tyr	Phe	Lys	Lys	Val
			245					250						255
Ile	Gly	Glu	Glu	Ala	Tyr	Thr	Ser	Cys	Phe	Pro	Leu	Val	Cys	Ser
			260					265					270	
Val	Pro	Ser	Ser	Glu	Gln	Ile	Arg	Gln	Leu	Thr				
			275				280							

(2) INFORMATION FOR SEQ ID NO:1189:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 957 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..957
(D) OTHER INFORMATION: / Ceres Seq. ID 1499811

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1189:

aaatgaaatg	atagagagag	taaagtggga	atttgacat	tggtgggttt	agggaaaaaa	60
cagagagaaa	gagatggatt	cgtcgtcagt	agggaaacacc	aacaggctact	gggtctctccg	120
ccacgggcaag	agcattcccca	acgagagagag	cctcgtcgtc	tcttccatgag	aaaatgggtgt	180
ccctcccgag	taccaggttag	ccctgatgg	tgctcgtcag	gctcgtctcg	ccggcgaatc	240
gttcctccag	caacttaagg	aaagtaacat	agaactggac	aaggttcggc	atttgctact	300
ccccctcttc	cagaaccact	cacaccgcta	gggttggttc	tgaggctcctc	aatctccctc	360

ttgatgtctc	tcaatgcaag	atgatggaag	atctgcgca	acgtatattt	ggacctacat	420
ttgaactcaa	gtcccatgac	aagtaccacg	agatatgggc	tcttgatgaa	aaagatccct	480
ttatgggacc	agaaggaggt	gaaagtgtgt	atgatgttgt	ttcccgactt	gccactgcca	540
tgaaatccat	ggaagctgaa	tatcaaaggt	gtgcaattct	gggtgtgagt	catgagagtc	600
ctctgcagat	gttcgagaac	gttttccatt	cagcaaaagca	acaggaagga	gatggtttgg	660
cagagaagtt	tcagtttgagc	agagttgctt	ctgtcttgtc	acagcacgcg	aagtttgctt	720
tgctcactgg	ggaactccga	ccccctcatc	gattggcaat	caatgtattc	agcttttgga	780
atgtcttttc	ttgaactctt	ttgttatcaa	ttcctatttc	ttcccatgtg	gcattctctg	840
aattgccaac	cttggtattag	cctgtttatt	atcacctctg	tttgttagag	aaaacatgaa	900
gatttactcc	tgtaataaga	aatcatgctc	atttatgtta	tatgtatctt	caaatct	

(2) INFORMATION FOR SEQ ID NO:1190:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1499812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1190:

Met	Met	Glu	Asp	Leu	Arg	Glu	Arg	Tyr	Phe	Gly	Pro	Thr	Phe	Glu	Leu
1			5					10					15		
Lys	Ser	His	Asp	Lys	Tyr	Pro	Glu	Ile	Trp	Ala	Leu	Asp	Glu	Lys	Asp
			20					25					30		
Pro	Phe	Met	Gly	Pro	Glu	Gly	Gly	Glu	Ser	Ala	Asp	Asp	Val	Val	Ser
			35				40					45			
Arg	Leu	Ala	Thr	Ala	Met	Lys	Ser	Met	Glu	Ala	Glu	Tyr	Gln	Arg	Cys
			50				55					60			
Ala	Ile	Leu	Val	Val	Ser	His	Gly	Asp	Pro	Leu	Gln	Met	Leu	Gln	Asn
			65				70				75			80	
Val	Phe	His	Ser	Ala	Lys	Gln	Gln	Glu	Gly	Asp	Gly	Leu	Ala	Glu	Lys
				85						90				95	
Phe	Gln	Leu	Ser	Arg	Val	Ala	Ser	Val	Leu	Ser	Gln	His	Arg	Lys	Phe
				100				105						110	
Ala	Leu	Leu	Thr	Gly	Glu	Leu	Arg	Pro	Leu	Ile					
				115				120							

(2) INFORMATION FOR SEQ ID NO:1191:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1499813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1191:

Met	Glu	Asp	Leu	Arg	Glu	Arg	Tyr	Phe	Gly	Pro	Thr	Phe	Glu	Leu	Lys
1			5					10					15		
Ser	His	Asp	Lys	Tyr	Pro	Glu	Ile	Trp	Ala	Leu	Asp	Glu	Lys	Asp	Pro
			20					25					30		
Phe	Met	Gly	Pro	Glu	Gly	Gly	Glu	Ser	Ala	Asp	Asp	Val	Val	Ser	Arg
				35			40					45			
Leu	Ala	Thr	Ala	Met	Lys	Ser	Met	Glu	Ala	Glu	Tyr	Gln	Arg	Cys	Ala
				50			55				60				
Ile	Leu	Val	Val	Ser	His	Gly	Asp	Pro	Leu	Gln	Met	Leu	Gln	Asn	Val
				65			70				75			80	
Phe	His	Ser	Ala	Lys	Gln	Gln	Glu	Gly	Asp	Gly	Leu	Ala	Glu	Lys	Phe

85 90 95
Gln Leu Ser Arg Val Ala Ser Val Leu Ser Gln His Arg Lys Phe Ala
100 105 110
Leu Leu Thr Gly Glu Leu Arg Pro Leu Ile
115 120

(2) INFORMATION FOR SEQ ID NO:1192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..89

(D) OTHER INFORMATION: / Ceres Seq. ID 1499814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1192:

Met Gly Pro Glu Gly Glu Ser Ala Asp Val Val Ser Arg Leu
1 5 10 15
Ala Thr Ala Met Lys Ser Met Glu Ala Glu Tyr Gln Arg Cys Ala Ile
20 25 30
Leu Val Val Ser His Gly Asp Pro Leu Gln Met Leu Gln Asn Val Phe
35 40 45
His Ser Ala Lys Gln Gln Glu Gly Asp Gly Leu Ala Glu Lys Phe Gln
50 55 60
Leu Ser Arg Val Ala Ser Val Leu Ser Gln His Arg Lys Phe Ala Leu
65 70 75 80
Leu Thr Gly Glu Leu Arg Pro Leu Ile
85

(2) INFORMATION FOR SEQ ID NO:1193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1112
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499823

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1193:

gagttcttcc ttccgtggaa agagcaaat ttacttttaa gaaatttgaa aacaaagttt 60
cattaacacag attggtggga tttaaattt gaattttgat cagtgaatca acgataaacg 120
attcgtcggt ttggaaggag ttggtgcacg gttaggtagg tcctcgacac ggtacggacc 180
ggcaacgggt ttccacggac cggtgaggaa gtggaagaa aagtggtgat acgtctcttc 240
ttcctctaag aaagacaata ataatagtct ctccggttcc ccgctgctc ccgcccgtgc 300
tgcagcttcc gtctgtaacg gtggttcgaa ttctgacggt agtaatggat cgcatttggt 360
gctgtataag tgggcaccat tgtctcagaa tggtaacggc aatgaagatg gtaaaagtga 420
gagtaattct ccagcggagg atacggtggc aacggtggca gaagatcctc caccgcccag 480
attcaaatatc gttccgatag cagtacttga ggaacagaag aaggaaatta cagaattga 540
ggaagatgat aagattgagc aggatgcaca gattgatgag gataataaag ttgagcagga 600
agacaagggt gatgaggaca aaactgtaga ggagtcgagc gagaagaaat cggaagtga 660
agtggaggaa aagcctgaca tcaatgatgt tccgatggaa gatattcagc aagttgaaga 720
aaaaatagta caggatgatc aagaaaaagt agtgcgacaa gatttgaacg aaagcactgt 780
ggaattagga ctgaacttaa atgcaaacga tgctgatgct gatgcagaaa acgaccaggaa 840
agaggacaag ccattagaag aatgataaac tgggtgcatt gttttgggtc ctacacctca 900
actctcaata tgaattagga agaaagacat tacagaaaga acaaacgcat ctagatatat 960
ggacgcagat ccttgatttg gtctgtaaac ccattggotta ttccttttga tgttaatgga 1020
aagactcat tgattcagac tgatcattca attcatagga gattcttgct tttttgtctg 1080
aattttattt tgattcaaca ttcagaacat tt

(2) INFORMATION FOR SEQ ID NO:1194:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 244 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..244
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499824
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1194:
Met Glu Gly Val Gly Ala Arg Leu Gly Arg Ser Ser Thr Arg Tyr Gly
1 5 10 15
Pro Ala Thr Val Phe Thr Gly Pro Val Arg Lys Trp Lys Lys Trp
 20 25 30
Val His Val Ser Pro Ser Ser Lys Asp Asn Asn Asn Ser Ser Ser
 35 40 45
Gly Ser Ala Ala Ala Pro Ala Ala Ala Ala Ser Val Val Asn Gly
50 55 60
Gly Ser Asn Ser Asp Gly Ser Asn Gly Ser His Leu Leu Leu Tyr Lys
65 70 75 80
Trp Ala Pro Leu Ser Gln Asn Gly Asn Gly Asn Glu Asp Gly Lys Ser
 85 90 95
Glu Ser Asn Ser Pro Ser Glu Asp Thr Val Ala Thr Val Ala Glu Asp
 100 105 110
Pro Pro Arg Arg Arg Phe Lys Tyr Val Pro Ile Ala Val Leu Glu Glu
 115 120 125
Gln Lys Lys Glu Ile Thr Glu Ile Glu Glu Asp Asp Lys Ile Glu Gln
130 135 140
Asp Asp Lys Ile Asp Glu Asp Asn Lys Val Glu Gln Glu Asp Lys Val
145 150 155 160
Asp Glu Asp Lys Thr Val Glu Glu Ser Ser Glu Lys Lys Ser Glu Val
 165 170 175
Glu Val Glu Glu Lys Pro Asp Ile Asn Asp Val Pro Met Glu Asp Ile
 180 185 190
Gln Gln Val Glu Glu Lys Ile Val Gln Asp Asp Glu Glu Lys Val Val
 195 200 205
Arg Gln Asp Leu Asn Glu Ser Thr Val Asp Leu Gly Leu Asn Leu Asn
210 215 220
Ala Asn Asp Ala Asp Ala Asp Ala Glu Asn Asp Pro Lys Glu Asp Lys
225 230 235 240
Pro Leu Glu Glu

(2) INFORMATION FOR SEQ ID NO:1195:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1851 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..1851
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499825
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1195:
aaaaaaaaacat tcactcggtta actcttctcc tccatccaat ttcactttct ctcaactcatt 60
tttattcgctc gtcgctcgctc cctctgattt gttctttttt ctctaaattc gcttcgcttc 120
ttctcagttc tacgaattct cgaattctct tggttttctc catcccgta tacgtttaag 180
aacattgcaa gaaagtgaag aaaaaaaaaa caggaaggga ctgatccgta tggtagagatt 240
gagataagtt ttggttatca atgcaataat aagaagatag gaatccctga agataaaatt 300
gctgatggtc gtgaggttct tggtagggtt aggctacaaa agactagcag tttctcttgt 360

ttatcaggag	ctgctttaag	tggaaacccc	acttttagcca	atactaataat	ctgcaatgga	420
gtcattgttg	ctgagatatt	gcccgtctctg	gattctccgga	aatcttttcag	gaaagttccg	480
tcttcgctgt	cgctttcgaa	gcttgatata	ctctctccct	ctctccattgg	aagtaggtg	540
agtctaagct	gcagctcgtc	tactagtcog	agtcctcctg	agcctgaatc	ttgttaactgt	600
acgtcaaatg	gttctccctc	ttctgttaat	gaaggggttc	ttctctctgc	tatggaagtt	660
caagtgtcgg	gtggtgctgc	aggggaagat	agagttcaa	ctgtttgtct	tgaggagaat	720
ggttggttgt	tttgcgctat	ctatgatgga	tccaacggaa	gagatgctgc	tgattttctgt	780
gcattgtact	tatatagact	cattgtgttt	catcttcaagt	tgcttgatgc	tcaaatgaag	840
caaacaaagt	ccgatgatga	tgccgaaaaa	ttggaattgt	tatcaaatat	aagtaagtga	900
gattactctt	ccactgattt	gttcaggcaa	ggagtactag	attgcttgaa	ccgtgcgctt	960
tttcaggcgg	aaacccgattt	cctaaggatg	gttgagcaag	aaatggaaga	aagaccggat	1020
ttagtatcgt	ttggaattgt	gtttttggto	actctcctgg	ttgggaagga	tctatacgtc	1080
cttaaatcttg	gtgatagcag	agctgttcta	gcgacctaca	atggtaataa	gaagctgcga	1140
gctgttcacg	tcacagagga	tcatacagtt	gataacgaag	tcgaagaagc	tagactctta	1200
agtgagcatc	ttgatgatcc	taagatcgtt	attggtggga	aaatcaaaag	aaagcttaaa	1260
gttactctgt	ctctcggagt	tggttacttg	aagaaggaga	aactaaatga	tgactcatgt	1320
gagatccctc	gcgttcgtaa	cccttttgagc	ccgccttatg	tttcagtgga	accatogagt	1380
agagttcaca	agataacgga	atcagatcac	tttgttatag	ttgcgaagca	tggtttgttt	1440
gattttctta	gcaacagga	agcgattggg	ctcgtccatt	ccctcgtttc	tagtaatcct	1500
tcgtgtgatc	cagcaaaagt	tctgcttgaa	cgtcttgtag	ctaaagctgc	tgctcgtgct	1560
ggctttacct	tggaaagaat	gacgaatggt	ccggctggta	ggagaagag	atcatcatgac	1620
gatgtgacta	taatggtaat	cactctaggt	accgatcaac	gtacctcaaa	agctcttacg	1680
tcctgtgatg	tttgatgatg	atggcgacaa	atgtgtggat	ggtaaaaagt	taattagtct	1740
catcatgatct	cttttagact	ttggaactga	tcactagttt	ttcaattctt	tggaaactggt	1800
ataatattat	ttcatgtata	gtccgtatat	atatatcatt	gtagtagtct	t	

(2) INFORMATION FOR SEQ ID NO:1196:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 493 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..493

(D) OTHER INFORMATION: / Ceres Seq. ID 1499826

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1196:

Met	Gln	Glu	Gly	Thr	Asp	Pro	Tyr	Gly	Glu	Ile	Glu	Ile	Ser	Phe	Gly
1			5					10					15		
Tyr	Gln	Cys	Asn	Asn	Lys	Lys	Ile	Gly	Ile	Pro	Glu	Asp	Lys	Ile	Ala
			20					25					30		
Asp	Gly	Arg	Glu	Val	Leu	Gly	Gly	Phe	Arg	Leu	Gln	Lys	Thr	Ser	Ser
			35					40					45		
Phe	Ser	Cys	Leu	Ser	Gly	Ala	Ala	Leu	Ser	Gly	Asn	Pro	Thr	Leu	Ala
			50					55					60		
Asn	Thr	Asn	Ile	Cys	Asn	Gly	Val	Ile	Gly	Ser	Glu	Ile	Leu	Pro	Ser
			65					70					75		
Leu	Asp	Ser	Pro	Lys	Ser	Phe	Arg	Lys	Val	Pro	Ser	Ser	Pro	Ala	Leu
			85					90					95		
Ser	Lys	Leu	Asp	Ile	Leu	Ser	Pro	Ser	Leu	His	Gly	Ser	Met	Val	Ser
			100					105					110		
Leu	Ser	Cys	Ser	Ser	Ser	Thr	Ser	Pro	Ser	Pro	Pro	Glu	Pro	Glu	Ser
			115					120					125		
Cys	Tyr	Leu	Thr	Ser	Met	Ser	Ser	Pro	Ser	Ser	Val	Asn	Glu	Gly	Phe
			130					135					140		
Leu	Leu	Ser	Ala	Met	Glu	Val	Gln	Val	Ala	Gly	Gly	Ala	Ala	Gly	Glu
			145					150					155		
Asp	Arg	Val	Gln	Ala	Val	Cys	Ser	Glu	Glu	Asn	Gly	Trp	Leu	Phe	Cys
			165					170					175		
Ala	Ile	Tyr	Asp	Gly	Phe	Asn	Gly	Arg	Asp	Ala	Ala	Asp	Phe	Leu	Ala
			180					185					190		

Cys Thr Leu Tyr Glu Ser Ile Val Phe His Leu Gln Leu Leu Asp Arg
195 200 205
Gln Met Lys Gln Thr Lys Ser Asp Asp Gly Glu Lys Leu Glu Leu
210 215 220
Leu Ser Asn Ile Ser Asn Val Asp Tyr Ser Ser Thr Asp Leu Phe Arg
225 230 235 240
Gln Gly Val Leu Asp Cys Leu Asn Arg Ala Leu Phe Gln Ala Glu Thr
245 250 255
Asp Phe Leu Arg Met Val Glu Gln Glu Met Glu Glu Arg Pro Asp Leu
260 265 270
Val Ser Val Gly Ser Cys Val Leu Val Thr Leu Leu Val Gly Lys Asp
275 280 285
Leu Tyr Val Leu Asn Leu Gly Asp Ser Arg Ala Val Leu Ala Thr Tyr
290 295 300
Asn Gly Asn Lys Lys Leu Gln Ala Val Gln Leu Thr Glu Asp His Thr
305 310 315 320
Val Asp Asn Glu Val Glu Glu Ala Arg Leu Leu Ser Glu His Leu Asp
325 330 335
Asp Pro Lys Ile Val Ile Gly Gly Lys Ile Lys Gly Lys Leu Lys Val
340 345 350
Thr Arg Ala Leu Gly Val Gly Tyr Leu Lys Lys Glu Lys Leu Asn Asp
355 360 365
Ala Leu Met Glu Ile Leu Arg Val Arg Asn Leu Leu Ser Pro Pro Tyr
370 375 380
Val Ser Val Glu Pro Ser Met Arg Val His Lys Ile Thr Glu Ser Asp
385 390 395 400
His Phe Val Ile Val Ala Ser Asp Gly Leu Phe Asp Phe Phe Ser Asn
405 410 415
Glu Glu Ala Ile Gly Leu Val His Ser Phe Val Ser Ser Asn Pro Ser
420 425 430
Gly Asp Pro Ala Lys Phe Leu Leu Glu Arg Leu Val Ala Lys Ala Ala
435 440 445
Ala Arg Ala Gly Phe Thr Leu Glu Glu Leu Thr Asn Val Pro Ala Gly
450 455 460
Arg Arg Arg Arg Tyr His Asp Asp Val Thr Ile Met Val Ile Thr Leu
465 470 475 480
Gly Thr Asp Gln Arg Thr Ser Lys Ala Ser Thr Phe Val
485 490

(2) INFORMATION FOR SEQ ID NO:1197:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 384 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..384

(D) OTHER INFORMATION: / Ceres Seq. ID 1499827

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1197:

Met Val Ser Leu Ser Cys Ser Ser Ser Thr Ser Pro Ser Pro Glu
1 5 10 15
Pro Glu Ser Cys Tyr Leu Thr Ser Met Ser Ser Pro Ser Ser Val Asn
20 25 30
Glu Gly Phe Leu Leu Ser Ala Met Glu Val Gln Val Ala Gly Gly Ala
35 40 45
Ala Gly Glu Asp Arg Val Gln Ala Val Cys Ser Glu Glu Asn Gly Trp
50 55 60
Leu Phe Cys Ala Ile Tyr Asp Gly Phe Asn Gly Arg Asp Ala Ala Asp
65 70 75 80
Phe Leu Ala Cys Thr Leu Tyr Glu Ser Ile Val Phe His Leu Gln Leu

(2) INFORMATION FOR SEQ ID NO:1198:

(A) LENGTH: 360 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..360

(D) OTHER INFORMATION: / Ceres Seq. ID 1499828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1198:

Met	Ser	Ser	Pro	Ser	Ser	Val	Asn	Glu	Gly	Phe	Leu	Leu	Ser	Ala	Met
1			5					10					15		
Glu	Val	Gln	Val	Ala	Gly	Gly	Ala	Ala	Gly	Glu	Asp	Arg	Val	Gln	Ala
			20					25					30		
Val	Cys	Ser	Glu	Glu	Asn	Gly	Trp	Leu	Phe	Cys	Ala	Ile	Tyr	Asp	Gly
			35				40					45			
Phe	Asn	Gly	Arg	Asp	Ala	Ala	Asp	Phe	Leu	Ala	Cys	Thr	Leu	Tyr	Glu
	50					55				60					
Ser	Ile	Val	Phe	His	Leu	Gln	Leu	Leu	Asp	Arg	Gln	Met	Lys	Gln	Thr
65					70					75					80

Lys Ser Asp Asp Asp Gly Glu Lys Leu Glu Leu Leu Ser Asn Ile Ser
85 90 95
Asn Val Asp Tyr Ser Ser Thr Asp Leu Phe Arg Gln Gly Val Leu Asp
100 105 110
Cys Leu Asn Arg Ala Leu Phe Gln Ala Glu Thr Asp Phe Leu Arg Met
115 120 125
Val Glu Gln Glu Met Glu Glu Arg Pro Asp Leu Val Ser Val Gly Ser
130 135 140
Cys Val Leu Val Thr Leu Leu Val Gly Lys Asp Leu Tyr Val Leu Asn
145 150 155 160
Leu Gly Asp Ser Arg Ala Val Leu Ala Thr Tyr Asn Gly Asn Lys Lys
165 170 175
Leu Gln Ala Val Gln Leu Thr Glu Asp His Thr Val Asp Asn Glu Val
180 185 190
Glu Glu Ala Arg Leu Leu Ser Glu His Leu Asp Asp Pro Lys Ile Val
195 200 205
Ile Gly Gly Lys Ile Lys Gly Lys Leu Lys Val Thr Arg Ala Leu Gly
210 215 220
Val Gly Tyr Leu Lys Lys Glu Lys Leu Asn Asp Ala Leu Met Glu Ile
225 230 235 240
Leu Arg Val Arg Asn Leu Leu Ser Pro Pro Tyr Val Ser Val Glu Pro
245 250 255
Ser Met Arg Val His Lys Ile Thr Glu Ser Asp His Phe Val Ile Val
260 265 270
Ala Ser Asp Gly Leu Phe Asp Phe Phe Ser Asn Glu Glu Ala Ile Gly
275 280 285
Leu Val His Ser Phe Val Ser Ser Asn Pro Ser Gly Asp Pro Ala Lys
290 295 300
Phe Leu Leu Glu Arg Leu Val Ala Lys Ala Ala Ala Arg Ala Gly Phe
305 310 315 320
Thr Leu Glu Glu Leu Thr Asn Val Pro Ala Gly Arg Arg Arg Arg Tyr
325 330 335
His Asp Asp Val Thr Ile Met Val Ile Thr Leu Gly Thr Asp Gln Arg
340 345 350
Thr Ser Lys Ala Ser Thr Phe Val
355 360

(2) INFORMATION FOR SEQ ID NO:1199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1810 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1810
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499829

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1199:

atacctacaa	gacgacgagt	gttccccattt	ccttggtcta	tttcaagaca	tggactcttc	60
tctcttgct	tctcgattag	aaggttttaa	tagcaacgac	aataatacta	atcaaaagaa	120
acgcccaga	aaagacgacg	aaggcggtag	tggtggcgcg	ggaggaacag	aagttctagg	180
agctgtta	ggtataata	aggctgcttt	tggagatata	ctcgcgacgc	ttttgttgtt	240
agacgaggaa	gctaacaacg	aacaagaaca	gtgggatttt	gaatctatta	aagagaagtc	300
tttactgaa	gctaatacta	agaagaaggt	gaaaacaatg	gatggttatt	acaatacaat	360
gcaagatcat	tactctgcag	ctggtgaaac	cgatgggttcg	cgttcaaaac	gcgcacggaa	420
aaccgcgggt	gcggtctggt	tttccgcggt	agcttccggg	gcggacacaa	ccggtttagc	480
tgctccgggt	ccgacgcggg	atatcgctag	cggttccggg	tcaggaccca	gcataggag	540
gttatgggtt	aaagaacgaa	ccacggactg	gtgggacaga	gtaagccggc	ctgattttcc	600
agaagacgag	tttcggcgag	agttccggtat	gagcaaatcg	acgtttaaac	taatatgcga	660
ggagctagat	acgacgggtg	cgaagaaaaa	cacgatgtta	agagacgcga	ttccagctcc	720
aaaacgcgta	ggcggttgcg	tttggcggtt	ggcgaagaga	gctccgcctc	gccacgtgtc	780

ggagcgtttc	ggtctgggaa	tetcaacttg	ccacaaacta	gtcatcgaag	tctgccgcgc	840
gattcatcag	gtttctcatg	ccaagtatct	cctctggccg	tcggattcag	agataaaactc	900
aacgaaagcc	aaattcgaa	cgttccacaa	aataccaaac	ctcgtcggtg	caattctacac	960
cacacatat	ccgatcatcg	ctccgaaaag	ccacgtggcg	gcgtatttta	acaagagaca	1020
cacggagagg	aatcagaaga	cgtcgtactc	gataacagta	caaggagtgg	tcaacgccga	1080
cgggatcttc	accgacgttt	gtatcggaaa	cccaggatct	ctcaccgacg	atcagatcct	1140
ggagaaatct	tctgctttac	ggcaaaagag	ggcgcgtggg	atgttacctg	acagctggat	1200
agttggaaac	tctgggtttc	cgttgactga	ttatcttctt	gtaccgtaca	cgagacagaa	1260
tctgacgtgg	acgcagcacg	cgtttaacga	gagtatcggg	gagattcagg	ggattgacgc	1320
ggctgcgttt	gagaggctca	aaggacggtg	ggcttggttg	cagaaacgga	cggaggtgaa	1380
gcttcaggat	ctgcgctacg	tgtttggagc	ttgtgtgtgt	ttgcataaca	tttgtgagat	1440
gaggaagagg	gagatgttgc	cggagttgaa	gtttgaggtt	tttgatgatg	tggcgggtgc	1500
ggagaataat	atccgatctg	ctagtgcggt	taatacaggg	gatcatatct	ctcacaatct	1560
cttgcacgtg	ggacttgccg	ggacaagaac	tctataggct	ctgtttttca	ccttttctta	1620
ttttgaaact	gattttttat	tgcaaatctt	ttttccaaat	taggaataaa	aacattttag	1680
ggatttggtt	gatacagaaa	gaatagtgtg	attgagagta	gaagtggctg	atgatattgt	1740
ttgtgttact	tattagcatt	gtgtaactct	tatttcactg	attttctata	caaattgaa	1800
ctgaaacctt						

(2) INFORMATION FOR SEQ ID NO:1200:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 531 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..531

(D) OTHER INFORMATION: / Ceres Seq. ID 1499830

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1200:

Tyr	Leu	Gln	Asp	Asp	Glu	Cys	Ser	His	Phe	Leu	Gly	Leu	Phe	Gln	Asp
1			5					10						15	
Met	Asp	Ser	Ser	Pro	Ser	Ala	Phe	Gly	Leu	Glu	Gly	Phe	Asn	Ser	Asn
			20					25					30		
Asp	Asn	Asn	Thr	Asn	Gln	Lys	Lys	Arg	Pro	Arg	Lys	Asp	Asp	Glu	Gly
			35					40					45		
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Thr	Glu	Val	Leu	Gly	Ala	Val	Asn	Gly
			50					55				60			
Asn	Asn	Lys	Ala	Ala	Phe	Gly	Asp	Ile	Leu	Ala	Thr	Leu	Leu	Leu	Leu
			70					75						80	
Asp	Glu	Glu	Ala	Lys	Gln	Gln	Gln	Glu	Gln	Trp	Asp	Phe	Glu	Ser	Ile
			85					90					95		
Lys	Glu	Lys	Ser	Leu	Leu	Glu	Ala	Asn	His	Lys	Lys	Val	Lys	Thr	
			100					105					110		
Met	Asp	Gly	Tyr	Tyr	Asn	Gln	Met	Gln	Asp	His	Tyr	Ser	Ala	Ala	Gly
			115					120					125		
Glu	Thr	Asp	Gly	Ser	Arg	Ser	Lys	Arg	Ala	Arg	Lys	Thr	Ala	Val	Ala
			130					135				140			
Ala	Val	Val	Ser	Ala	Val	Ala	Ser	Gly	Ala	Asp	Thr	Thr	Gly	Leu	Ala
			145					150				155			
Ala	Pro	Val	Pro	Thr	Ala	Asp	Ile	Ala	Ser	Gly	Ser	Gly	Ser	Gly	Pro
			165					170					175		
Ser	His	Arg	Arg	Leu	Trp	Val	Lys	Glu	Arg	Thr	Thr	Asp	Trp	Trp	Asp
			180					185					190		
Arg	Val	Ser	Arg	Pro	Asp	Phe	Pro	Glu	Asp	Glu	Phe	Arg	Arg	Glu	Phe
			195					200					205		
Arg	Met	Ser	Lys	Ser	Thr	Phe	Asn	Leu	Ile	Cys	Glu	Glu	Leu	Asp	Thr
			210					215				220			
Thr	Val	Thr	Lys	Lys	Asn	Thr	Met	Leu	Arg	Asp	Ala	Ile	Pro	Ala	Pro
			225					230				235			240
Lys	Arg	Val	Gly	Val	Cys	Val	Trp	Arg	Leu	Ala	Thr	Gly	Ala	Pro	Leu

Met	Asp	Ser	Ser	Pro	Ser	Ala	Phe	Gly	Leu	Glu	Gly	Phe	Asn	Ser	Asn
1			5						10					15	
Asp	Asn	Asn	Thr	Asn	Gln	Lys	Lys	Arg	Pro	Arg	Lys	Asp	Asp	Glu	Gly
			20					25					30		
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Thr	Glu	Val	Leu	Gly	Ala	Val	Asn	Gly
			35				40					45			
Asn	Asn	Lys	Ala	Ala	Phe	Gly	Asp	Ile	Leu	Ala	Thr	Leu	Leu	Leu	Leu
			50			55					60				
Asp	Glu	Glu	Ala	Lys	Gln	Gln	Gln	Glu	Gln	Trp	Asp	Phe	Glu	Ser	Ile
65					70					75				80	
Lys	Glu	Lys	Ser	Leu	Leu	Glu	Ala	Asn	His	Lys	Lys	Lys	Val	Lys	Thr
			85						90					95	

Met Asp Gly Tyr Tyr Asn Gln Met Gln Asp His Tyr Ser Ala Ala Gly
100 105 110
Glu Thr Asp Gly Ser Arg Ser Lys Arg Ala Arg Lys Thr Ala Val Ala
115 120 125
Ala Val Val Ser Ala Val Ala Ser Gly Ala Asp Thr Thr Gly Leu Ala
130 135 140
Ala Pro Val Pro Thr Ala Asp Ile Ala Ser Gly Ser Gly Pro
145 150 155 160
Ser His Arg Arg Leu Trp Val Lys Glu Arg Thr Thr Asp Trp Trp Asp
165 170 175
Arg Val Ser Arg Pro Asp Phe Pro Glu Asp Glu Phe Arg Arg Glu Phe
180 185 190
Arg Met Ser Lys Ser Thr Phe Asn Leu Ile Cys Glu Glu Leu Asp Thr
195 200 205
Thr Val Thr Lys Lys Asn Thr Met Leu Arg Asp Ala Ile Pro Ala Pro
210 215 220
Lys Arg Val Gly Val Cys Val Trp Arg Leu Ala Thr Gly Ala Pro Leu
225 230 235 240
Arg His Val Ser Glu Arg Phe Gly Leu Gly Ile Ser Thr Cys His Lys
245 250 255
Leu Val Ile Glu Val Cys Arg Ala Ile Tyr Asp Val Leu Met Pro Lys
260 265 270
Tyr Leu Leu Trp Pro Ser Asp Ser Glu Ile Asn Ser Thr Lys Ala Lys
275 280 285
Phe Glu Ser Val His Lys Ile Pro Asn Val Val Gly Ser Ile Tyr Thr
290 295 300
Thr His Ile Pro Ile Ile Ala Pro Lys Val His Val Ala Ala Tyr Phe
305 310 315 320
Asn Lys Arg His Thr Glu Arg Asn Gln Lys Thr Ser Tyr Ser Ile Thr
325 330 335
Val Gln Gly Val Val Asn Ala Asp Gly Ile Phe Thr Asp Val Cys Ile
340 345 350
Gly Asn Pro Gly Ser Leu Thr Asp Asp Gln Ile Leu Glu Lys Ser Ser
355 360 365
Leu Ser Arg Gln Arg Ala Ala Arg Gly Met Leu Arg Asp Ser Trp Ile
370 375 380
Val Gly Asn Ser Gly Phe Pro Leu Thr Asp Tyr Leu Leu Val Pro Tyr
385 390 395 400
Thr Arg Gln Asn Leu Thr Trp Thr Gln His Ala Phe Asn Glu Ser Ile
405 410 415
Gly Glu Ile Gln Gly Ile Ala Thr Ala Ala Phe Glu Arg Leu Lys Gly
420 425 430
Arg Trp Ala Cys Leu Gln Lys Arg Thr Glu Val Lys Leu Gln Asp Leu
435 440 445
Pro Tyr Val Leu Gly Ala Cys Cys Val Leu His Asn Ile Cys Glu Met
450 455 460
Arg Lys Glu Glu Met Leu Pro Glu Leu Lys Phe Glu Val Phe Asp Asp
465 470 475 480
Val Ala Val Pro Glu Asn Asn Ile Arg Ser Ala Ser Ala Val Asn Thr
485 490 495
Arg Asp His Ile Ser His Asn Leu Leu His Arg Gly Leu Ala Gly Thr
500 505 510
Arg Thr Leu
515

(2) INFORMATION FOR SEQ ID NO:1202:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 419 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..419

(D) OTHER INFORMATION: / Ceres Seq. ID 1499832

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1202:

Met	Asp	Gly	Tyr	Tyr	Asn	Gln	Met	Gln	Asp	His	Tyr	Ser	Ala	Ala	Gly
1				5						10				15	
Glu	Thr	Asp	Gly	Ser	Arg	Ser	Lys	Arg	Ala	Arg	Lys	Thr	Ala	Val	Ala
			20				25						30		
Ala	Val	Val	Ser	Ala	Val	Ala	Ser	Gly	Ala	Asp	Thr	Thr	Gly	Leu	Ala
		35				40					45				
Ala	Pro	Val	Pro	Thr	Ala	Asp	Ile	Ala	Ser	Gly	Ser	Gly	Ser	Gly	Pro
	50				55					60					
Ser	His	Arg	Arg	Leu	Trp	Val	Lys	Glu	Arg	Thr	Thr	Asp	Trp	Trp	Asp
	65				70				75					80	
Arg	Val	Ser	Arg	Pro	Asp	Phe	Pro	Glu	Asp	Glu	Phe	Arg	Arg	Glu	Phe
			85					90						95	
Arg	Met	Ser	Lys	Ser	Thr	Phe	Asn	Leu	Ile	Cys	Glu	Glu	Leu	Asp	Thr
			100					105					110		
Thr	Val	Thr	Lys	Lys	Asn	Thr	Met	Leu	Arg	Asp	Ala	Ile	Pro	Ala	Pro
		115				120						125			
Lys	Arg	Val	Gly	Val	Cys	Val	Trp	Arg	Leu	Ala	Thr	Gly	Ala	Pro	Leu
		130			135							140			
Arg	His	Val	Ser	Glu	Arg	Phe	Gly	Leu	Gly	Ile	Ser	Thr	Cys	His	Lys
	145				150				155					160	
Leu	Val	Ile	Glu	Val	Cys	Arg	Ala	Ile	Tyr	Asp	Val	Leu	Met	Pro	Lys
		165						170					175		
Tyr	Leu	Leu	Trp	Pro	Ser	Asp	Ser	Glu	Ile	Asn	Ser	Thr	Lys	Ala	Lys
		180						185					190		
Phe	Glu	Ser	Val	His	Lys	Ile	Pro	Asn	Val	Val	Gly	Ser	Ile	Tyr	Thr
		195				200						205			
Thr	His	Ile	Pro	Ile	Ile	Ala	Pro	Lys	Val	His	Val	Ala	Ala	Tyr	Phe
	210				215						220				
Asn	Lys	Arg	His	Thr	Glu	Arg	Asn	Gln	Lys	Thr	Ser	Tyr	Ser	Ile	Thr
	225				230					235				240	
Val	Gln	Gly	Val	Val	Asn	Ala	Asp	Gly	Ile	Phe	Thr	Asp	Val	Cys	Ile
		245						250					255		
Gly	Asn	Pro	Gly	Ser	Leu	Thr	Asp	Asp	Gln	Ile	Leu	Glu	Lys	Ser	Ser
		260					265						270		
Leu	Ser	Arg	Gln	Arg	Ala	Ala	Arg	Gly	Met	Leu	Arg	Asp	Ser	Trp	Ile
		275					280				285				
Val	Gly	Asn	Ser	Gly	Phe	Pro	Leu	Thr	Asp	Tyr	Leu	Leu	Val	Pro	Tyr
	290				295						300				
Thr	Arg	Gln	Asn	Leu	Thr	Trp	Thr	Gln	His	Ala	Phe	Asn	Glu	Ser	Ile
	305				310					315				320	
Gly	Glu	Ile	Gln	Gly	Ile	Ala	Thr	Ala	Ala	Phe	Glu	Arg	Leu	Lys	Gly
		325						330					335		
Arg	Trp	Ala	Cys	Leu	Gln	Lys	Arg	Thr	Glu	Val	Lys	Leu	Gln	Asp	Leu
		340						345					350		
Pro	Tyr	Val	Leu	Gly	Ala	Cys	Cys	Val	Leu	His	Asn	Ile	Cys	Glu	Met
		355				360					365				
Arg	Lys	Glu	Glu	Met	Leu	Pro	Glu	Leu	Lys	Phe	Glu	Val	Phe	Asp	Asp
	370				375					380					
Val	Ala	Val	Pro	Glu	Asn	Asn	Ile	Arg	Ser	Ala	Ser	Ala	Val	Asn	Thr
	385				390				395					400	
Arg	Asp	His	Ile	Ser	His	Asn	Leu	Leu	His	Arg	Gly	Leu	Ala	Gly	Thr
			405					410					415		

(2) INFORMATION FOR SEQ ID NO:1203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1540

(D) OTHER INFORMATION: / Ceres Seq. ID 1499833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1203:

aaaaaatctg	aaattctcag	gcgagattcc	ggaagcaaaa	cattcctaaa	tttcgccaaag	60
tgatccgcga	tgggagaaga	gaagtctctg	cttcagttcc	tgagttttcc	ttcactcaag	120
acctctgatt	tcgctctcac	cgaagaacct	tcattggaggc	tggaagaacaa	cgtgtcgtcg	180
aatcgccgga	gaggaaacaa	gagaagcggg	ggcgttttta	ccaattttgc	gtccctttcc	240
gtagcgatta	ggagagatcg	gagakaattc	acatttaacg	gtcgtaatgg	cggcgagggc	300
ggagcgcttc	cgtcggttcc	ggtggtgatt	ccgaagggaag	aggatgaatt	cgcgcctacc	360
tcggccacgc	tgttgaaaaa	ccccattgct	ttactgtcga	tagtaccgaa	agacgcgcga	420
ctattctctc	ccggagcggt	cgccggagcc	ggcgcaaaat	cagtgcgcgc	accgcttgac	480
cgaataaagc	tcctaatgca	gacacatggt	gttcgagctg	ggcaacaaa	tgctaaagaag	540
gctattgggt	tcattgaggc	cattactctt	atcggaagg	aagaagggtat	taaaaggttat	600
tggaaggaaa	atctaccctca	ggtgataaag	attgtacctt	atagcgcagt	ccagttgttt	660
gcattatgaa	catacaagaa	actcttcag	gggaagacg	gtcaattgtc	agtcctcgga	720
aggtcgcggt	ctgggtgctt	tgctggcatg	acgtctactc	tgattacata	ccctttagat	780
gtgctgagat	tgaggttagc	tgttgaacca	gggtatcgaa	ccatgtccca	ggttgccctg	840
aaactgctgc	gggagggaag	agttgcatca	ttctacaacg	gtctaggctc	ttcgctttta	900
agtagctcgc	cttaacattgc	catcaacttc	tgctgtcttg	atctggtata	gaaatctctg	960
ccagagaagc	atcaacaaaa	gacacaatca	tctttgttaa	cagcagtagt	agctgctgct	1020
attgtaccgt	gtactttgcta	tcattgggat	accattagaa	gacagatgca	attgaagggt	1080
actccatata	aatcgcttat	agacgcttcc	tcaggatata	ttgcgcgtga	aggagttggt	1140
ggcttgcacc	gtggctttgt	ccccaatgca	ctcaaaaagc	tgccaaaacag	cagattatag	1200
cttacacatc	tcgacatcgt	caagaaactc	atagcagcga	gtgagaagga	gatccaaaaga	1260
atcgccgagt	ataaccgcga	gaaagcaagt	ctcaacacaa	ccgatgaaca	aacctgaaga	1320
cgcgaatttg	gatttcacaa	aggtcatatt	tgcccggtat	cttatgacct	ttgtttgtgt	1380
gttttgtta	ttggaatgta	ataagttgta	tggtctctcc	ataattcaaa	atgtgcttga	1440
attgaatcct	gaagccagag	agggtataaa	atggctgttt	gtgttacggt	tggtcgcgct	1500
ggttttgat	aaaccgaatt	taaccggggt	gtacactcg			

(2) INFORMATION FOR SEQ ID NO:1204:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 415 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..415

(D) OTHER INFORMATION: / Ceres Seq. ID 1499834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1204:

Met	Gly	Glu	Glu	Lys	Ser	Leu	Leu	Gln	Phe	Arg	Ser	Phe	Pro	Ser	Leu	
1			5					10					15			
Lys	Thr	Ser	Asp	Phe	Ala	Leu	Thr	Glu	Pro	Ser	Trp	Arg	Leu	Glu		
			20					25				30				
Asn	Asn	Val	Ser	Ser	Asn	Arg	Arg	Gly	Asn	Lys	Arg	Ser	Gly	Gly		
			35				40				45					
Val	Phe	Thr	Asn	Phe	Ala	Ser	Leu	Ser	Val	Ala	Ile	Arg	Arg	Asp	Arg	
			50				55				60					
Arg	Xaa	Ser	Thr	Phe	Asn	Gly	Arg	Asn	Gly	Gly	Gly	Gly	Gly	Ala	Phe	
			65				70				75			80		
Ala	Ser	Val	Ser	Val	Val	Ile	Pro	Lys	Glu	Glu	Asp	Glu	Phe	Ala	Pro	
							85				90			95		
Thr	Ser	Ala	Gln	Leu	Leu	Lys	Asn	Pro	Ile	Ala	Leu	Leu	Ser	Ile	Val	

```

100          105          110
Pro Lys Asp Ala Ala Leu Phe Phe Ala Gly Ala Phe Ala Gly Ala Ala
115          120          125
Ala Lys Ser Val Thr Ala Pro Leu Asp Arg Ile Lys Leu Leu Met Gln
130          135          140
Thr His Gly Val Arg Ala Gly Gln Gln Ser Ala Lys Lys Ala Ile Gly
145          150          155          160
Phe Ile Glu Ala Ile Thr Leu Ile Gly Lys Glu Gly Ile Lys Gly
165          170          175
Tyr Trp Lys Gly Asn Leu Pro Gln Val Ile Arg Ile Val Pro Tyr Ser
180          185          190
Ala Val Gln Leu Phe Ala Tyr Glu Thr Tyr Lys Lys Leu Phe Arg Gly
195          200          205
Lys Asp Gly Gln Leu Ser Val Leu Gly Arg Leu Gly Ala Gly Ala Cys
210          215          220
Ala Gly Met Thr Ser Thr Leu Ile Thr Tyr Pro Leu Asp Val Leu Arg
225          230          235          240
Leu Arg Leu Ala Val Glu Pro Gly Tyr Arg Thr Met Ser Gln Val Ala
245          250          255
Leu Asn Met Leu Arg Glu Glu Gly Val Ala Ser Phe Tyr Asn Gly Leu
260          265          270
Gly Pro Ser Leu Leu Ser Ile Ala Pro Tyr Ile Ala Ile Asn Phe Cys
275          280          285
Val Phe Asp Leu Val Lys Lys Ser Leu Pro Glu Lys Tyr Gln Gln Lys
290          295          300
Thr Gln Ser Ser Leu Leu Thr Ala Val Val Ala Ala Ile Ala Thr
305          310          315          320
Gly Thr Cys Tyr Pro Leu Asp Thr Ile Arg Arg Gln Met Gln Leu Lys
325          330          335
Gly Thr Pro Tyr Lys Ser Val Leu Asp Ala Phe Ser Gly Ile Ile Ala
340          345          350
Arg Glu Gly Val Val Gly Leu Tyr Arg Gly Phe Val Pro Asn Ala Leu
355          360          365
Lys Ser Met Pro Asn Ser Ser Ile Lys Leu Thr Thr Phe Asp Ile Val
370          375          380
Lys Lys Leu Ile Ala Ala Ser Glu Lys Glu Ile Gln Arg Ile Ala Asp
385          390          395          400
Asp Asn Arg Lys Lys Ala Ser Pro Asn Thr Thr Asp Glu Gln Thr
405          410          415

```

(2) INFORMATION FOR SEQ ID NO:1205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..273
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499835

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1205:

```

Met Gln Thr His Gly Val Arg Ala Gly Gln Gln Ser Ala Lys Lys Ala
1          5          10          15
Ile Gly Phe Ile Glu Ala Ile Thr Leu Ile Gly Lys Glu Glu Gly Ile
20          25          30
Lys Gly Tyr Trp Lys Gly Asn Leu Pro Gln Val Ile Arg Ile Val Pro
35          40          45
Tyr Ser Ala Val Gln Leu Phe Ala Tyr Glu Thr Tyr Lys Lys Leu Phe
50          55          60
Arg Gly Lys Asp Gly Gln Leu Ser Val Leu Gly Arg Leu Gly Ala Gly
65          70          75          80

```

Ala Cys Ala Gly Met Thr Ser Thr Leu Ile Thr Tyr Pro Leu Asp Val
85 90 95
Leu Arg Leu Arg Leu Ala Val Glu Pro Gly Tyr Arg Thr Met Ser Gln
100 105 110
Val Ala Leu Asn Met Leu Arg Glu Gly Val Ala Ser Phe Tyr Asn
115 120 125
Gly Leu Gly Pro Ser Leu Leu Ser Ile Ala Pro Tyr Ile Ala Ile Asn
130 135 140
Phe Cys Val Phe Asp Leu Val Lys Lys Ser Leu Pro Glu Lys Tyr Gln
145 150 155 160
Gln Lys Thr Gln Ser Ser Leu Leu Thr Ala Val Val Ala Ala Ala Ile
165 170 175
Ala Thr Gly Thr Cys Tyr Pro Leu Asp Thr Ile Arg Arg Gln Met Gln
180 185 190
Leu Lys Gly Thr Pro Tyr Lys Ser Val Leu Asp Ala Phe Ser Gly Ile
195 200 205
Ile Ala Arg Glu Gly Val Val Gly Leu Tyr Arg Gly Phe Val Pro Asn
210 215 220
Ala Leu Lys Ser Met Pro Asn Ser Ser Ile Lys Leu Thr Thr Phe Asp
225 230 235 240
Ile Val Lys Lys Leu Ile Ala Ala Ser Glu Lys Glu Ile Gln Arg Ile
245 250 255
Ala Asp Asp Asn Arg Lys Lys Ala Ser Pro Asn Thr Thr Asp Glu Gln
260 265 270
Thr

(2) INFORMATION FOR SEQ ID NO:1206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1109 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1109
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1206:

aaaaaaacca	ataaaaattgg	tcgcttcgca	aaaactgaga	tvtgagttct	tccttcggtg	60
gaaagagcaa	attttacttt	taagaaattt	gaaaacaaag	tttcattaaa	cgagttggtg	120
ggatttttaa	tttgaatttt	gatcagtgaa	tcaacgataa	acgattcgct	gttatggaag	180
gagttgtgtc	acgggttaggc	aggctctcga	cacggtagcg	accggcaacg	gttttcaccg	240
gtccggtgcg	gaagtggaag	aagaagtggg	tacacgtctc	tccatccact	aagaaagaca	300
ataataatag	ctcctccggt	tcgcccgctg	ctgcagcttc	cgctgtaaat	gggtggttcga	360
attctgcagg	cgataatgga	tcgctattgt	tgctgtataa	gtgggcacca	ttgtcccaga	420
acggtaacgg	gaatgaagat	tgtaaaaagt	agagtaattc	tcgcagcgag	gacacgggtg	480
cgacggtggc	agaagatcct	cgcggcgcca	gattcaaaaa	cggtcccgata	gcagtaactg	540
aggaacagaa	gaaggaaaatt	acagaaaattg	aggaacgatga	taagattgag	ggagatgaca	600
agattgatga	ggataataag	gtcgcagcagg	aagacaagggt	tgatgaggag	aaaactgtag	660
aggagtcgag	cgagaagaaa	gcggaagtgt	aagtggaaagt	ggaggaaaag	ccgtgatatac	720
atgatgttcc	aatggaagat	attcagcagg	atgaagaaaa	aatagtacag	gatgatgaag	780
aaaaagtagt	gcgacaagat	ttgaacgaaa	gcactgtgga	tttaggactg	aacttaaatg	840
caaacactgc	tgatgctgat	gcagaaaacg	accgcgaaga	ggacaagcca	ttagaagaat	900
gataaactgg	gtgcatttgt	ttggttcctc	accctcaact	ctcaatatca	attaggaaga	960
aagacattac	agaaagaaca	aagcagtcac	tagatatgga	cgcagatcct	tgatttggct	1020
tgtaaaccca	tggtcttacc	cttttgatgt	taatggaat	gactcattga	ttcagactga	1080
tcattcaatt	cataggcaga	ttcttgtctc				

(2) INFORMATION FOR SEQ ID NO:1207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..242
(D) OTHER INFORMATION: / Ceres Seq. ID 1499845
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1207:

Met	Glu	Gly	Val	Gly	Ala	Arg	Leu	Gly	Arg	Ser	Ser	Thr	Arg	Tyr	Gly
1			5					10					15		
Pro	Ala	Thr	Val	Phe	Thr	Gly	Pro	Val	Arg	Lys	Trp	Lys	Lys	Lys	Trp
			20				25					30			
Val	His	Val	Ser	Pro	Ser	Thr	Lys	Lys	Asp	Asn	Asn	Asn	Ser	Ser	Ser
			35				40				45				
Gly	Ser	Ala	Ala	Ala	Ala	Ala	Ser	Val	Val	Asn	Gly	Gly	Ser	Asn	Ser
			50			55					60				
Asp	Gly	Ser	Asn	Gly	Ser	His	Leu	Leu	Leu	Tyr	Lys	Trp	Ala	Pro	Leu
			65			70				75				80	
Ser	Gln	Asn	Gly	Asn	Gly	Asn	Glu	Asp	Gly	Lys	Ser	Glu	Ser	Asn	Ser
			85						90				95		
Pro	Ser	Glu	Asp	Thr	Val	Ala	Thr	Val	Ala	Glu	Asp	Pro	Pro	Arg	Arg
			100					105					110		
Arg	Phe	Lys	Tyr	Val	Pro	Ile	Ala	Val	Leu	Glu	Glu	Gln	Lys	Lys	Glu
			115				120					125			
Ile	Thr	Glu	Ile	Glu	Asp	Asp	Lys	Ile	Glu	Glu	Asp	Asp	Lys	Ile	
			130			135					140				
Asp	Glu	Asp	Asn	Lys	Val	Glu	Gln	Glu	Asp	Lys	Val	Asp	Glu	Asp	Lys
			145			150				155				160	
Thr	Val	Glu	Glu	Ser	Ser	Glu	Lys	Lys	Ala	Glu	Val	Glu	Val	Glu	Val
			165					170					175		
Glu	Glu	Lys	Pro	Asp	Ile	Asn	Asp	Val	Pro	Met	Glu	Asp	Ile	Gln	Gln
			180				185						190		
Asp	Glu	Glu	Lys	Ile	Val	Gln	Asp	Asp	Glu	Glu	Lys	Val	Val	Arg	Gln
			195				200					205			
Asp	Leu	Asn	Glu	Ser	Thr	Val	Asp	Leu	Gly	Leu	Asn	Leu	Asn	Ala	Asn
			210			215					220				
Asp	Ala	Asp	Ala	Asp	Ala	Glu	Asn	Asp	Pro	Lys	Glu	Asp	Lys	Pro	Leu
			225			230				235				240	

Glu Glu

(2) INFORMATION FOR SEQ ID NO:1208:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 604 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..604

(D) OTHER INFORMATION: / Ceres Seq. ID 1499850

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1208:

gcactgcttc	attctctata	accaagtata	agcttgagg	gggtattttt	totaaaaggg	60
attgagtttt	taagatcatg	tctatgacag	tggagataag	agttccaaac	ttggattgtg	120
aaggatgtgc	ttctaagctt	aggaagactc	tactcaagct	taaaggagtg	gaagaagtg	180
aaagttagaga	tggaaaccca	aaaagtgcag	gctcgaggat	accggttaga	ggaaaagaa	240
gtattgaaa	cggtacgacg	tgccggtaag	gcagctgaac	tgtggccata	ccggttagtg	300
aatagccatt	ttgcctcttt	ctataaatat	cttctcttacg	tgaccaacca	ctattactct	360
gatgcacacc	gtacggatcc	caccggtgtg	gtccacactt	tcttccacac	tcttcgggtt	420
tactcgggtg	ctgtggctgg	agatgagatc	gcggcttcga	tgttttagcg	tgataatccc	480
catgcttgta	ctattatgta	gtcttttagt	atacaaaaat	atgttttcag	tctactctct	540

tcgtccaaat ttgatttgat gtgatttttt ttgtacaact aatgttggaat tgagaaagta 600
aaat

(2) INFORMATION FOR SEQ ID NO:1209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..63
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499851

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1209:

Met	Ser	Met	Thr	Val	Glu	Ile	Arg	Val	Pro	Asn	Leu	Asp	Cys	Glu	Gly	
1				5					10					15		
Cys	Ala	Ser	Lys	Leu	Arg	Lys	Thr	Leu	Leu	Lys	Leu	Lys	Gly	Val	Glu	
			20					25					30			
Glu	Val	Glu	Ser	Arg	Asp	Gly	Asn	Pro	Lys	Ser	Asp	Gly	Ser	Arg	Ile	
			35				40					45				
Pro	Val	Arg	Gly	Lys	Glu	Gly	Ile	Glu	Ser	Gly	Thr	Thr	Cys	Arg		
			50			55						60				

(2) INFORMATION FOR SEQ ID NO:1210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..103
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1210:

Met	Glu	Thr	Gln	Lys	Val	Thr	Ala	Arg	Gly	Tyr	Arg	Leu	Glu	Glu	Lys	
1				5					10					15		
Lys	Val	Leu	Lys	Ala	Val	Arg	Arg	Ala	Gly	Lys	Ala	Ala	Glu	Leu	Trp	
			20					25					30			
Pro	Tyr	Arg	Leu	Gly	Asn	Ser	His	Phe	Ala	Ser	Phe	Tyr	Lys	Tyr	Pro	
			35				40					45				
Ser	Tyr	Val	Thr	Asn	His	Tyr	Tyr	Ser	Asp	Ala	His	Arg	Thr	Asp	Pro	
			50			55					60					
Thr	Gly	Gly	Val	His	Thr	Phe	Phe	His	Thr	Pro	Ala	Val	Tyr	Ser	Val	
			65			70			75					80		
Ala	Val	Ala	Gly	Asp	Glu	Ile	Ala	Ala	Ser	Met	Phe	Ser	Asp	Asp	Asn	
			85					90					95			
Pro	His	Ala	Cys	Thr	Ile	Met										
			100													

(2) INFORMATION FOR SEQ ID NO:1211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..65
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499853

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1211:

Met His Thr Val Arg Ile Pro Pro Val Val Ser Thr Leu Ser Ser Thr

1	5	10	15
Leu Leu Arg Phe Thr Arg Leu Leu Trp Leu Glu Met Arg Ser Arg Leu			
20	25	30	
Arg Cys Leu Ala Met Ile Ile Pro Met Leu Val Leu Leu Cys Ser Leu			
35	40	45	
Leu Val Tyr Lys Asn Met Phe Ser Val His Leu Leu Arg Pro Asn Leu			
50	55	60	

Ile
65

(2) INFORMATION FOR SEQ ID NO:1212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..835
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499854

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1212:

aacttaattt	atcttaggc	catgggaaga	aaagtcttct	gcgttaataa	tttctagatc	60
tttccacaac	attcataccg	aactccctta	aatcttgaaa	cgaccaattt	cttcaaaaac	120
atagattgtt	tgcatggcg	acagacaacg	acgtggaagt	tggaacagag	acacctctgt	180
tttcgggaag	gtttttgagg	aacagagatt	tatatctctt	cttgcccttt	ctcttaggtt	240
ttcttgatca	agaatcatca	aacggagatg	atgatgatgt	tgcttcatcg	cgtgagagaa	300
tcattttagt	caaccctttt	acacaaggaa	tgattgtgct	cgaaggtcca	tcaggaaatga	360
atcctctgct	tcgtagctta	ctggagtcac	gtgaggaagg	tcgtcctcct	cgctccaagg	420
cttcacatga	tgcatggccg	atcgttgaga	ttgatggcgt	tgaaggagag	tgtgtgatct	480
gtttgggaga	gtggaagtcc	gaggagacgg	tgaaggagat	ccgctgtaag	cataggtttc	540
acggttggat	tatagagaaa	tggttagggt	ttcatgggtc	gtgtcctggt	tgtaggtaacg	600
agatgctctg	tgatggagat	gagattggga	agaaaagaaa	cgatgggaa	gagatttggg	660
ttaggttca	tttcaacgat	ggtcggagaa	ttagagattt	ttctgcgcag	gacggtggaa	720
acagtgtatg	tggtgagtc	gagaattagg	attacataa	gaagcttttg	taaaaaaac	780
ttgtgccttt	ttttgtctt	gttctgggaa	aaggttgatg	aacttttttt	gtctt	

(2) INFORMATION FOR SEQ ID NO:1213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..204
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1213:

Met Ala Thr Glu Gln Asp Ala Glu Val Gly Thr Glu Thr Pro Ser Val			
1	5	10	15
Ser Gly Arg Phe Leu Arg Asn Arg Asp Leu Tyr Leu Phe Leu Pro Phe			
20	25	30	
Leu Leu Gly Phe Ser Asp Gln Glu Ser Ser Asn Gly Asp Asp Asp Asp			
35	40	45	
Val Ala Ser Ser Arg Glu Arg Ile Ile Leu Val Asn Pro Phe Thr Gln			
50	55	60	
Gly Met Ile Val Leu Glu Gly Ser Ser Gly Met Asn Pro Leu Leu Arg			
65	70	75	80
Ser Leu Leu Glu Ser Arg Glu Glu Gly Arg Pro Pro Ala Ser Lys Ala			
85	90	95	
Ser Ile Asp Ala Met Pro Ile Val Glu Ile Asp Gly Cys Glu Gly Glu			
100	105	110	

Cys Val Ile Cys Leu Glu Glu Trp Lys Ser Glu Glu Thr Val Lys Glu
115 120 125
Met Pro Cys Lys His Arg Phe His Gly Gly Cys Ile Glu Lys Trp Leu
130 135 140
Gly Phe His Gly Ser Cys Pro Val Cys Arg Tyr Glu Met Pro Val Asp
145 150 155 160
Gly Asp Glu Ile Gly Lys Lys Arg Asn Asp Gly Asn Glu Ile Trp Val
165 170 175
Arg Phe Ser Phe Asn Asp Gly Arg Arg Ile Arg Asp Phe Ser Ala Gln
180 185 190
Asp Gly Gly Asn Ser Asp Gly Val Glu Ser Glu Asn
195 200

(2) INFORMATION FOR SEQ ID NO:1214:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 139 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..139
(D) OTHER INFORMATION: / Ceres Seq. ID 1499856

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1214:

Met Ile Val Leu Glu Gly Ser Ser Gly Met Asn Pro Leu Leu Arg Ser
1 5 10 15
Leu Leu Glu Ser Arg Glu Glu Gly Arg Pro Pro Ala Ser Lys Ala Ser
20 25 30
Ile Asp Ala Met Pro Ile Val Glu Ile Asp Gly Cys Glu Gly Glu Cys
35 40 45
Val Ile Cys Leu Glu Glu Trp Lys Ser Glu Glu Thr Val Lys Glu Met
50 55 60
Pro Cys Lys His Arg Phe His Gly Gly Cys Ile Glu Lys Trp Leu Gly
65 70 75 80
Phe His Gly Ser Cys Pro Val Cys Arg Tyr Glu Met Pro Val Asp Gly
85 90 95
Asp Glu Ile Gly Lys Lys Arg Asn Asp Gly Asn Glu Ile Trp Val Arg
100 105 110
Phe Ser Phe Asn Asp Gly Arg Arg Ile Arg Asp Phe Ser Ala Gln Asp
115 120 125
Gly Gly Asn Ser Asp Gly Val Glu Ser Glu Asn
130 135

(2) INFORMATION FOR SEQ ID NO:1215:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..130
(D) OTHER INFORMATION: / Ceres Seq. ID 1499857

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1215:

Met Asn Pro Leu Leu Arg Ser Leu Leu Glu Ser Arg Glu Glu Gly Arg
1 5 10 15
Pro Pro Ala Ser Lys Ala Ser Ile Asp Ala Met Pro Ile Val Glu Ile
20 25 30
Asp Gly Cys Glu Gly Glu Cys Val Ile Cys Leu Glu Glu Trp Lys Ser
35 40 45
Glu Glu Thr Val Lys Glu Met Pro Cys Lys His Arg Phe His Gly Gly

50		55		60
Cys Ile Glu Lys Trp	Leu Gly Phe His Gly Ser	Cys Pro Val	Cys Arg	
65	70	75	80	
Tyr Glu Met Pro Val Asp Gly Asp Glu Ile Gly Lys Lys Arg Asn Asp				
	85	90	95	
Gly Asn Glu Ile Trp Val Arg Phe Ser Phe Asn Asp Gly Arg Arg Ile				
	100	105	110	
Arg Asp Phe Ser Ala Gln Asp Gly Gly Asn Ser Asp Gly Val Glu Ser				
	115	120	125	
Glu Asn				
130				

(2) INFORMATION FOR SEQ ID NO:1216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1745 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1745
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499875

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1216:

aaacaagaaa	gagattagga	agagagagac	ggcgatggcg	gctacaggat	ctggagcggtc	60
tcaattcatt	tccagttccg	gcggtaaacg	aagcttctcc	aattctccac	tcactcgagaa	120
ctctgattct	aatcagatta	ttgtctctga	gaagaagagc	tggaagaatt	tctttgctta	180
cttagggcct	ggttttcttg	tttcaatcgc	atatattgat	cctggaaact	ttgagaactga	240
tctgcaagct	ggagcacact	accaagtatga	attactttgg	atcatattgg	ttggcctcatg	300
tgccgctttg	gtgattcaat	ctctggctgc	taactcttgg	gtgtgcacag	gaaaacatttt	360
ggctgagcaa	gttagagccg	agttacccaa	agttccaaac	tttatgttat	gggtcctgtgc	420
tgaaattgca	gtagttgott	gtgacatacc	ggaagtatat	ggaacagctt	ttgtcttgaa	480
catgctcttt	agcataccgg	gttggatcgg	tggtctcttg	acaggcttaa	gtacgctgatg	540
tcttctcgca	cttcaaaaaa	acgggggtgag	aaagctggag	tctttgatag	cgtttcttgt	600
gttccacaatt	gctatatgct	tctttgttga	gcttcattac	tcaagccagc	accagcaga	660
agtcactaat	ggctctcttg	ttctcgaact	taaaggaaat	gggtgcaact	gtctcgcaat	720
ctctttgtgc	ggagccatgg	ttatgcgcga	taattctctc	ctccactcgg	ccttggttct	780
ctcgaggaaa	atccctcggt	ccgcttctgg	tatcaaggaa	gcttgccagg	tttacttgat	840
agaaagtggg	ttggctctta	tgttgccctt	tctcataaac	gtctctgtaa	tatcagtaag	900
cggggctggt	tgtaatgccc	ccaacttaag	ccctgaagat	cgagctaatt	gtgaggatttt	960
ggaactaaac	aaggctcttg	ttctgctacg	gaacgttgtg	ggaaaatgga	gctcaaaagct	1020
atttgcaatc	gcgctctctg	ctcttggtca	gagctcgagc	ataaccggaa	gtctcgtgg	1080
acaattatga	atgcaggcgt	ttcttgatct	cagactcgag	ccatggctga	gaaacttact	1140
aacaagatgt	ttagctataa	tcccgagctc	aattgttgct	ctcatcgctg	gttcagctgat	1200
agctggaaag	ttaatcatca	ttgcctcgat	gatcttatcc	tttgagctcc	cgtttgcggt	1260
ggttcctctt	ctaaaattca	caagttgcaa	aaccaagatg	gggtcacatg	tcaaccacaa	1320
ggcgattaca	gctttgactt	gggtcatctg	tggtttaaat	atgggaaata	acatatacta	1380
tctagttaag	agtttcatca	aactgcttat	ccacagtcac	atgaagctta	tctcgtcgtg	1440
cttctgtgga	attcttgggt	tcgcaggoat	tgctctctat	ttagccgcga	tagcttacct	1500
tgcttctcgg	aaaaacagag	tagccacttc	tctctctatt	tcaagagact	cacaaaaagt	1560
ggagacactt	ccaagacagg	acattgtcaa	catgcagcta	ccatgtagag	tatctacctc	1620
cgatgttggc	tgagtcatca	ttaaagcttag	gattccaata	aagttagatc	taaaccaagt	1680
tcataaaaac	cttctgatag	tgtagtagaa	taaaggttat	atgaatcggt	ttgcgctctt	1740
tctttt						

(2) INFORMATION FOR SEQ ID NO:1217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..543

(D) OTHER INFORMATION: / Ceres Seq. ID 1499876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1217:

Asn Lys Lys Glu Ile Arg Lys Arg Glu Thr Ala Met Ala Ala Thr Gly
1 5 10 15
Ser Gly Arg Ser Gln Phe Ile Ser Ser Ser Gly Gly Asn Arg Ser Phe
20 25 30
Ser Asn Ser Ser Pro Leu Ile Glu Asn Ser Asp Ser Asn Gln Ile Ile Val
35 40 45
Ser Glu Lys Lys Ser Trp Lys Asn Phe Phe Ala Tyr Leu Gly Pro Gly
50 55 60
Phe Leu Val Ser Ile Ala Tyr Ile Asp Pro Gly Asn Phe Glu Thr Asp
65 70 75 80
Leu Gln Ala Gly Ala His Tyr Lys Tyr Glu Leu Leu Trp Ile Ile Leu
85 90 95
Val Ala Ser Cys Ala Ala Leu Val Ile Gln Ser Leu Ala Ala Asn Leu
100 105 110
Gly Val Val Thr Gly Lys His Leu Ala Glu Gln Cys Arg Ala Glu Tyr
115 120 125
Ser Lys Val Pro Asn Phe Met Leu Trp Val Val Ala Glu Ile Ala Val
130 135 140
Val Ala Cys Asp Ile Pro Glu Val Ile Gly Thr Ala Phe Ala Leu Asn
145 150 155 160
Met Leu Phe Ser Ile Pro Val Trp Ile Gly Val Leu Leu Thr Gly Leu
165 170 175
Ser Thr Leu Ile Leu Leu Ala Leu Gln Lys Tyr Gly Val Arg Lys Leu
180 185 190
Glu Phe Leu Ile Ala Phe Leu Val Phe Thr Ile Ala Ile Cys Phe Phe
195 200 205
Val Glu Leu His Tyr Ser Lys Pro Asp Pro Gly Glu Val Leu His Gly
210 215 220
Leu Phe Val Pro Gln Leu Lys Gly Asn Gly Ala Thr Gly Leu Ala Ile
225 230 235 240
Ser Leu Leu Gly Ala Met Val Met Pro His Asn Leu Phe Leu His Ser
245 250 255
Ala Leu Val Leu Ser Arg Lys Ile Pro Arg Ser Ala Ser Gly Ile Lys
260 265 270
Glu Ala Cys Arg Phe Tyr Leu Ile Glu Ser Gly Leu Ala Leu Met Val
275 280 285
Ala Phe Leu Ile Asn Val Ser Val Ile Ser Val Ser Gly Ala Val Cys
290 295 300
Asn Ala Pro Asn Leu Ser Pro Glu Asp Arg Ala Asn Cys Glu Asp Leu
305 310 315 320
Asp Leu Asn Lys Ala Ser Phe Leu Leu Arg Asn Val Val Gly Lys Trp
325 330 335
Ser Ser Lys Leu Phe Ala Ile Ala Leu Leu Ala Ser Gly Gln Ser Ser
340 345 350
Thr Ile Thr Gly Thr Tyr Ala Gly Gln Tyr Val Met Gln Gly Phe Leu
355 360 365
Asp Leu Arg Leu Glu Pro Trp Leu Arg Asn Leu Leu Thr Arg Cys Leu
370 375 380
Ala Ile Ile Pro Ser Leu Ile Val Ala Leu Ile Gly Gly Ser Ala Gly
385 390 395 400
Ala Gly Lys Leu Ile Ile Ile Ala Ser Met Ile Leu Ser Phe Glu Leu
405 410 415
Pro Phe Ala Leu Val Pro Leu Leu Lys Phe Thr Ser Cys Lys Thr Lys
420 425 430
Met Gly Ser His Val Asn Pro Met Ala Ile Thr Ala Leu Thr Trp Val
435 440 445
Ile Gly Gly Leu Ile Met Gly Ile Asn Ile Tyr Tyr Leu Val Ser Ser

450										455										460																																			
Phe	Ile	Lys	Leu	Leu	Ile	His	Ser	His	Met	Lys	Lys	Leu	Ile	Leu	Val	Val	Val	Val	Val	Phe	Ile	Lys	Leu	Leu	Ile	His	Ser	His	Met	Lys	Lys	Leu	Ile	Leu	Val	Val	Phe	Ile	Lys	Leu	Leu	Ile	His	Ser	His	Met	Lys	Lys	Leu	Ile	Leu	Val	Val		
465																				470																		475																	
Phe	Cys	Gly	Ile	Leu	Gly	Phe	Ala	Gly	Ile	Ala	Leu	Tyr	Leu	Ala	Ala	Ala	Ala	Ala	Ala	Phe	Ala	Gly	Ile	Ala	Leu	Tyr	Leu	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Phe	Ala	Gly	Ile	Ala	Leu	Tyr	Leu	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala
																				485																		490																	
Ile	Ala	Tyr	Leu	Val	Phe	Arg	Lys	Asn	Arg	Val	Ala	Thr	Ser	Leu	Leu	Leu	Leu	Leu	Leu	Ile	Ala	Tyr	Leu	Val	Phe	Arg	Lys	Asn	Arg	Val	Ala	Thr	Ser	Leu	Leu	Leu	Ile	Ala	Tyr	Leu	Val	Phe	Arg	Lys	Asn	Arg	Val	Ala	Thr	Ser	Leu	Leu	Leu		
																				500																		505																	
Ile	Ser	Arg	Asp	Ser	Gln	Asn	Val	Glu	Thr	Leu	Pro	Gln	Gln	Asp	Ile	Ile	Ile	Ile	Ile	Ile	Ser	Arg	Asp	Ser	Gln	Asn	Val	Glu	Thr	Leu	Pro	Gln	Gln	Asp	Ile	Ile	Ile	Ser	Arg	Asp	Ser	Gln	Asn	Val	Glu	Thr	Leu	Pro	Gln	Gln	Asp	Ile	Ile		
																				515																		520																	
Val	Asn	Met	Gln	Leu	Pro	Cys	Arg	Val	Ser	Thr	Ser	Asp	Val	Gly	Gly	Gly	Gly	Gly	Gly	Val	Asn	Met	Gln	Leu	Pro	Cys	Arg	Val	Ser	Thr	Ser	Asp	Val	Gly	Gly	Gly	Val	Asn	Met	Gln	Leu	Pro	Cys	Arg	Val	Ser	Thr	Ser	Asp	Val	Gly	Gly	Gly		
																				530																		535																	
(2) INFORMATION FOR SEQ ID NO:1218:																																																							
(i) SEQUENCE CHARACTERISTICS:																																																							
(A) LENGTH: 532 amino acids																																																							
(B) TYPE: amino acid																																																							
(C) STRANDEDNESS:																																																							
(D) TOPOLOGY: linear																																																							
(ii) MOLECULE TYPE: peptide																																																							
(ix) FEATURE:																																																							
(A) NAME/KEY: peptide																																																							
(B) LOCATION: 1..532																																																							
(D) OTHER INFORMATION: / Ceres Seq. ID 1499877																																																							
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1218:																																																							
Met	Ala	Ala	Thr	Gly	Ser	Gly	Arg	Ser	Gln	Phe	Ile	Ser	Ser	Ser	Ser	Gly	Gly	Gly	Gly	Met	Ala	Ala	Thr	Gly	Ser	Gly	Arg	Ser	Gln	Phe	Ile	Ser	Ser	Ser	Gly	Gly	Gly	Met	Ala	Ala	Thr	Gly	Ser	Gly	Arg	Ser	Gln	Phe	Ile	Ser	Ser	Ser	Gly	Gly	Gly
1																				5																	10																		
Gly	Asn	Arg	Ser	Phe	Ser	Asn																																																	

Asn Cys Glu Asp Leu Asp Leu Asn Lys Ala Ser Phe Leu Leu Arg Asn
305 310 315 320
Val Val Gly Lys Trp Ser Ser Lys Leu Phe Ala Ile Ala Leu Leu Ala
325 330 335
Ser Gly Gln Ser Ser Thr Ile Thr Gly Thr Tyr Ala Gly Gln Tyr Val
340 345 350
Met Gln Gly Phe Leu Asp Leu Arg Leu Glu Pro Trp Leu Arg Asn Leu
355 360 365
Leu Thr Arg Cys Leu Ala Ile Ile Pro Ser Leu Ile Val Ala Leu Ile
370 375 380
Gly Gly Ser Ala Gly Ala Gly Lys Leu Ile Ile Ile Ala Ser Met Ile
385 390 395 400
Leu Ser Phe Glu Leu Leu Pro Phe Ala Leu Val Pro Leu Leu Lys Phe Thr
405 410 415
Ser Cys Lys Thr Lys Met Gly Ser His Val Asn Pro Met Ala Ile Thr
420 425 430
Ala Leu Thr Trp Val Ile Gly Gly Leu Ile Met Gly Ile Asn Ile Tyr
435 440 445
Tyr Leu Val Ser Ser Phe Ile Lys Leu Leu Ile His Ser His Met Lys
450 455 460
Leu Ile Leu Val Val Phe Cys Gly Ile Leu Gly Phe Ala Gly Ile Ala
465 470 475 480
Leu Tyr Leu Ala Ala Ile Ala Tyr Leu Val Phe Arg Lys Asn Arg Val
485 490 495
Ala Thr Ser Leu Leu Ile Ser Arg Asp Ser Gln Asn Val Glu Thr Leu
500 505 510
Pro Arg Gln Asp Ile Val Asn Met Gln Leu Pro Cys Arg Val Ser Thr
515 520 525
Ser Asp Val Gly
530

(2) INFORMATION FOR SEQ ID NO:1219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..409
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499878

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1219:

Met Leu Trp Val Val Ala Glu Ile Ala Val Val Ala Cys Asp Ile Pro
1 5 10 15
Glu Val Ile Gly Thr Ala Phe Ala Leu Asn Met Leu Phe Ser Ile Pro
20 25 30
Val Trp Ile Gly Val Leu Leu Thr Gly Leu Ser Thr Leu Ile Leu Leu
35 40 45
Ala Leu Gln Lys Tyr Gly Val Arg Lys Leu Glu Phe Leu Ile Ala Phe
50 55 60
Leu Val Phe Thr Ile Ala Ile Cys Phe Phe Val Glu Leu His Tyr Ser
65 70 75 80
Lys Pro Asp Pro Gly Glu Val Leu His Gly Leu Phe Val Pro Gln Leu
85 90 95
Lys Gly Asn Gly Ala Thr Gly Leu Ala Ile Ser Leu Leu Gly Ala Met
100 105 110
Val Met Pro His Asn Leu Phe Leu His Ser Ala Leu Val Leu Ser Arg
115 120 125
Lys Ile Pro Arg Ser Ala Ser Gly Ile Lys Glu Ala Cys Arg Phe Tyr
130 135 140
Leu Ile Glu Ser Gly Leu Ala Leu Met Val Ala Phe Leu Ile Asn Val

145				150				155				160
Ser	Val	Ile	Ser	Val	Ser	Gly	Ala	Val	Cys	Asn	Ala	Pro
				165					170			175
Pro	Glu	Asp	Arg	Ala	Asn	Cys	Glu	Asp	Leu	Asp	Leu	Asn
			180					185				190
Phe	Leu	Leu	Arg	Asn	Val	Val	Gly	Lys	Trp	Ser	Ser	Lys
			195				200					205
Ile	Ala	Leu	Leu	Ala	Ser	Gly	Gln	Ser	Ser	Thr	Ile	Thr
			210			215				220		225
Ala	Gly	Gln	Tyr	Val	Met	Gln	Gly	Phe	Leu	Asp	Leu	Arg
				230				235				240
Trp	Leu	Arg	Asn	Leu	Leu	Thr	Arg	Cys	Leu	Ala	Ile	Ile
			245					250				255
Ile	Val	Ala	Leu	Ile	Gly	Gly	Ser	Ala	Gly	Ala	Gly	Lys
			260				265					270
Ile	Ala	Ser	Met	Ile	Leu	Ser	Phe	Glu	Leu	Pro	Phe	Ala
			275				280				285	290
Leu	Leu	Lys	Phe	Thr	Ser	Cys	Lys	Thr	Lys	Met	Gly	Ser
			290			295					300	305
Pro	Met	Ala	Ile	Thr	Ala	Leu	Thr	Trp	Val	Ile	Gly	Gly
				310						315		320
Gly	Ile	Asn	Ile	Tyr	Tyr	Leu	Val	Ser	Ser	Phe	Ile	Lys
			325					330				335
His	Ser	His	Met	Lys	Leu	Ile	Leu	Val	Val	Phe	Cys	Gly
			340					345				350
Phe	Ala	Gly	Ile	Ala	Leu	Tyr	Leu	Ala	Ala	Ile	Ala	Tyr
			355				360				365	370
Arg	Lys	Asn	Arg	Val	Ala	Thr	Ser	Leu	Leu	Ile	Ser	Arg
			370			375					380	385
Asn	Val	Glu	Thr	Leu	Pro	Arg	Gln	Asp	Ile	Val	Asn	Met
				390						395		400
Cys	Arg	Val	Ser	Thr	Ser	Asp	Val	Gly				
				405								

(2) INFORMATION FOR SEQ ID NO:1220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 700 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..700
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1220:

acctgttctc	atattagttt	gtttatacaac	tcacttagaa	taattagtag	tacatttcag	60
ccaaattcat	attcttgaga	gaaaagaaat	cgaagatggc	aacaaaaatcc	accggaggtg	120
ccgagaaaaac	caagtcgata	gaagtgaaga	agaaactaat	caacgtgttg	atcgtcgatg	180
atgatccatt	aaaccgtaga	ctccacgaga	tgatcatcaa	aacgatcgga	ggaattttctc	240
agactgcaaa	gaatggcgag	gaggcagtg	tcctccaccg	tgacggcgaa	gcatctttcg	300
acctattctt	aatggataag	gaaatgectg	agaggggatg	agtttcgaca	actaagaagc	360
taagagaaat	gaaagtgaac	tcaatgatcg	ttggggtaac	gtcagtagct	gaccaagaag	420
aagagcgtaa	ggtctttatg	gaagctgggc	tcaaccattg	cttgaaaaaa	cccttaacca	480
aggccaagat	cttcccgctc	attagccacc	tcttcgatgc	ttgatggatg	aaggctcatt	540
aatgtatcta	tattttcaat	catgaaatca	cctacacgtg	tattttgacac	aaaaatctgc	600
atttgttggt	atataggggt	tctcatatct	atgttttgatt	tattttctta	tcgtccgagg	660
taaaatcatg	caagtcattt	cttttggcta	ataaaatatt			

(2) INFORMATION FOR SEQ ID NO:1212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..142
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499900
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1221:
Met Ala Thr Lys Ser Thr Gly Gly Thr Glu Lys Thr Lys Ser Ile Glu
1 5 10 15
Val Lys Lys Lys Leu Ile Asn Val Leu Ile Val Asp Asp Asp Pro Leu
 20 25 30
Asn Arg Arg Leu His Glu Met Ile Ile Lys Thr Ile Gly Gly Ile Ser
 35 40 45
Gln Thr Ala Lys Asn Gly Glu Glu Ala Val Ile Leu His Arg Asp Gly
 50 55 60
Glu Ala Ser Phe Asp Leu Ile Leu Met Asp Lys Glu Met Pro Glu Arg
65 70 75 80
Asp Gly Val Ser Thr Thr Lys Lys Leu Arg Glu Met Lys Val Thr Ser
 85 90 95
Met Ile Val Gly Val Thr Ser Val Ala Asp Gln Glu Glu Glu Arg Lys
 100 105 110
Ala Phe Met Glu Ala Gly Leu Asn His Cys Leu Glu Lys Pro Leu Thr
 115 120 125
Lys Ala Lys Ile Phe Pro Leu Ile Ser His Leu Phe Asp Ala
130 135 140

(2) INFORMATION FOR SEQ ID NO:1222:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..104
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499901
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1222:
Met Ile Ile Lys Thr Ile Gly Gly Ile Ser Gln Thr Ala Lys Asn Gly
1 5 10 15
Glu Glu Ala Val Ile Leu His Arg Asp Gly Glu Ala Ser Phe Asp Leu
 20 25 30
Ile Leu Met Asp Lys Glu Met Pro Glu Arg Asp Gly Val Ser Thr Thr
 35 40 45
Lys Lys Leu Arg Glu Met Lys Val Thr Ser Met Ile Val Gly Val Thr
 50 55 60
Ser Val Ala Asp Gln Glu Glu Arg Lys Ala Phe Met Glu Ala Gly
65 70 75 80
Leu Asn His Cys Leu Glu Lys Pro Leu Thr Lys Ala Lys Ile Phe Pro
 85 90 95
Leu Ile Ser His Leu Phe Asp Ala
 100

(2) INFORMATION FOR SEQ ID NO:1223:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 520 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -

(B) LOCATION: 1..520

(D) OTHER INFORMATION: / Ceres Seq. ID 1499902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1223:

aaggtgtcgg	atcttgatga	agcttcgaag	attcttgtgc	cggagtctgt	gaaaaagctc	60
cgggaaactta	tgggttacat	attttacaaa	cggcggttgg	caagactggt	tcctacttgt	120
ctttctccatg	atttcatcga	acatgctttg	acaagagata	atatggaaga	gaagagagaa	180
ctgattaaag	ccataccaaa	agacagaata	atctcagaga	ttccaaagct	caaacaccca	240
acattgataa	tatgggggga	gcatgatcaa	gtgttcccat	tggagatggg	caagagactt	300
gagaagcatg	taggagataa	tgggaaactc	gttatcatca	agagaacttg	tcatactttt	360
aacttcgaga	aacctaaaaa	gtttatcaaa	cttctcaaat	ctttctctct	agagactagt	420
aaaccacaga	ttctgtcttc	taatgtttga	ttcttagtca	tcgttttgaa	gatcctctca	480
taastaattt	ccaaggatta	ataacatata	tatcattttc			

(2) INFORMATION FOR SEQ ID NO:1224:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1499903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1224:

Lys	Val	Ser	Asp	Leu	Asp	Glu	Ala	Ser	Lys	Ile	Leu	Val	Pro	Glu	Ser	
1			5					10						15		
Val	Lys	Lys	Leu	Arg	Glu	Leu	Met	Gly	Tyr	Ile	Phe	Tyr	Lys	Pro	Ala	
			20					25					30			
Leu	Ala	Arg	Leu	Val	Pro	Thr	Cys	Leu	Leu	His	Asp	Phe	Ile	Glu	His	
			35				40					45				
Ala	Leu	Thr	Arg	Asp	Asn	Met	Glu	Glu	Lys	Arg	Glu	Leu	Ile	Lys	Ala	
			50			55					60					
Ile	Pro	Lys	Asp	Arg	Ile	Ile	Ser	Glu	Ile	Pro	Lys	Leu	Lys	Gln	Pro	
65			70					75						80		
Thr	Leu	Ile	Ile	Trp	Gly	Glu	His	Asp	Gln	Val	Phe	Pro	Leu	Glu	Met	
			85					90						95		
Gly	Lys	Arg	Leu	Glu	Lys	His	Val	Gly	Asp	Asn	Gly	Lys	Leu	Val	Ile	
			100					105						110		
Ile	Lys	Arg	Thr	Gly	His	Ile	Phe	Asn	Phe	Glu	Lys	Pro	Lys	Lys	Phe	
			115				120					125				
Ile	Lys	Leu	Leu	Lys	Ser	Phe	Leu	Leu	Glu	Thr	Ser	Lys	Pro	Gln	Ile	
			130			135					140					
Pro	Val	Ser	Asn	Val												
145																

(2) INFORMATION FOR SEQ ID NO:1225:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..126

(D) OTHER INFORMATION: / Ceres Seq. ID 1499904

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1225:

Met	Gly	Tyr	Ile	Phe	Tyr	Lys	Pro	Ala	Leu	Ala	Arg	Leu	Val	Pro	Thr	
1			5					10						15		
Cys	Leu	Leu	His	Asp	Phe	Ile	Glu	His	Ala	Leu	Thr	Arg	Asp	Asn	Met	
			20					25					30			
Glu	Glu	Lys	Arg	Glu	Leu	Ile	Lys	Ala	Ile	Pro	Lys	Asp	Arg	Ile	Ile	

35 40 45
Ser Glu Ile Pro Lys Leu Lys Gln Pro Thr Leu Ile Ile Trp Gly Glu
50 55 60
His Asp Gln Val Phe Pro Leu Glu Met Gly Lys Arg Leu Glu Lys His
65 70 75 80
Val Gly Asp Asn Gly Lys Leu Val Ile Ile Lys Arg Thr Gly His Ile
85 90 95
Phe Asn Phe Glu Lys Pro Lys Lys Phe Ile Lys Leu Leu Lys Ser Phe
100 105 110
Leu Leu Glu Thr Ser Lys Pro Gln Ile Pro Val Ser Asn Val
115 120 125

(2) INFORMATION FOR SEQ ID NO:1226:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1499905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1226:

Met Glu Glu Lys Arg Glu Leu Ile Lys Ala Ile Pro Lys Asp Arg Ile
1 5 10 15
Ile Ser Glu Ile Pro Lys Leu Lys Gln Pro Thr Leu Ile Ile Trp Gly
20 25 30
Glu His Asp Gln Val Phe Pro Leu Glu Met Gly Lys Arg Leu Glu Lys
35 40 45
His Val Gly Asp Asn Gly Lys Leu Val Ile Ile Lys Arg Thr Gly His
50 55 60
Ile Phe Asn Phe Glu Lys Pro Lys Lys Phe Ile Lys Leu Leu Lys Ser
65 70 75 80
Phe Leu Leu Glu Thr Ser Lys Pro Gln Ile Pro Val Ser Asn Val
85 90 95

(2) INFORMATION FOR SEQ ID NO:1227:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 982 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..982

(D) OTHER INFORMATION: / Ceres Seq. ID 1499906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1227:

agaacacaaa caaaaacaca ttgtaacatt agtttaagca taagctctct ttatgtcgaa 60
taataataat tcttcgacca ccggtgaatca agaaacgacg acgtctctgt aagttctaat 120
cacattgctt actgatcaat ctctcctaac ctcaccagga tcatcttctt ctcttcacc 180
gagacctctc ggtggtacac cggcgagaag aacggcgact ggattatccg gcaagcactc 240
taatttcagg gggatttcgac tacgtaacgg aaaaatggga tcggagatta gagagccacg 300
taaaacgaca agaatttggc tcgggactta tcgggtaccg gagatggctg ccgcccgtta 360
cgacgtggct cggttagctt taaaaggacc aggccgtttt gaattttcct gggttagct 420
ttgacttacg tggctccggt ttcaaaactct gctgcggata taagagcgcg tgctagtaga 480
gcagcggaga tgaagcaacc ggcacgggtt ggggatgaga aggtatttga accggttcaa 540
cccggcaaaag aggaagaatt agaagaatgt tcggtgaact cgtgttctgt gtagtttatg 600
gatgaggaag cgaattgtga tatgccgact ttgttgacgg agatggccta gggatgtgtg 660
atgagttcac cgagaatgat gatacatccg acgatggaaag atgattcgcc aggaatcat 720
gaaggagata atctttggag ttataaatga atccattgaa gctgctctct tttttattgt 780
tttcgggtcg aatgagattt tccccctttt tttttctttt tgggtcgctg ttatggaaag 840

tcaaataggt tattaatatg atctattaat atttttgaaa cataatgagt ttgaatttga 900
atttttccat ttttatataa atatggttta tatgagggaa aaatagatac atatcgaaga 960
tataagaatt gtttttctgc tt

(2) INFORMATION FOR SEQ ID NO:1228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..121
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499907

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1228:

Met	Ser	Asn	Asn	Asn	Asn	Ser	Pro	Thr	Thr	Val	Asn	Gln	Glu	Thr	Thr	
1			5						10				15			
Thr	Ser	Arg	Glu	Val	Ser	Ile	Thr	Leu	Pro	Thr	Asp	Gln	Ser	Pro	Gln	
			20					25				30				
Thr	Ser	Pro	Gly	Ser	Ser	Ser	Ser	Pro	Ser	Pro	Arg	Pro	Ser	Gly	Gly	
			35				40				45					
Ser	Pro	Ala	Arg	Arg	Thr	Ala	Thr	Gly	Leu	Ser	Gly	Lys	His	Ser	Ile	
			50			55				60						
Phe	Arg	Gly	Ile	Arg	Leu	Arg	Asn	Gly	Lys	Trp	Val	Ser	Glu	Ile	Arg	
			65			70			75							
Glu	Pro	Arg	Lys	Thr	Thr	Arg	Ile	Trp	Leu	Gly	Thr	Tyr	Pro	Val	Pro	
			85					90					95			
Glu	Met	Ala	Ala	Ala	Ala	Tyr	Asp	Val	Ala	Ala	Leu	Ala	Leu	Lys	Gly	
			100				105				110					
Pro	Gly	Arg	Phe	Glu	Phe	Ser	Trp	Val								
			115			120										

(2) INFORMATION FOR SEQ ID NO:1229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..86
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1229:

Met	Lys	Gln	Pro	Asp	Gln	Gly	Gly	Asp	Glu	Lys	Val	Leu	Glu	Pro	Val	
1			5					10					15			
Gln	Pro	Gly	Lys	Glu	Glu	Glu	Leu	Glu	Glu	Val	Ser	Cys	Asn	Ser	Cys	
			20					25				30				
Ser	Leu	Glu	Phe	Met	Asp	Glu	Glu	Ala	Met	Leu	Asn	Met	Pro	Thr	Leu	
			35				40				45					
Leu	Thr	Glu	Met	Ala	Glu	Gly	Met	Leu	Met	Ser	Pro	Pro	Arg	Met	Met	
			50			55				60						
Ile	His	Pro	Thr	Met	Glu	Asp	Asp	Ser	Pro	Glu	Asn	His	Glu	Gly	Asp	
			65			70			75							
Asn	Leu	Trp	Ser	Tyr	Lys											
			85													

(2) INFORMATION FOR SEQ ID NO:1230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 932 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..932

(D) OTHER INFORMATION: / Ceres Seq. ID 1499909

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1230:

aactgtttga	tttctgagga	gaatccattg	tttccattcg	aagaaaaactc	taactttctc	60
gttgaaagctt	tgagctctct	acctctttat	ctccggagat	gtataataac	atgggaacctc	120
aaccggggat	cgcaagacct	ccaggaaaacc	ctgagccttg	tccatttggt	aatcctttca	180
ctggagctgg	ctcgggtttt	atccgtgggtg	gtttggggagc	gtagggggag	agaattttag	240
gatcgarcct	tgagtatgtt	cagagcaata	taagcccgta	ctctctgat	ccgcaatact	300
atttccaaagt	gaatgatcaa	tatgtgagga	ataaactgaa	ggttgttctg	tttctttcc	360
tacacccggg	acactggacc	agaatatctg	aaccagttgg	tggtagggctc	tcatacaagc	420
ctccaataata	tgatatcaat	gctcccagac	ttgtacattc	cctttatggc	atttggtacc	480
tacgttgtttc	ttgctggctt	ttcattggga	cttaatggaa	agtttacacc	ggaagctttg	540
aattggctgtg	ttgtgaaagg	attggttggt	tggtttttgc	aagtaagtct	cctgaaagta	600
acaactctcat	caacttgtag	tggaagagga	ccattactag	atattgtggc	atacggaggg	660
tatgcttttg	ctggctctgtg	tcttgccggc	tttgccaaaa	taattgtggg	atactcgtag	720
tacggcttgga	tgccatggac	ttgtctatgc	actgggattt	tcttggtgaa	gacgatgaaa	780
cggtgtctgt	ttgctgaagt	aagaagttac	gattcgagca	aacatcacta	cctctctctg	840
tttttagcct	tggtccagtt	ccactttttg	atatggcttg	gtaacattag	tgtttaattg	900
cttcttttgaa	atgaaaaaag	acgtttttgt	gt			

- (2) INFORMATION FOR SEQ ID NO:1231:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..159

(D) OTHER INFORMATION: / Ceres Seq. ID 1499910

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1231:

Met	Ile	Ser	Met	Leu	Pro	Asp	Leu	Tyr	Ile	Pro	Phe	Met	Ala	Phe	Gly	
1			5						10						15	
Thr	Tyr	Val	Val	Leu	Ala	Gly	Leu	Ser	Leu	Gly	Leu	Asn	Gly	Lys	Phe	
			20						25						30	
Thr	Pro	Glu	Ala	Leu	Asn	Trp	Leu	Phe	Val	Lys	Gly	Leu	Val	Gly	Trp	
		35				40					45					
Phe	Leu	Gln	Val	Met	Leu	Leu	Lys	Val	Thr	Leu	Leu	Ser	Ser	Gly	Ser	
	50					55				60						
Gly	Glu	Ala	Pro	Leu	Leu	Asp	Ile	Val	Ala	Tyr	Gly	Gly	Tyr	Ala	Phe	
	65					70				75					80	
Ala	Gly	Leu	Cys	Leu	Ala	Gly	Phe	Ala	Lys	Ile	Met	Trp	Gly	Tyr	Ser	
			85						90					95		
Tyr	Tyr	Ala	Leu	Met	Pro	Trp	Thr	Cys	Leu	Cys	Thr	Gly	Ile	Phe	Leu	
		100						105					110			
Val	Lys	Thr	Met	Lys	Arg	Val	Leu	Phe	Ala	Glu	Val	Arg	Ser	Tyr	Asp	
		115						120					125			
Ser	Ser	Lys	His	His	Tyr	Leu	Leu	Leu	Phe	Leu	Ala	Leu	Val	Gln	Phe	
		130						135					140			
Pro	Leu	Leu	Ile	Trp	Leu	Gly	Asn	Ile	Ser	Val	Asn	Trp	Leu	Leu		
	145							150					155			

- (2) INFORMATION FOR SEQ ID NO:1232:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 156 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..156
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1232:

Met Leu Pro Asp Leu Tyr Ile Pro Phe Met Ala Phe Gly Thr Tyr Val
1 5 10 15
Val Leu Ala Gly Leu Ser Leu Gly Leu Asn Gly Lys Phe Thr Pro Glu
20 25 30
Ala Leu Asn Trp Leu Phe Val Lys Gly Leu Val Gly Trp Phe Leu Gln
35 40 45
Val Met Leu Leu Lys Val Thr Leu Leu Ser Leu Gly Ser Gly Glu Ala
50 55 60
Pro Leu Leu Asp Ile Val Ala Tyr Gly Gly Tyr Ala Phe Ala Gly Leu
65 70 75 80
Cys Leu Ala Gly Phe Ala Lys Ile Met Trp Gly Tyr Ser Tyr Tyr Ala
85 90 95
Leu Met Pro Trp Thr Cys Leu Cys Thr Gly Ile Phe Leu Val Lys Thr
100 105 110
Met Lys Arg Val Leu Phe Ala Glu Val Arg Ser Tyr Asp Ser Ser Lys
115 120 125
His His Tyr Leu Leu Leu Phe Leu Ala Leu Val Gln Phe Pro Leu Leu
130 135 140
Ile Trp Leu Gly Asn Ile Ser Val Asn Trp Leu Leu
145 150 155

(2) INFORMATION FOR SEQ ID NO:1233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499912

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1233:

Met Ala Phe Gly Thr Tyr Val Val Leu Ala Gly Leu Ser Leu Gly Leu
1 5 10 15
Asn Gly Lys Phe Thr Pro Glu Ala Leu Asn Trp Leu Phe Val Lys Gly
20 25 30
Leu Val Gly Trp Phe Leu Gln Val Met Leu Leu Lys Val Thr Leu Leu
35 40 45
Ser Leu Gly Ser Gly Glu Ala Pro Leu Leu Asp Ile Val Ala Tyr Gly
50 55 60
Gly Tyr Ala Phe Ala Gly Leu Cys Leu Ala Gly Phe Ala Lys Ile Met
65 70 75 80
Trp Gly Tyr Ser Tyr Tyr Ala Leu Met Pro Trp Thr Cys Leu Cys Thr
85 90 95
Gly Ile Phe Leu Val Lys Thr Met Lys Arg Val Leu Phe Ala Glu Val
100 105 110
Arg Ser Tyr Asp Ser Ser Lys His His Tyr Leu Leu Leu Phe Leu Ala
115 120 125
Leu Val Gln Phe Pro Leu Leu Ile Trp Leu Gly Asn Ile Ser Val Asn
130 135 140
Trp Leu Leu
145

(2) INFORMATION FOR SEQ ID NO:1234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 619 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..619
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499924
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1234:

atttcggcg	actgtgaatt	atgtggtcgg	cgacgttacc	tttcccttct	tttgtggctt	60
cttcattctt	tctacctaat	tacaggaacc	gtaggtttcc	aaagattaaa	gcttcgctct	120
ttaattacc	tctagcgagc	aaaatcatgg	tcagaaattt	accgttttct	mcaagtgaag	180
attttctaaa	gagagagttt	tcagcttttg	gagagatagc	tgaagtgaag	cttatcaaa	240
atgaggcaat	gcagagatca	aaaggttatg	cttttattca	attcacgtct	caagatgatg	300
ctttttttgc	catagagacc	atggaccgtc	ggatgtacaa	tggaaagaatg	atttatatag	360
acattgcgaa	accgcgtaaa	cgtgatttcc	aaggactacc	gaggacttct	ggctcccctg	420
agaagtcgga	tgtgccagaa	gaagccgccta	atgatgaggt	tgctgattgc	tggtattagt	480
tgttagtatc	aagctcacca	aactgtaact	gaactgcat	aaatcagatg	tcaaatatg	540
cttcttatta	ggaatttgat	caatgtgaag	aatgttgttt	actgataaac	aattattgac	600
acggttccag	ttacagctc					

(2) INFORMATION FOR SEQ ID NO:1235:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 152 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..152
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499925
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1235:

Met	Trp	Ser	Ala	Thr	Leu	Ser	Phe	Pro	Ser	Phe	Val	Ala	Ser	Ser	Ser	
1					5					10					15	
Ser	Leu	Pro	Asn	Tyr	Arg	Asn	Arg	Arg	Phe	Pro	Lys	Ile	Lys	Ala	Ser	
			20					25					30			
Leu	Phe	Asn	Tyr	Pro	Leu	Ala	Ser	Lys	Ile	Met	Val	Arg	Asn	Leu	Pro	
			35				40					45				
Phe	Ser	Xaa	Ser	Glu	Asp	Phe	Leu	Lys	Arg	Glu	Phe	Ser	Ala	Phe	Gly	
		50				55				60						
Glu	Ile	Ala	Glu	Val	Lys	Leu	Ile	Lys	Asp	Glu	Ala	Met	Gln	Arg	Ser	
65					70				75					80		
Lys	Gly	Tyr	Ala	Phe	Ile	Gln	Phe	Thr	Ser	Gln	Asp	Asp	Ala	Phe	Leu	
					85				90				95			
Ala	Ile	Glu	Thr	Met	Asp	Arg	Arg	Met	Tyr	Asn	Gly	Arg	Met	Ile	Tyr	
			100					105					110			
Ile	Asp	Ile	Ala	Lys	Pro	Gly	Lys	Arg	Asp	Phe	Gln	Gly	Leu	Pro	Arg	
			115				120					125				
Thr	Ser	Gly	Pro	Pro	Glu	Lys	Ser	Asp	Val	Pro	Glu	Glu	Ala	Ala	Asn	
			130				135				140					
Asp	Glu	Val	Ala	Asp	Cys	Trp	Tyr									
145					150											

(2) INFORMATION FOR SEQ ID NO:1236:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 110 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1499926

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1236:

Met	Val	Arg	Asn	Leu	Pro	Phe	Ser	Xaa	Ser	Glu	Asp	Phe	Leu	Lys	Arg	
1			5					10						15		
Glu	Phe	Ser	Ala	Phe	Gly	Glu	Ile	Ala	Glu	Val	Lys	Leu	Ile	Lys	Asp	
			20				25						30			
Glu	Ala	Met	Gln	Arg	Ser	Lys	Gly	Tyr	Ala	Phe	Ile	Gln	Phe	Thr	Ser	
			35				40					45				
Gln	Asp	Asp	Ala	Phe	Leu	Ala	Ile	Glu	Thr	Met	Asp	Arg	Arg	Met	Tyr	
			50				55				60					
Asn	Gly	Arg	Met	Ile	Tyr	Ile	Asp	Ile	Ala	Lys	Pro	Gly	Lys	Arg	Asp	
65			70					75						80		
Phe	Gln	Gly	Leu	Pro	Arg	Thr	Ser	Gly	Pro	Pro	Glu	Lys	Ser	Asp	Val	
			85					90						95		
Pro	Glu	Glu	Ala	Ala	Asn	Asp	Glu	Val	Ala	Asp	Cys	Trp	Tyr			
			100					105					110			

(2) INFORMATION FOR SEQ ID NO:1237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..76
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1237:

Met	Gln	Arg	Ser	Lys	Gly	Tyr	Ala	Phe	Ile	Gln	Phe	Thr	Ser	Gln	Asp	
1			5					10					15			
Asp	Ala	Phe	Leu	Ala	Ile	Glu	Thr	Met	Asp	Arg	Arg	Met	Tyr	Asn	Gly	
			20				25					30				
Arg	Met	Ile	Tyr	Ile	Asp	Ile	Ala	Lys	Pro	Gly	Lys	Arg	Asp	Phe	Gln	
			35				40					45				
Gly	Leu	Pro	Arg	Thr	Ser	Gly	Pro	Pro	Glu	Lys	Ser	Asp	Val	Pro	Glu	
			50				55				60					
Glu	Ala	Ala	Asn	Asp	Glu	Val	Ala	Asp	Cys	Trp	Tyr					
65			70					75								

(2) INFORMATION FOR SEQ ID NO:1238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..622
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499928

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1238:

acctcaaatc	cataatcgct	ctacttctct	ctctctctag	attcgaaaaa	atggcgaaac	60
tggtgatgtt	gttggttctc	tgtatcttac	cggcgatagc	catggcggca	aggaggggaa	120
atatgggaaa	gaatacaatg	gtgggttcaa	gtagcaccta	ctgtgacatt	tgcaaatctg	180
gcttcgagac	tectgaatcc	tectacttca	tcccgggtgc	aacggtgaa	ctatcatgca	240
aagacaggaa	gacaatggaa	gaggtttaca	cagacaaagc	tgtatcagac	aaagaaggaa	300
agtataagtt	cattgtccac	gacgatcaga	catgctaaca	acatgggatt	tgagaaagaa	360
gtgagtgatg	tgttctgctc	tgctttgttt	cagaagtata	tggttgatga	agatgaggat	420
gatattaaaa	accatctctc	atctctctgt	ttaatcttat	gatctgctgt	tttcttcatt	480
aatgagtttc	gagttatgga	agagatatat	tctgtatttg	tttgattact	tatttgttgt	540
ctttagagat	gttgactctg	tgatcggat	aactatctgt	ttgtgtaagc	ttcttatata	600
ttgatgtgtc	atttccctgc	tt				

(2) INFORMATION FOR SEQ ID NO:1239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499929

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1239:

Phe	Lys	Ser	Ile	Ile	Ala	Leu	Leu	Leu	Ser	Leu	Ser	Arg	Phe	Glu	Lys	
1				5					10					15		
Met	Ala	Lys	Leu	Val	Met	Leu	Leu	Val	Leu	Cys	Ile	Leu	Pro	Ala	Ile	
			20					25					30			
Ala	Met	Ala	Ala	Arg	Arg	Gly	Asn	Ile	Gly	Lys	Asn	Thr	Met	Val	Val	
			35				40					45				
Gln	Gly	Ser	Thr	Tyr	Cys	Asp	Ile	Cys	Lys	Phe	Gly	Phe	Glu	Thr	Pro	
						55					60					
Glu	Ser	Ser	Tyr	Phe	Ile	Pro	Gly	Ala	Thr	Val	Lys	Leu	Ser	Cys	Lys	
65					70					75				80		
Asp	Arg	Lys	Thr	Met	Glu	Glu	Val	Tyr	Thr	Asp	Lys	Ala	Val	Ser	Asp	
				85					90					95		
Lys	Glu	Gly	Lys	Tyr	Lys	Phe	Ile	Val	His	Asp	Asp	Gln	Thr	Cys		
				100				105					110			

(2) INFORMATION FOR SEQ ID NO:1240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1240:

Met	Ala	Lys	Leu	Val	Met	Leu	Leu	Val	Leu	Cys	Ile	Leu	Pro	Ala	Ile	
1				5						10				15		
Ala	Met	Ala	Ala	Arg	Arg	Gly	Asn	Ile	Gly	Lys	Asn	Thr	Met	Val	Val	
			20					25					30			
Gln	Gly	Ser	Thr	Tyr	Cys	Asp	Ile	Cys	Lys	Phe	Gly	Phe	Glu	Thr	Pro	
			35					40				45				
Glu	Ser	Ser	Tyr	Phe	Ile	Pro	Gly	Ala	Thr	Val	Lys	Leu	Ser	Cys	Lys	
			50				55				60					
Asp	Arg	Lys	Thr	Met	Glu	Glu	Val	Tyr	Thr	Asp	Lys	Ala	Val	Ser	Asp	
65					70					75				80		
Lys	Glu	Gly	Lys	Tyr	Lys	Phe	Ile	Val	His	Asp	Asp	Gln	Thr	Cys		
				85					90					95		

(2) INFORMATION FOR SEQ ID NO:1241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499931

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1241:
Met Leu Leu Val Leu Cys Ile Leu Pro Ala Ile Ala Met Ala Ala Arg
1 5 10 15
Arg Gly Asn Ile Gly Lys Asn Thr Met Val Val Gln Gly Ser Thr Tyr
20 25 30
Cys Asp Ile Cys Lys Phe Gly Phe Glu Thr Pro Glu Ser Ser Tyr Phe
35 40 45
Ile Pro Gly Ala Thr Val Lys Leu Ser Cys Lys Asp Arg Lys Thr Met
50 55 60
Glu Glu Val Tyr Thr Asp Lys Ala Val Ser Asp Lys Glu Gly Lys Tyr
65 70 75 80
Lys Phe Ile Val His Asp Asp Gln Thr Cys
85 90

(2) INFORMATION FOR SEQ ID NO:1242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1010 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1010
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1242:

acaatcaaa	atgacactag	ctagacattt	tcgttttcat	ctccccacga	atcaaaaagat	60
ggcttttgcc	attgcttctg	ctctcaactc	cacactcaoa	ttatccacga	gcagagtcca	120
aaatcctacc	cagagaagac	cacatgtagc	gtccacatca	tccaccggtg	gaagattaat	180
gagagagcgc	ttgttggtgg	ttctgcccgg	caaagaagtt	tctagcgtct	gtgaaccact	240
tcctccggac	cgctccttat	ggttcctcgg	tagctctcca	cctgaatggc	tcgatggcag	300
cttacctggt	gatttcggtt	tcgatcctct	cggtttaggg	tctggtatcc	gacacccctca	360
aatggtttg	acaagctgag	cttatacata	gccggtgggc	aatgctggcc	gtgacaggta	420
tcataatacc	agaatgtmhh	cgagcggwta	ggtttcattg	aaaatttctc	atggtatgac	480
gcagggtctc	gtgagtactt	bgcggattcc	actacgctgt	ttgtggctca	aatggtttta	540
atgggctggg	cagaaggtak	aagatgggct	gatttgatta	aaaccgggtc	tgttgacata	600
gaaccaaagt	accgcataaa	agtaaatcct	aaaccgggat	ttggttaccc	tggagggttg	660
tggttcgatt	ttatgatgtg	ggggagaggt	tctcctgaac	cggtaatggt	tttgaggact	720
aaagagatta	agaacggagc	gctcgcgatg	cttgctttcc	ttgggttctg	tttccaaagt	780
acctacacata	gccaaagatc	aattgagaat	ctcatggctc	atctggtggc	tcctgggtcat	840
tgcaacgctc	tttcggcatt	tacatcacat	taatgaggat	tagcttgggg	cgaataataa	900
attttttata	tattttatga	tgttgaactt	ttgtatagtg	tcactgcggc	ttgttacaa	960
ttctgcttac	tttaattaaca	tgtaaaatat	attatatata	tatgtagaag		

(2) INFORMATION FOR SEQ ID NO:1243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1243:

Gln Ser Lys Met Thr Leu Ala Arg His Phe Arg Phe His Leu Pro Thr
1 5 10 15
Asn Gln Lys Met Ala Phe Ala Ile Ala Ser Ala Leu Thr Ser Thr Leu
20 25 30
Thr Leu Ser Thr Ser Arg Val Gln Asn Pro Thr Gln Arg Arg Pro His
35 40 45
Val Ala Ser Thr Ser Ser Thr Gly Arg Leu Met Arg Glu Arg Leu

50	55	60
Val Val Val Arg Ala Gly Lys Glu Val Ser Ser Val Cys Glu Pro Leu		
65	70	75
Pro Pro Asp Arg Pro Leu Trp Phe Pro Gly Ser Ser Pro Pro Glu Trp		80
	85	90
Leu Asp Gly Ser Leu Pro Gly Asp Phe Gly Phe Asp Pro Leu Gly Leu		95
	100	105
Gly Ser Gly Ser Gly His Pro Gln Met Val Cys Thr Ser		110
	115	120
		125

(2) INFORMATION FOR SEQ ID NO:1244:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1499937

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1244:

Met Thr Leu Ala Arg His Phe Arg Phe His Leu Pro Thr Asn Gln Lys		
1	5	10
Met Ala Phe Ala Ile Ala Ser Ala Leu Thr Ser Thr Leu Thr Leu Ser		15
	20	25
Thr Ser Arg Val Gln Asn Pro Thr Gln Arg Arg Pro His Val Ala Ser		30
	35	40
Thr Ser Ser Thr Gly Gly Arg Leu Met Arg Glu Arg Leu Val Val Val		45
	50	55
Arg Ala Gly Lys Glu Val Ser Ser Val Cys Glu Pro Leu Pro Pro Asp		60
	65	70
Arg Pro Leu Trp Phe Pro Gly Ser Ser Pro Pro Glu Trp Leu Asp Gly		75
	85	90
Ser Leu Pro Gly Asp Phe Gly Phe Asp Pro Leu Gly Leu Gly Ser Gly		95
	100	105
Ser Gly His Pro Gln Met Val Cys Thr Ser		110
	115	120

(2) INFORMATION FOR SEQ ID NO:1245:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1499938

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1245:

Met Val Leu Met Gly Trp Ala Glu Gly Xaa Arg Trp Ala Asp Leu Ile		
1	5	10
Lys Pro Gly Ser Val Asp Ile Glu Pro Lys Tyr Pro His Lys Val Asn		15
	20	25
Pro Lys Pro Asp Val Gly Tyr Pro Gly Gly Leu Trp Phe Asp Phe Met		30
	35	40
Met Trp Gly Arg Gly Ser Pro Glu Pro Val Met Val Leu Arg Thr Lys		45
	50	55
Glu Ile Lys Asn Gly Arg Leu Ala Met Leu Ala Phe Leu Gly Phe Cys		60
	65	70
Phe Gln Ala Thr Tyr Thr Ser Gln Asp Pro Ile Glu Asn Leu Met Ala		75
	85	90
		95

His Leu Ala Asp Pro Gly His Cys Asn Val Phe Ser Ala Phe Thr Ser
100 105 110
His

(2) INFORMATION FOR SEQ ID NO:1246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 568 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..568
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499939

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1246:

acggatccac	cggagagatc	tggtctgcca	ttccctcgct	ccttcccggtg	aaccacaaac	60
ctaacgcgga	rmggcgcggg	ccggcmrcgg	ggcgaggtgc	gcgtagctgc	cgctgattgt	120
cgccggatcc	atccaccatg	ggcggtgcca	acggccagaa	gtccaaagatg	gcccgcgagc	180
gcaacttgga	gaagaacaag	ggggccaagg	ggagccagct	cgagaccaac	aagaaggcca	240
tgagcatcca	gtgcaaaagt	tgcatgcaaa	cattcatgtg	taccacgagt	gaagtgaagt	300
gccgggagca	cgccgaggcc	aagcatccca	agacagacgt	gtaccagtcg	ttcccccatc	360
tgaagaagtg	aaaggcctga	acttagcaac	cagtgctggt	ttggtcacta	cgatcgggcc	420
agggggcggt	cctgtgtgtg	aggggtgttc	ttccgtgtta	tcttcccgtc	agtcatcgct	480
cctgtcctat	gttaacctac	ataagaaaag	gatgtgggtg	ccacttctag	tgaaactact	540
gtctgctgtt	aaaacctggt	tggtttcg				

(2) INFORMATION FOR SEQ ID NO:1247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..122
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499940

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1247:

Gly	Ser	Thr	Gly	Glu	Ile	Trp	Ser	Ala	Ile	Pro	Ser	Leu	Leu	Pro	Val
1				5					10					15	
Asn	His	Lys	Pro	Asn	Ala	Xaa	Xaa	Arg	Gly	Pro	Xaa	Xaa	Gly	Arg	Gly
			20					25					30		
Ala	Arg	Ser	Cys	Arg	Arg	Leu	Ser	Pro	Asp	Pro	Ser	Thr	Met	Gly	Gly
		35					40					45			
Gly	Asn	Gly	Gln	Lys	Ser	Lys	Met	Ala	Arg	Glu	Arg	Asn	Leu	Glu	Lys
		50				55				60					
Asn	Lys	Gly	Ala	Lys	Gly	Ser	Gln	Leu	Glu	Thr	Asn	Lys	Lys	Ala	Met
65					70					75				80	
Ser	Ile	Gln	Cys	Lys	Val	Cys	Met	Gln	Thr	Phe	Met	Cys	Thr	Thr	Xaa
			85					90					95		
Glu	Val	Lys	Cys	Arg	Glu	His	Ala	Glu	Ala	Lys	His	Pro	Lys	Thr	Asp
			100				105						110		
Val	Tyr	Gln	Cys	Phe	Pro	His	Leu	Lys	Lys						
			115				120								

(2) INFORMATION FOR SEQ ID NO:1248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1499941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1248:

```
Met Gly Gly Asn Gly Gln Lys Ser Lys Met Ala Arg Glu Arg Asn
1          5          10          15
Leu Glu Lys Asn Lys Gly Ala Lys Gly Ser Gln Leu Glu Thr Asn Lys
20          25          30
Lys Ala Met Ser Ile Gln Cys Lys Val Cys Met Gln Thr Phe Met Cys
35          40          45
Thr Thr Xaa Glu Val Lys Cys Arg Glu His Ala Glu Ala Lys His Pro
50          55          60
Lys Thr Asp Val Tyr Gln Cys Phe Pro His Leu Lys Lys
65          70          75
```

(2) INFORMATION FOR SEQ ID NO:1249:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..67

(D) OTHER INFORMATION: / Ceres Seq. ID 1499942

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1249:

```
Met Ala Arg Gly Arg Asn Leu Glu Lys Asn Lys Gly Ala Lys Gly Ser
1          5          10          15
Gln Leu Glu Thr Asn Lys Lys Ala Met Ser Ile Gln Cys Lys Val Cys
20          25          30
Met Gln Thr Phe Met Cys Thr Thr Xaa Glu Val Lys Cys Arg Glu His
35          40          45
Ala Glu Ala Lys His Pro Lys Thr Asp Val Tyr Gln Cys Phe Pro His
50          55          60
Leu Lys Lys
65
```

(2) INFORMATION FOR SEQ ID NO:1250:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 531 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..531

(D) OTHER INFORMATION: / Ceres Seq. ID 1499943

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1250:

```
acaacattc aaaagctatt agcgattott cttctctctg attcaatctt cttcatagtt      60
tctaagctct caaattcttg acgaagcaat ggctcgtacg aagcaaaactg caagaaaatc      120
acacggaggga aaagctccga ggactctgct cgctaccaag gcggcgaggga aatctgcgcc      180
gactactgga ggagtcgaaga aaacctcaccc ttaccgtccc ggaacctgctg cttctcgtga      240
gattcgtaaa taccagaaga gcacagagtt gttgatccgt aaacttctct ttcaacgtct      300
tgttcgtgaa atcgctcaaag attacaagac ggatctgaga ttccagagcc atcgctgtgt      360
agctcttcaa gaagctgctg aagcatattt ggttggtttt tttagaataa caaatctgtg      420
tgccattcat gccaaagagg ttacgatcat gcctaaagat gttcaattgg cagaaggatt      480
cgtggagagc gtgcttagat tcgaattaaa atcatcaact attattctat t
```

(2) INFORMATION FOR SEQ ID NO:1251:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..147
(D) OTHER INFORMATION: / Ceres Seq. ID 1499944
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1251:
Met Ala Arg Thr Lys Gln Thr Ala Arg Lys Ser His Gly Gly Lys Ala
1 5 10 15
Pro Arg Thr Leu Ala Thr Lys Ala Arg Lys Ser Ala Pro Thr
20 25 30
Thr Gly Gly Val Lys Lys Pro His Arg Tyr Arg Pro Gly Thr Val Ala
35 40 45
Leu Arg Glu Ile Arg Lys Tyr Gln Lys Ser Thr Glu Leu Leu Ile Arg
50 55 60
Lys Leu Pro Phe Gln Arg Leu Val Arg Glu Ile Ala Gln Asp Tyr Lys
65 70 75 80
Thr Asp Leu Arg Phe Gln Ser His Ala Xaa Leu Ala Leu Gln Glu Ala
85 90 95
Ala Glu Ala Tyr Leu Val Gly Leu Phe Glu Asp Thr Asn Leu Cys Ala
100 105 110
Ile His Ala Lys Arg Val Thr Ile Met Pro Lys Asp Val Gln Leu Ala
115 120 125
Glu Gly Phe Val Glu Ser Val Leu Arg Phe Glu Leu Lys Ser Ser Thr
130 135 140
Ile Ile Leu
145

(2) INFORMATION FOR SEQ ID NO:1252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1308 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1308
(D) OTHER INFORMATION: / Ceres Seq. ID 1499960
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1252:

atatatttc	ataaataaac	ctctcaaac	ccacacttcc	tcacccatca	cacaatccctc	60
aaaaacagag	aacccaaaaa	acagagcaat	ctctaaaaaa	ctctcaagaaa	ctctcaactaaa	120
atgggttcaa	cggcgagag	acaattaa	ccggtgcaag	tcacccagca	cgaagctgccc	180
ctcttcgcc	tgcaactagc	cagtgcttcc	gttcttccga	tggctttaa	atccgcctta	240
gagcttgacc	ttcttgagat	tatggccaag	aatggttctc	ccatgtctcc	taccgagatc	300
gcttctaacc	ttccgacc	aaacccctgaa	gctccgggtca	tgctcgaccg	tatctccctg	360
cttcttaagt	cttactccgt	cttaacctgc	tccaacctga	aactttccgg	tgatggcggtt	420
gaacggattt	acgggcttgg	tcgggtttgc	aagtatttga	ccaagaacga	agatgggtgtt	480
tccattgtcg	ctctttgtct	tatgaaccaa	gacaagggttc	tcattggaag	ctggtagccat	540
ttgaagagat	caattcttga	tgggtgggatt	ccattcaaca	aggcttatgg	aatgagcgccg	600
ttcgatgacc	acgggaactga	ccctagattc	aacaagggtc	ttacaacatg	aatgtctaac	660
catctacaac	tcaccatgaa	gaagattctt	gagacctata	agggttttga	aggggttgact	720
tcttttggtg	atgttggtgg	tggtcattgt	gctacactca	aaatgattgt	ctccaagtac	780
cctaacttta	aaggcatcaa	ctttgatctc	ccacatgtca	ttgaagatgc	tccttctcat	840
cttggttattg	agcatgttgg	aggagatatg	tttgtaagt	tccttaaaag	tgatgccata	900
ttcatgaagt	ggatatgtca	tgactggagt	gacgaacatt	cggtgaaatt	cttgaaaaac	960
tgctacagat	cacttccaga	ggatggaaaa	gtgatattag	cagagattgat	acttccagag	1020
acaccagact	caagctctct	aacccaacaa	gtagtccatg	tcgatttgcat	ttgttggct	1080
cacaatcccg	gaggcaaa	acgaaccgag	aaagagtttg	aggcattatg	caaagcatca	1140
ggcttcaagg	gcatacaagt	tgcttgcgac	gcttttgggt	ttacccctat	tgagttactc	1200

aagaagctctt aaaaacaaac aatgttccta tgaagatgat ttatatgtaa acattatctc 1260
atatctcctt ccacgggttc aaaaactatgc tgtttaataa tggttttt

(2) INFORMATION FOR SEQ ID NO:1253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..363
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499961

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1253:

Met	Gly	Ser	Thr	Ala	Glu	Thr	Gln	Leu	Thr	Pro	Val	Gln	Val	Thr	Asp
1				5					10					15	
Asp	Glu	Ala	Ala	Leu	Phe	Ala	Met	Gln	Leu	Ala	Ser	Ala	Ser	Val	Leu
			20					25					30		
Pro	Met	Ala	Leu	Lys	Ser	Ala	Leu	Glu	Leu	Asp	Leu	Leu	Glu	Ile	Met
		35					40					45			
Ala	Lys	Asn	Gly	Ser	Pro	Met	Ser	Pro	Thr	Glu	Ile	Ala	Ser	Lys	Leu
	50					55				60					
Pro	Thr	Lys	Asn	Pro	Glu	Ala	Pro	Val	Met	Leu	Asp	Arg	Ile	Leu	Arg
	65				70				75					80	
Leu	Leu	Thr	Ser	Tyr	Ser	Val	Leu	Thr	Cys	Ser	Asn	Arg	Lys	Leu	Ser
				85					90					95	
Gly	Asp	Gly	Val	Glu	Arg	Ile	Tyr	Gly	Leu	Gly	Pro	Val	Cys	Lys	Tyr
			100					105					110		
Leu	Thr	Lys	Asn	Glu	Asp	Gly	Val	Ser	Ile	Ala	Ala	Leu	Cys	Leu	Met
			115				120					125			
Asn	Gln	Asp	Lys	Val	Leu	Met	Glu	Ser	Trp	Tyr	His	Leu	Lys	Asp	Ala
	130					135					140				
Ile	Leu	Asp	Gly	Gly	Ile	Pro	Phe	Asn	Lys	Ala	Tyr	Gly	Met	Ser	Ala
	145				150					155					160
Phe	Glu	Tyr	His	Gly	Thr	Asp	Pro	Arg	Phe	Asn	Lys	Val	Phe	Asn	Asn
				165					170					175	
Gly	Met	Ser	Asn	His	Ser	Thr	Ile	Thr	Met	Lys	Lys	Ile	Leu	Glu	Thr
			180					185					190		
Tyr	Lys	Gly	Phe	Glu	Gly	Leu	Thr	Ser	Leu	Val	Asp	Val	Gly	Gly	Gly
		195					200					205			
Ile	Gly	Ala	Thr	Leu	Lys	Met	Ile	Val	Ser	Lys	Tyr	Pro	Asn	Leu	Lys
					215						220				
Gly	Ile	Asn	Phe	Asp	Leu	Pro	His	Val	Ile	Glu	Asp	Ala	Pro	Ser	His
	225				230					235					240
Pro	Gly	Ile	Glu	His	Val	Gly	Gly	Asp	Met	Phe	Val	Ser	Val	Pro	Lys
				245					250					255	
Gly	Asp	Ala	Ile	Phe	Met	Lys	Trp	Ile	Cys	His	Asp	Trp	Ser	Asp	Glu
			260					265					270		
His	Cys	Val	Lys	Phe	Leu	Lys	Asn	Cys	Tyr	Glu	Ser	Leu	Pro	Glu	Asp
		275					280					285			
Gly	Lys	Val	Ile	Leu	Ala	Glu	Cys	Ile	Leu	Pro	Glu	Thr	Pro	Asp	Ser
		290				295						300			
Ser	Leu	Ser	Thr	Lys	Gln	Val	Val	His	Val	Asp	Cys	Ile	Met	Leu	Ala
	305					310				315				320	
His	Asn	Pro	Gly	Gly	Lys	Glu	Arg	Thr	Glu	Lys	Glu	Phe	Glu	Ala	Leu
				325					330					335	
Ala	Lys	Ala	Ser	Gly	Phe	Lys	Gly	Ile	Lys	Val	Val	Cys	Asp	Ala	Phe
				340				345					350		
Gly	Val	Asn	Leu	Ile	Glu	Leu	Leu	Lys	Lys	Leu					
		355				360									

(2) INFORMATION FOR SEQ ID NO:1254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..340
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499962

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1254:

Met Gln Leu Ala Ser Ala Ser Val Leu Pro Met Ala Leu Lys Ser Ala
1 5 10 15
Leu Glu Leu Asp Leu Leu Glu Ile Met Ala Lys Asn Gly Ser Pro Met
20 25 30
Ser Pro Thr Glu Ile Ala Ser Lys Leu Pro Thr Lys Asn Pro Glu Ala
35 40 45
Pro Val Met Leu Asp Arg Ile Leu Arg Leu Leu Thr Ser Tyr Ser Val
50 55 60
Leu Thr Cys Ser Asn Arg Lys Leu Ser Gly Asp Gly Val Glu Arg Ile
65 70 75 80
Tyr Gly Leu Gly Pro Val Cys Lys Tyr Leu Thr Lys Asn Glu Asp Gly
85 90 95
Val Ser Ile Ala Ala Leu Cys Leu Met Asn Gln Asp Lys Val Leu Met
100 105 110
Glu Ser Trp Tyr His Leu Lys Asp Ala Ile Leu Asp Gly Gly Ile Pro
115 120 125
Phe Asn Lys Ala Tyr Gly Met Ser Ala Phe Glu Tyr His Gly Thr Asp
130 135 140
Pro Arg Phe Asn Lys Val Phe Asn Asn Gly Met Ser Asn His Ser Thr
145 150 155 160
Ile Thr Met Lys Lys Ile Leu Glu Thr Tyr Lys Gly Phe Glu Gly Leu
165 170 175
Thr Ser Leu Val Asp Val Gly Gly Ile Gly Ala Thr Leu Lys Met
180 185 190
Ile Val Ser Lys Tyr Pro Asn Leu Lys Gly Ile Asn Phe Asp Leu Pro
195 200 205
His Val Ile Glu Asp Ala Pro Ser His Pro Gly Ile Glu His Val Gly
210 215 220
Gly Asp Met Phe Val Ser Val Pro Lys Gly Asp Ala Ile Phe Met Lys
225 230 235 240
Trp Ile Cys His Asp Trp Ser Asp Glu His Cys Val Lys Phe Leu Lys
245 250 255
Asn Cys Tyr Glu Ser Leu Pro Glu Asp Gly Lys Val Ile Leu Ala Glu
260 265 270
Cys Ile Leu Pro Glu Thr Pro Asp Ser Ser Leu Ser Thr Lys Gln Val
275 280 285
Val His Val Asp Cys Ile Met Leu Ala His Asn Pro Gly Gly Lys Glu
290 295 300
Arg Thr Glu Lys Glu Phe Glu Ala Leu Ala Lys Ala Ser Gly Phe Lys
305 310 315 320
Gly Ile Lys Val Val Cys Asp Ala Phe Gly Val Asn Leu Ile Glu Leu
325 330 335
Leu Lys Lys Leu
340

(2) INFORMATION FOR SEQ ID NO:1255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..330
(D) OTHER INFORMATION: / Ceres Seq. ID 1499963

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1255:

```
Met Ala Leu Lys Ser Ala Leu Glu Leu Asp Leu Leu Glu Ile Met Ala
1      5      10      15
Lys Asn Gly Ser Pro Met Ser Pro Thr Glu Ile Ala Ser Lys Leu Pro
20      25      30
Thr Lys Asn Pro Glu Ala Pro Val Met Leu Asp Arg Ile Leu Arg Leu
35      40      45
Leu Thr Ser Tyr Ser Val Leu Thr Cys Ser Asn Arg Lys Leu Ser Gly
50      55      60
Asp Gly Val Glu Arg Ile Tyr Gly Leu Gly Pro Val Cys Lys Tyr Leu
65      70      75      80
Thr Lys Asn Glu Asp Gly Val Ser Ile Ala Ala Leu Cys Leu Met Asn
85      90      95
Gln Asp Lys Val Leu Met Glu Ser Trp Tyr His Leu Lys Asp Ala Ile
100     105     110
Leu Asp Gly Gly Ile Pro Phe Asn Lys Ala Tyr Gly Met Ser Ala Phe
115     120     125
Glu Tyr His Gly Thr Asp Pro Arg Phe Asn Lys Val Phe Asn Asn Gly
130     135     140
Met Ser Asn His Ser Thr Ile Thr Met Lys Lys Ile Leu Glu Thr Tyr
145     150     155     160
Lys Gly Phe Glu Gly Leu Thr Ser Leu Val Asp Val Gly Gly Gly Ile
165     170     175
Gly Ala Thr Leu Lys Met Ile Val Ser Lys Tyr Pro Asn Leu Lys Gly
180     185     190
Ile Asn Phe Asp Leu Pro His Val Ile Glu Asp Ala Pro Ser His Pro
195     200     205
Gly Ile Glu His Val Gly Gly Asp Met Phe Val Ser Val Pro Lys Gly
210     215     220
Asp Ala Ile Phe Met Lys Trp Ile Cys His Asp Trp Ser Asp Glu His
225     230     235     240
Cys Val Lys Phe Leu Lys Asn Cys Tyr Glu Ser Leu Pro Glu Asp Gly
245     250     255
Lys Val Ile Leu Ala Glu Cys Ile Leu Pro Glu Thr Pro Asp Ser Ser
260     265     270
Leu Ser Thr Lys Gln Val Val His Val Asp Cys Ile Met Leu Ala His
275     280     285
Asn Pro Gly Gly Lys Glu Arg Thr Glu Lys Glu Phe Glu Ala Leu Ala
290     295     300
Lys Ala Ser Gly Phe Lys Gly Ile Lys Val Val Cys Asp Ala Phe Gly
305     310     315     320
Val Asn Leu Ile Glu Leu Leu Lys Lys Leu
325     330
```

(2) INFORMATION FOR SEQ ID NO:1256:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 916 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..916
(D) OTHER INFORMATION: / Ceres Seq. ID 1499964

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1256:

acgaaagaag agaacaaaga agaaattttg aaaatagtga aaatggtaac cgtaagccaa

```

agtcacacga cgacgtttct cttcttcacc acattttctt tgatattcgg atcaatctca 120
gocgtccggt tgcttccacg accaaacact acaacaacca acgatctaga tttcatccga 180
acaagctgca acgtactctt atatccagac gtctgcttca cgtoactctc cggctacgcc 240
tctgccgttc aagacagtcg ggcgaggcta gccaaagctcg caatcgccgt ttcactttaa 300
caagccaaat ccactcgccg ttttctctcc aaactctcac gctctgccgc taaatactcc 360
ggtgatggcc accaaacagc ttccgcgcta atccgagact ggtttcgaa cgtcgaagac 420
gcgngtggag gagatgagag gatctctccg tcaactacgc gacatgaacg gcagaggagg 480
cggcacggca gctcgagggt cggtagaaac gtttaggttc cagatgagta acgtgcagac 540
gtggatgagt gcagcattga cggatgagga cactgttacg aatggatttg aagatatgga 600
cgaaggagga ttgattaaaga cgaccgtttg tgatcggttc gaggaagtga agaggctaac 660
gagtaaatgct cttgcccttg tcaacactta cgccaacaat ggagctccat gaccatgaga 720
ccatgagacc atgaggagtt ttaactttga tttaagtgtc ttttatata atttaataca 780
ttgtgggggt taagtttagag ttatgtgtcg atttcatcat gttttacatt tgtttttgta 840
tcattccgagt ttcttatggt taaaggggtc agagagatgt tgtatctttg atttactaat 900
caaaactgcac gatgat

```

(2) INFORMATION FOR SEQ ID NO:1257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..99
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1257:

```

Thr Lys Glu Glu Asn Lys Glu Glu Ile Leu Lys Ile Val Lys Met Val
1 5 10 15
Thr Val Ser Gln Ser His Thr Thr Thr Phe Leu Phe Phe Thr Thr Phe
20 25 30
Leu Leu Ile Phe Gly Ser Ile Ser Ala Val Arg Leu Leu Pro Arg Pro
35 40 45
Asn Thr Thr Thr Thr Asn Asp Leu Asp Phe Ile Arg Thr Ser Cys Asn
50 55 60
Ala Thr Leu Tyr Pro Asp Val Cys Phe Thr Ser Leu Ser Gly Tyr Ala
65 70 75 80
Ser Ala Val Gln Asp Ser Pro Ala Arg Leu Ala Lys Leu Ala Ile Gly
85 90 95
Val Ser Leu

```

(2) INFORMATION FOR SEQ ID NO:1258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..116
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1258:

```

Glu Arg Arg Glu Gln Arg Arg Asn Phe Glu Asn Ser Glu Asn Gly Asn
1 5 10 15
Arg Lys Pro Lys Ser His Asp Asp Val Ser Leu Leu His His Ile Ser
20 25 30
Leu Asp Ile Arg Ile Asn Leu Ser Arg Pro Phe Ala Ser Thr Thr Lys
35 40 45
His Tyr Asn Asn Gln Arg Ser Arg Phe His Pro Asn Lys Leu Gln Arg
50 55 60

```

(2) INFORMATION FOR SEQ ID NO:1259:

- (ii) MOLECULE TYPE: peptide

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..92

- (D) OTHER INFORMATION: / Ceres Seq. ID 1499967

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1259:

(2) INFORMATION FOR SEQ ID NO:1260:

- (ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..257

- (D) OTHER INFORMATION: / Ceres Seq. ID 1499968

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1260:

(2) INFORMATION FOR SEQ ID NO:1261:

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..85

- (D) OTHER INFORMATION: / Ceres Seq. ID 1499969

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1261:

```

Ile Val Phe Asp Gln Val Thr Lys Ser Ile Glu Gly Leu Leu Pro Leu
1           5           10           15
Pro Lys Ile His Asn Pro Asn Asp Pro Arg Ile Glu Phe Lys Glu
           20           25           30
Leu Glu Ala Glu Lys Ala Val Ile Asp Val Lys Ala His Thr Leu Val
           35           40           45
Arg Glu Leu Trp Ala Gly Leu Gly Tyr Leu Ile Leu Gln Thr Ala Gly
           50           55           60
Phe Met Arg Leu Thr Phe Trp Glu Leu Ser Trp Asp Val Met Glu Pro
65           70           75           80
Ile Cys Phe Tyr Val
           85

```

(2) INFORMATION FOR SEQ ID NO:1262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..573

(D) OTHER INFORMATION: / Ceres Seq. ID 1499970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1262:

```

ggagaagacg tcgtgattat ccgagtagta gctcagattc cgaatcagaa tcggagtcgg      60
aatattctga ttctgaggag agtgagagtg aagatgagag aagaagggaag aagaggaaga      120
gaaagagagag ggaagaggaa gagaagagaga ggaagagaa gagaagagag aaagataaga      180
agaagaggaa caagtctgat aaagatggag ataagaagag gaaggagaa aagaagaaga      240
agtcctgaaa agtgaagaaa ggagctgtta ctgaatcatg gggcaagtat ggaatcatca      300
gagaaactga tatgtggaat aaacgtccag agttcacagc atggttgctt gaagtaaaaga      360
aggttaattt ggaaagcttg ccaccttggg aagagaagaa aatgtttaaa gattttatgg      420
aggatcataa tactgtgtaca ttacctcga aaaaatacta tgacattgat ggttactata      480
gaactaaagt ggaaaaagag atgaaaaagg gtttgaagaa agctgggatt agtgaacgta      540
ctgtgttcaa tgatgaggaa caacgccgac tgg

```

(2) INFORMATION FOR SEQ ID NO:1263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..190

(D) OTHER INFORMATION: / Ceres Seq. ID 1499971

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1263:

```

Arg Arg Arg Arg Asp Tyr Pro Ser Ser Ser Asp Ser Glu Ser Glu
1           5           10           15
Ser Glu Ser Glu Tyr Ser Asp Ser Glu Glu Ser Glu Ser Glu Asp Glu
           20           25           30
Arg Arg Arg Lys Lys Arg Lys Arg Lys Glu Arg Glu Glu Glu Lys
           35           40           45
Glu Arg Lys Arg Arg Arg Arg Glu Lys Asp Lys Lys Lys Arg Asn Lys
           50           55           60
Ser Asp Ser Lys Asp Gly Asp Lys Lys Arg Lys Glu Lys Lys Lys Lys
65           70           75           80
Ser Glu Lys Val Lys Lys Lys Gly Ala Val Thr Glu Ser Trp Gly Lys Tyr
           85           90           95
Gly Ile Ile Arg Glu Thr Asp Met Trp Asn Lys Arg Pro Glu Phe Thr
           100          105          110
Ala Trp Leu Leu Glu Val Lys Lys Val Asn Leu Glu Ser Leu Pro Pro

```


(2) INFORMATION FOR SEQ ID NO:1264:

(A) LENGTH: 1770 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

```
(ix) FEATURE:
```

(A) NAME/KEY: -

(B) LOCATION: 1..1770

(D) OTHER INFORMATION: / Ceres Seq. ID 1499972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1264:

(2) INFORMATION FOR SEQ ID NO:1265:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 525 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..525

(D) OTHER INFORMATION: / Ceres Seq. ID 1499973
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1265:

Met	Glu	Glu	Lys	Ser	Lys	Ser	Arg	Gly	Trp	Cys	Gly	Trp	Phe	Ile	Ala	
1			5					10						15		
Ile	Ile	Val	Leu	Ala	Ser	Val	Ile	Leu	Ala	Val	Val	Tyr	Thr	Val	Lys	
		20					25					30				
Leu	Arg	Thr	Lys	Lys	Ser	Gly	Asp	Asp	Asp	Gly	Gly	Cys	Pro	Val	Pro	
		35					40					45				
Gly	Pro	Pro	Gly	Ala	Ile	Asp	Lys	Lys	Tyr	Ala	Asp	Ala	Leu	Lys	Leu	
		50					55					60				
Ala	Leu	Gln	Phe	Phe	Asp	Ile	Gln	Lys	Ser	Gly	Lys	Leu	Glu	Asn	Asn	
65					70				75						80	
Lys	Ile	Pro	Trp	Arg	Gly	Asp	Ser	Gly	Leu	Lys	Asp	Gly	Ser	Glu	Asp	
			85						90					95		
Asn	Leu	Asp	Leu	Ser	Lys	Gly	Leu	Tyr	Asp	Ala	Gly	Asp	His	Ile	Lys	
			100						105				110			
Phe	Gly	Phe	Pro	Met	Ala	Phe	Thr	Ala	Thr	Val	Leu	Ser	Trp	Ser	Ile	
			115				120						125			
Leu	Glu	Tyr	Gly	Asp	Gln	Met	Asn	Ala	Val	Asn	Gln	Leu	Asp	Pro	Ala	
			130				135				140					
Lys	Asp	Ser	Leu	Arg	Trp	Ile	Thr	Asp	Tyr	Leu	Ile	Lys	Ala	His	Pro	
145					150					155					160	
Ser	Asp	Asn	Val	Leu	Tyr	Ile	Gln	Val	Gly	Asp	Pro	Lys	Val	Asp	His	
			165						170					175		
Pro	Cys	Trp	Glu	Arg	Pro	Glu	Asp	Met	Lys	Glu	Lys	Arg	Pro	Leu	Thr	
			180						185					190		
Lys	Ile	Asp	Val	Asp	Thr	Pro	Gly	Thr	Glu	Val	Ala	Ala	Glu	Thr	Ala	
			195					200					205			
Ala	Ala	Met	Ala	Ser	Ala	Ser	Leu	Val	Phe	Lys	Asp	Ser	Asp	Pro	Thr	
			210				215						220			
Tyr	Ser	Ala	Thr	Leu	Leu	Lys	His	Ala	Lys	Gln	Leu	Phe	Asp	Phe	Ala	
225					230					235					240	
Asp	Thr	Lys	Arg	Gly	Ser	Tyr	Ser	Val	Asn	Ile	Pro	Glu	Val	Gln	Lys	
			245						250					255		
Phe	Tyr	Asn	Ser	Thr	Gly	Tyr	Gly	Asp	Glu	Leu	Leu	Trp	Ala	Ala	Ser	
			260					265						270		
Trp	Leu	Tyr	His	Ala	Thr	Glu	Asp	Lys	Thr	Tyr	Leu	Asp	Tyr	Val	Ser	
			275					280					285			
Asn	His	Gly	Lys	Glu	Phe	Ala	Ser	Phe	Gly	Asn	Pro	Thr	Trp	Phe	Ser	
			290				295					300				
Trp	Asp	Asn	Lys	Leu	Ala	Gly	Thr	Gln	Val	Leu	Leu	Ser	Arg	Leu	Leu	
305					310					315					320	
Phe	Phe	Lys	Lys	Asp	Leu	Ser	Gly	Ser	Lys	Gly	Leu	Gly	Asn	Tyr	Arg	
			325						330					335		
Asn	Thr	Ala	Lys	Ala	Val	Met	Cys	Gly	Leu	Leu	Pro	Lys	Ser	Pro	Thr	
			340					345					350			
Ser	Thr	Ala	Ser	Arg	Thr	Asn	Gly	Gly	Leu	Ile	Trp	Val	Ser	Glu	Trp	
			355					360					365			
Asn	Ser	Met	Gln	Gln	Ser	Val	Ser	Ser	Ala	Phe	Leu	Ala	Ser	Leu	Phe	
			370				375					380				
Ser	Asp	Tyr	Met	Leu	Thr	Ser	Arg	Ile	His	Lys	Ile	Ser	Cys	Asp	Gly	
385					390					395					400	
Lys	Ile	Phe	Lys	Ala	Thr	Glu	Leu	Arg	Asp	Phe	Ala	Lys	Ser	Gln	Ala	
			405							410				415		
Asp	Tyr	Met	Leu	Gly	Lys	Asn	Pro	Leu	Gly	Thr	Ser	Phe	Val	Val	Gly	
			420						425					430		
Tyr	Gly	Asp	Lys	Tyr	Pro	Gln	Phe	Val	His	His	Arg	Gly	Ala	Ser	Ile	
			435					440					445			
Pro	Ala	Asp	Ala	Thr	Thr	Gly	Cys	Leu	Asp	Gly	Phe	Lys	Trp	Phe	Asn	
			450				455					460				
Ser	Thr	Lys	Pro	Asn	Pro	Asn	Ile	Ala	Tyr	Gly	Ala	Leu	Val	Gly	Gly	

465				470				475				480			
Pro	Phe	Phe	Asn	Glu	Thr	Phe	Thr	Asp	Ser	Arg	Glu	Asn	Pro	Met	Gln
				485				490					495		
Asn	Glu	Pro	Thr	Thr	Tyr	Asn	Asn	Ala	Leu	Leu	Val	Gly	Leu	Leu	Ser
			500					505					510		
Ser	Leu	Val	Thr	Thr	Ser	Ser	Thr	Leu	Gln	Ser	Leu	Lys			
			515					520				525			

(2) INFORMATION FOR SEQ ID NO:1266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..409
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1266:

Met	Ala	Phe	Thr	Ala	Thr	Val	Leu	Ser	Trp	Ser	Ile	Leu	Glu	Tyr	Gly
1				5					10					15	
Asp	Gln	Met	Asn	Ala	Val	Asn	Gln	Leu	Asp	Pro	Ala	Lys	Asp	Ser	Leu
			20					25					30		
Arg	Trp	Ile	Thr	Asp	Tyr	Leu	Ile	Lys	Ala	His	Pro	Ser	Asp	Asn	Val
			35					40					45		
Leu	Tyr	Ile	Gln	Val	Gly	Asp	Pro	Lys	Val	Asp	His	Pro	Cys	Trp	Glu
			50			55					60				
Arg	Pro	Glu	Asp	Met	Lys	Glu	Lys	Arg	Pro	Leu	Thr	Lys	Ile	Asp	Val
			65			70				75				80	
Asp	Thr	Pro	Gly	Thr	Glu	Val	Ala	Ala	Glu	Thr	Ala	Ala	Ala	Met	Ala
			85						90					95	
Ser	Ala	Ser	Leu	Val	Phe	Lys	Asp	Ser	Asp	Pro	Thr	Tyr	Ser	Ala	Thr
			100					105					110		
Leu	Leu	Lys	His	Ala	Lys	Gln	Leu	Phe	Asp	Phe	Ala	Asp	Thr	Lys	Arg
			115				120					125			
Gly	Ser	Tyr	Ser	Val	Asn	Ile	Pro	Glu	Val	Gln	Lys	Phe	Tyr	Asn	Ser
			130			135					140				
Thr	Gly	Tyr	Gly	Asp	Glu	Leu	Leu	Trp	Ala	Ala	Ser	Trp	Leu	Tyr	His
			145			150					155			160	
Ala	Thr	Glu	Asp	Lys	Thr	Tyr	Leu	Asp	Tyr	Val	Ser	Asn	His	Gly	Lys
			165						170					175	
Glu	Phe	Ala	Ser	Phe	Gly	Asn	Pro	Thr	Trp	Phe	Ser	Trp	Asp	Asn	Lys
			180					185					190		
Leu	Ala	Gly	Thr	Gln	Val	Leu	Leu	Ser	Arg	Leu	Leu	Phe	Phe	Lys	Lys
			195				200					205			
Asp	Leu	Ser	Gly	Ser	Lys	Gly	Leu	Gly	Asn	Tyr	Arg	Asn	Thr	Ala	Lys
			210			215					220				
Ala	Val	Met	Cys	Gly	Leu	Leu	Pro	Lys	Ser	Pro	Thr	Ser	Thr	Ala	Ser
			225			230				235				240	
Arg	Thr	Asn	Gly	Gly	Leu	Ile	Trp	Val	Ser	Glu	Trp	Asn	Ser	Met	Gln
			245						250					255	
Gln	Ser	Val	Ser	Ser	Ala	Phe	Leu	Ala	Ser	Leu	Phe	Ser	Asp	Tyr	Met
			260				265						270		
Leu	Thr	Ser	Arg	Ile	His	Lys	Ile	Ser	Cys	Asp	Gly	Lys	Ile	Phe	Lys
			275				280					285			
Ala	Thr	Glu	Leu	Arg	Asp	Phe	Ala	Lys	Ser	Gln	Ala	Asp	Tyr	Met	Leu
			290			295					300				
Gly	Lys	Asn	Pro	Leu	Gly	Thr	Ser	Phe	Val	Val	Gly	Tyr	Gly	Asp	Lys
			305			310				315				320	
Tyr	Pro	Gln	Phe	Val	His	His	Arg	Gly	Ala	Ser	Ile	Pro	Ala	Asp	Ala
			325						330					335	

Thr Thr Gly Cys Leu Asp Gly Phe Lys Trp Phe Asn Ser Thr Lys Pro
340 345 350
Asn Pro Asn Ile Ala Tyr Gly Ala Leu Val Gly Gly Pro Phe Phe Asn
355 360 365
Glu Thr Phe Thr Asp Ser Arg Glu Asn Pro Met Gln Asn Glu Pro Thr
370 375 380
Thr Tyr Asn Asn Ala Leu Leu Val Gly Leu Ser Ser Leu Val Thr
385 390 395 400
Thr Ser Ser Thr Leu Gln Ser Leu Lys
405

(2) INFORMATION FOR SEQ ID NO:1267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..391
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1267:

Met Asn Ala Val Asn Gln Leu Asp Pro Ala Lys Asp Ser Leu Arg Trp
1 5 10 15
Ile Thr Asp Tyr Leu Ile Lys Ala His Pro Ser Asp Asn Val Leu Tyr
20 25 30
Ile Gln Val Gly Asp Pro Lys Val Asp His Pro Cys Trp Glu Arg Pro
35 40 45
Glu Asp Met Lys Glu Lys Arg Pro Leu Thr Lys Ile Asp Val Asp Thr
50 55 60
Pro Gly Thr Glu Val Ala Ala Glu Thr Ala Ala Ala Met Ala Ser Ala
65 70 75 80
Ser Leu Val Phe Lys Asp Ser Asp Pro Thr Tyr Ser Ala Thr Leu Leu
85 90 95
Lys His Ala Lys Gln Leu Phe Asp Phe Ala Asp Thr Lys Arg Gly Ser
100 105 110
Tyr Ser Val Asn Ile Pro Glu Val Gln Lys Phe Tyr Asn Ser Thr Gly
115 120 125
Tyr Gly Asp Glu Leu Leu Trp Ala Ala Ser Trp Leu Tyr His Ala Thr
130 135 140
Glu Asp Lys Thr Tyr Leu Asp Tyr Val Ser Asn His Gly Lys Glu Phe
145 150 155 160
Ala Ser Phe Gly Asn Pro Thr Trp Phe Ser Trp Asp Asn Lys Leu Ala
165 170 175
Gly Thr Gln Val Leu Leu Ser Arg Leu Leu Phe Phe Lys Lys Asp Leu
180 185 190
Ser Gly Ser Lys Gly Leu Gly Asn Tyr Arg Asn Thr Ala Lys Ala Val
195 200 205
Met Cys Gly Leu Leu Pro Lys Ser Pro Thr Ser Thr Ala Ser Arg Thr
210 215 220
Asn Gly Gly Leu Ile Trp Val Ser Glu Trp Asn Ser Met Gln Gln Ser
225 230 235 240
Val Ser Ser Ala Phe Leu Ala Ser Leu Phe Ser Asp Tyr Met Leu Thr
245 250 255
Ser Arg Ile His Lys Ile Ser Cys Asp Gly Lys Ile Phe Lys Ala Thr
260 265 270
Glu Leu Arg Asp Phe Ala Lys Ser Gln Ala Asp Tyr Met Leu Gly Lys
275 280 285
Asn Pro Leu Gly Thr Ser Phe Val Val Gly Tyr Gly Asp Lys Tyr Pro
290 295 300
Gln Phe Val His His Arg Gly Ala Ser Ile Pro Ala Asp Ala Thr Thr

(2) INFORMATION FOR SEQ ID NO:1268:

(A) LENGTH: 883 base pairs

(C) STRANDEDNESS: sing

(D) TOPOLOGY: linear

(D) TOPOLOGY: linear
MOLECULE TYPE: DNA (g

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(B) LOCATION: 1..883

(D) OTHER INFORMATION: / Ceres Seq. ID 1499976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1268:

(2) INFORMATION FOR SEQ ID NO:1269:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1499977

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1269:

Met	Gly	Gln	Ala	Leu	Gly	Cys	Ile	Gln	Val	Asp	Gln	Ser	Asn	Val	Ala
1				5				10						15	
Ile	Lys	Glu	Thr	Phe	Gly	Lys	Phe	Asp	Glu	Phe	Leu	Ser	Arg	Val	Val
			20					25					30		
Thr	Val	Cys	His	Gly	Val	Trp	Glu	Val	Lys	Ser	Leu	Val	Thr	Phe	Leu
			35				40					45			
Tyr	Val	Phe	Asn	Ser	Ser	Met	Phe	Ala	Ala	Arg	Gln	Arg	Leu	Arg	Ile
			50			55				60					
Met	Cys	Leu	Ser	Arg	Leu	Leu	Leu	Pro	Phe	Asn	Thr	Val	Pro		
65				70						75					

(2) INFORMATION FOR SEQ ID NO:1270:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 84 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..84
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499978
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1270:
Met Ser His Tyr Gly Tyr Glu Ile Val Gln Thr Leu Ile Val Asp Ile
1 5 10 15
Glu Pro Asp Val His Val Lys Arg Ala Met Asn Glu Ile Asn Ala Ala
 20 25 30
Ser Arg Met Arg Glu Ala Ala Ser Glu Lys Ala Glu Leu Val Ile Ser
 35 40 45
Asn Arg Lys Glu Thr Gln Gln Gln Ser Asp Val Lys Met Gln Lys Lys
 50 55 60
Arg Ile Glu Asn His Phe Gly Gly Phe Lys Arg Leu Lys Val Lys Gly
65 70 75 80
Leu Ile Lys Pro

(2) INFORMATION FOR SEQ ID NO:1271:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..59
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499979
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1271:
Met Asn Glu Ile Asn Ala Ala Ser Arg Met Arg Glu Ala Ala Ser Glu
1 5 10 15
Lys Ala Glu Leu Val Ile Ser Asn Arg Lys Glu Thr Gln Gln Gln Ser
 20 25 30
Asp Val Lys Met Gln Lys Lys Arg Ile Glu Asn His Phe Gly Gly Phe
 35 40 45
Lys Arg Leu Lys Val Lys Gly Leu Ile Lys Pro
 50 55

(2) INFORMATION FOR SEQ ID NO:1272:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1178 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..1178
 (D) OTHER INFORMATION: / Ceres Seq. ID 1499984
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1272:
ctcaaccccttt tgggtggaataa aaccagaaaaa tgggggttgca tccaatttcc gacgccaatg 60
aacacaatcc cttcggtctct ctcaccgcgc acgaattcta cgccaaacat tccgttagcc 120
actcctccgc ttctcatcac aaccctcgcg gtctcaaaact cttcactcaa tggttggtcac 180
cactccctcc aactaaaacca atcggtatca tcgctgtcgt ccatggcttc acgggggaat 240
ccagttggtt ccttcagctc acatcaatcc tcttcgctaa atccggtttc ataacctggc 300
caattgatca ccaaggccat ggattctccg atggactcat cgctcatatc cctgacatca 360

atcccgctgt	cgatgactgt	atctctttot	tcgatgactt	cgcgtaccgt	caaacaccgt	420
cagatctgcc	gtgtttttct	tactctgaat	ccctaggcgg	cgcgattgct	ctctacatct	480
cgcttcgtca	gagaggtgtt	tgggatggac	ttatcctcaa	cggagctatg	tgtggaatca	540
gcgataaatt	caaacgcgcg	tgccgcttgg	agcatattgt	atctcgtctc	gcgaatctta	600
tccctacttg	gcgcgtttatc	cccactcgcg	gatctattcc	cgatgtttcg	ttcaaggagc	660
cgtgggaagag	gaagcttgcc	atggctagcc	caaggaggac	ggtagggaaa	ccacggggccg	720
ctactgccta	tgagctgatt	cgtgtttgta	aggatctgca	ggggaggttt	gaggaagtgg	780
aggttcgcgt	tctgatttgg	cacggcggag	gtgatgttgt	atgcgacgta	gcgtgtgttg	840
aggagcttca	tcggagagcg	attagtggag	ataagacgat	caagatctac	cctgagttgt	900
ggcatcagat	gattggggaa	tcggaggaga	aagtcgatct	ggtttacggt	gatatgctga	960
gctggctcaa	gagtcgagct	gaaaggaagg	cacgcgcgcg	cgttgatgga	ggagcagctt	1020
agagtcctct	ttgagctctt	gggtgttgta	ttgtagtcca	ataggactgt	gccatctggc	1080
aagaaactat	ttatgttttt	actgtttcgt	aatcgtagca	catggtttac	agttaaacca	1140
atactcttgg	gtatcatcaa	taataataaa	aatcgtttg			

(2) INFORMATION FOR SEQ ID NO:1273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..339

(D) OTHER INFORMATION: / Ceres Seq. ID 1499985

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1273:

Gln	Pro	Phe	Gly	Gly	Lys	Asn	Gln	Lys	Met	Gly	Leu	His	Pro	Ile	Ser
1			5						10					15	
Asp	Ala	Asn	Glu	His	Asn	Pro	Phe	Gly	Ser	Leu	Thr	Ala	Asp	Glu	Phe
			20					25					30		
Tyr	Ala	Lys	His	Ser	Val	Ser	His	Ser	Ser	Ala	Phe	Ile	Thr	Asn	Pro
		35					40				45				
Arg	Gly	Leu	Lys	Leu	Phe	Thr	Gln	Trp	Trp	Ser	Pro	Leu	Pro	Pro	Thr
	50					55				60					
Lys	Pro	Ile	Gly	Ile	Ile	Ala	Val	Val	His	Gly	Phe	Thr	Gly	Glu	Ser
	65				70					75				80	
Ser	Trp	Phe	Leu	Gln	Leu	Thr	Ser	Ile	Leu	Phe	Ala	Lys	Ser	Gly	Phe
				85					90					95	
Ile	Thr	Cys	Ala	Ile	Asp	His	Gln	Gly	His	Gly	Phe	Ser	Asp	Gly	Leu
			100					105					110		
Ile	Ala	His	Ile	Pro	Asp	Ile	Asn	Pro	Val	Val	Asp	Asp	Cys	Ile	Ser
		115				120					125				
Phe	Phe	Asp	Asp	Phe	Arg	Ser	Arg	Gln	Thr	Pro	Ser	Asp	Leu	Pro	Cys
	130				135					140					
Phe	Leu	Tyr	Ser	Glu	Ser	Leu	Gly	Gly	Ala	Ile	Ala	Leu	Tyr	Ile	Ser
	145				150				155					160	
Leu	Arg	Gln	Arg	Gly	Val	Trp	Asp	Gly	Leu	Ile	Leu	Asn	Gly	Ala	Met
				165				170						175	
Cys	Gly	Ile	Ser	Asp	Lys	Phe	Lys	Pro	Pro	Trp	Pro	Leu	Glu	His	Leu
			180					185					190		
Leu	Phe	Val	Val	Ala	Asn	Leu	Ile	Pro	Thr	Trp	Arg	Val	Ile	Pro	Thr
		195					200					205			
Arg	Gly	Ser	Ile	Pro	Asp	Val	Ser	Phe	Lys	Glu	Pro	Trp	Lys	Arg	Lys
	210				215						220				
Leu	Ala	Met	Ala	Ser	Pro	Arg	Arg	Thr	Val	Ala	Lys	Pro	Arg	Ala	Ala
	225				230				235					240	
Thr	Ala	Tyr	Glu	Leu	Ile	Arg	Val	Cys	Lys	Asp	Leu	Gln	Gly	Arg	Phe
			245					250						255	
Glu	Glu	Val	Glu	Val	Pro	Leu	Leu	Ile	Val	His	Gly	Gly	Gly	Asp	Val
			260					265					270		
Val	Cys	Asp	Val	Ala	Cys	Val	Glu	Glu	Leu	His	Arg	Arg	Ala	Ile	Ser

(2) INFORMATION FOR SEQ ID NO:1274:

(A) LENGTH: 330 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

```
(ix) FEATURE:
```

(A) NAME/KEY: peptide

(B) LOCATION: 1..330

(D) OTHER INFORMATION: / Ceres Seq. ID 1499986

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1274:

Met	Gly	Leu	His	Pro	Ile	Ser	Asp	Ala	Asn	Glu	His	Asn	Pro	Phe	Gly
1				5				10						15	
Ser	Leu	Thr	Ala	Asp	Glu	Phe	Tyr	Ala	Lys	His	Ser	Val	Ser	His	Ser
			20					25					30		
Ser	Ala	Phe	Ile	Thr	Asn	Pro	Arg	Gly	Leu	Lys	Leu	Phe	Thr	Gln	Trp
		35					40					45			
Trp	Ser	Pro	Leu	Pro	Pro	Thr	Lys	Pro	Ile	Gly	Ile	Ile	Ala	Val	Val
	50					55					60				
His	Gly	Phe	Thr	Gly	Glu	Ser	Ser	Trp	Phe	Leu	Gln	Leu	Thr	Ser	Ile
65				70					75						80
Leu	Phe	Ala	Lys	Ser	Gly	Phe	Ile	Thr	Cys	Ala	Ile	Asp	His	Gln	Gly
				85					90					95	
His	Gly	Phe	Ser	Asp	Gly	Leu	Ile	Ala	His	Ile	Pro	Asp	Ile	Asn	Pro
			100					105					110		
Val	Val	Asp	Asp	Cys	Ile	Ser	Phe	Phe	Asp	Asp	Phe	Arg	Ser	Arg	Gln
		115					120					125			
Thr	Pro	Ser	Asp	Leu	Pro	Cys	Phe	Leu	Tyr	Ser	Glu	Ser	Leu	Gly	Gly
	130					135					140				
Ala	Ile	Ala	Leu	Tyr	Ile	Ser	Leu	Arg	Gln	Arg	Gly	Val	Trp	Asp	Gly
145				150						155					160
Leu	Ile	Leu	Asn	Gly	Ala	Met	Cys	Gly	Ile	Ser	Asp	Lys	Phe	Lys	Pro
				165					170					175	
Pro	Trp	Pro	Leu	Glu	His	Leu	Leu	Phe	Val	Val	Ala	Asn	Leu	Ile	Pro
			180					185					190		
Thr	Trp	Arg	Val	Ile	Pro	Thr	Arg	Gly	Ser	Ile	Pro	Asp	Val	Ser	Phe
	195						200					205			
Lys	Glu	Pro	Trp	Lys	Arg	Lys	Leu	Ala	Met	Ala	Ser	Pro	Arg	Arg	Thr
	210					215					220				
Val	Ala	Lys	Pro	Arg	Ala	Ala	Thr	Ala	Tyr	Glu	Leu	Ile	Arg	Val	Cys
225				230						235					240
Lys	Asp	Leu	Gln	Gly	Arg	Phe	Glu	Glu	Val	Glu	Val	Pro	Leu	Leu	Ile
				245					250					255	
Val	His	Gly	Gly	Gly	Asp	Val	Val	Cys	Asp	Val	Ala	Cys	Val	Glu	Glu
		260						265					270		
Leu	His	Arg	Arg	Ala	Ile	Ser	Glu	Asp	Lys	Thr	Ile	Lys	Ile	Tyr	Pro
		275					280					285			
Glu	Leu	Trp	His	Gln	Met	Ile	Gly	Glu	Ser	Glu	Glu	Lys	Val	Asp	Leu
	290					295					300				
Val	Tyr	Gly	Asp	Met	Leu	Ser	Trp	Leu	Lys	Ser	Arg	Ala	Glu	Arg	Lys
305					310					315					320

Ala Arg Ala Ala Val Asp Gly Gly Ala Ala
325 330

(2) INFORMATION FOR SEQ ID NO:1275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1591
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1275:

```
ctcttgcttt ttgtctctcc accaattttt tcttgcttt tctctotcca ccacataaaa 60
aaaaaaaaac ctactctttt cccctcaact cactgattga actgcttgat ttctgattga 120
tcactctgggt gggttttgat cgaagagtat tgttgattta gtggctgggt gctctccaaa 180
agagtaaggc cgagagagaa aatcaatggc ctctggcgcc ggagaggcgg ataaatcaact 240
tgaatccggg tcggggaccg cggatcccaa aataggcggt actgggagca ggagcgccgg 300
agaagaacga tacttcaggc cagatatact ggatttcagt aaatgggatt tgcattatggg 360
tcaaacctct actagcagcg tcttcaacaa ttccgcttcc acgagcgctc ccgacccggc 420
gatgcaggaa tgggagattt accctctccaa actcgatatg aagcacgtcc tcgctcaccg 480
tacttacggc actgtctacc cgggtgtcta cgccggccaa gaagtcgcag tgaagtgtgt 540
agattgggga gaagatgggt acgcccaccc agctgaaact acaactctcc gtgcttcttt 600
cgagcaagag gtcgcctgtt ggcagaagct cgatcatccc aacgttacca agtctatagg 660
agcatccatg ggaacctctg atctcgcgat cctctctgct ggtgatactg gcggacgtgg 720
taacggtgca catcctcgca gggcctgttg tgttgtggtt gaatatgttg ccggagcgac 780
gcttaagaag ttctctatca agaaatatag ggccaaacta cccatcaagg atgtcatcca 840
gctcgttttg gatctcgcta gagggtctag ttacctccac tccaaggcga ttgtacatag 900
ggagctgaag tcagagaaca tgcgtttaca gcctaacaag acgctgaaga cgcgtgattt 960
cgggtagctt agagtgaag ctcagaaccc toaagacatg acgggtgga cgtggaacact 1020
tggtacatct gcaccagagg ttcttgaagg aaagccttac aacaggaaat gcgattgcta 1080
tagctttggg gtatgcctct gggaaatata ctgctgtgac atgccctatg ctgactgtag 1140
ttttgctgat atctctcacc cggttgttca taggaatctg agaccagaga ttccgaaatg 1200
ctgcccgcgt gcagtggaac acatcatgaa gagatgctgg gaccogaatc cagacagcgg 1260
tcggagatg gaggaggtgg tgaagctgct tgaagccata gacacaagca aagtggtggg 1320
aatgatatgt ccggaccagt ttcagggggt cctctgtttc ttcaaacctc gaagccctctg 1380
aatctctctc cctctctttc ctttttgctc cgtgtctgat atattcttga gagctgcgtg 1440
attcttttga ttttgtattt accttgagct atgggagttg gattgggtgg ggttttgtca 1500
taagaatctt tctgcgctct atgtatttat taacttaaca cagtcgtgta taattcgatt 1560
aagctttatt ttattttttg atgttgattc c
```

(2) INFORMATION FOR SEQ ID NO:1276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..391
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1276:

```
Met Ala Ser Gly Gly Gly Glu Ala Asp Lys Ser Leu Glu Ile Gly Ser
1 5 10 15
Gly Thr Ala Asp Pro Lys Ile Gly Gly Thr Gly Ser Arg Ser Ala Gly
20 25 30
Glu Glu Arg Tyr Phe Arg Ala Asp Thr Leu Asp Phe Ser Lys Trp Asp
35 40 45
Leu His Met Gly Gln Thr Ser Thr Ser Ser Val Leu Thr Asn Ser Ala
50 55 60
```

Ser Thr Ser Ala Pro Ala Pro Ala Met Gln Glu Trp Glu Ile Asp Leu
65 70 75 80
Ser Lys Leu Asp Met Lys His Val Leu Ala His Gly Thr Tyr Gly Thr
85 90 95
Val Tyr Arg Gly Val Tyr Ala Gly Gln Glu Val Ala Val Lys Val Leu
100 105 110
Asp Trp Gly Glu Asp Gly Tyr Ala Thr Pro Ala Glu Thr Thr Thr Leu
115 120 125
Arg Ala Ser Phe Glu Gln Glu Val Ala Val Trp Gln Lys Leu Asp His
130 135 140
Pro Asn Val Thr Lys Phe Ile Gly Ala Ser Met Gly Thr Ser Asp Leu
145 150 155 160
Arg Ile Pro Pro Ala Gly Asp Thr Gly Gly Arg Gly Asn Gly Ala His
165 170 175
Pro Ala Arg Ala Cys Cys Val Val Val Glu Tyr Val Ala Gly Gly Thr
180 185 190
Leu Lys Lys Phe Leu Ile Lys Lys Tyr Arg Ala Lys Leu Pro Ile Lys
195 200 205
Asp Val Ile Gln Leu Ala Leu Asp Leu Ala Arg Gly Leu Ser Tyr Leu
210 215 220
His Ser Lys Ala Ile Val His Arg Asp Val Lys Ser Glu Asn Met Leu
225 230 235 240
Leu Gln Pro Asn Lys Thr Leu Lys Ile Ala Asp Phe Gly Val Ala Arg
245 250 255
Val Glu Ala Gln Asn Pro Gln Asp Met Thr Gly Gly Thr Gly Thr Leu
260 265 270
Gly Tyr Met Ala Pro Glu Val Leu Glu Gly Lys Pro Tyr Asn Arg Lys
275 280 285
Cys Asp Val Tyr Ser Phe Gly Val Cys Leu Trp Glu Ile Tyr Cys Cys
290 295 300
Asp Met Pro Tyr Ala Asp Cys Ser Phe Ala Glu Ile Ser His Ala Val
305 310 315 320
Val His Arg Asn Leu Arg Pro Glu Ile Pro Lys Cys Cys Pro His Ala
325 330 335
Val Ala Asn Ile Met Lys Arg Cys Trp Asp Pro Asn Pro Asp Arg Arg
340 345 350
Pro Glu Met Glu Glu Val Val Lys Leu Leu Glu Ala Ile Asp Thr Ser
355 360 365
Lys Gly Gly Gly Met Ile Ala Pro Asp Gln Phe Gln Gly Cys Leu Cys
370 375 380
Phe Phe Lys Pro Arg Gly Pro
385 390

(2) INFORMATION FOR SEQ ID NO:1277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..341
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1277:

Met Gly Gln Thr Ser Thr Ser Ser Val Leu Thr Asn Ser Ala Ser Thr
1 5 10 15
Ser Ala Pro Ala Pro Ala Met Gln Glu Trp Glu Ile Asp Leu Ser Lys
20 25 30
Leu Asp Met Lys Lys His Val Leu Ala His Gly Thr Tyr Gly Thr Val Tyr
35 40 45
Arg Gly Val Tyr Ala Gly Gln Glu Val Ala Val Lys Val Leu Asp Trp

50 55 60
Gly Glu Asp Gly Tyr Ala Thr Pro Ala Glu Thr Thr Thr Leu Arg Ala
65 70 75 80
Ser Phe Glu Gln Glu Val Ala Val Trp Gln Lys Leu Asp His Pro Asn
85 90 95
Val Thr Lys Phe Ile Gly Ala Ser Met Gly Thr Ser Asp Leu Arg Ile
100 105 110
Pro Pro Ala Gly Asp Thr Gly Gly Arg Gly Asn Gly Ala His Pro Ala
115 120 125
Arg Ala Cys Cys Val Val Val Glu Tyr Val Ala Gly Gly Thr Leu Lys
130 135 140
Lys Phe Leu Ile Lys Lys Tyr Arg Ala Lys Leu Pro Ile Lys Asp Val
145 150 155 160
Ile Gln Leu Ala Leu Asp Leu Ala Arg Gly Leu Ser Tyr Leu His Ser
165 170 175
Lys Ala Ile Val His Arg Asp Val Lys Ser Glu Asn Met Leu Leu Gln
180 185 190
Pro Asn Lys Thr Leu Lys Ile Ala Asp Phe Gly Val Ala Arg Val Glu
195 200 205
Ala Gln Asn Pro Gln Asp Met Thr Gly Gly Thr Gly Thr Leu Gly Tyr
210 215 220
Met Ala Pro Glu Val Leu Glu Gly Lys Pro Tyr Asn Arg Lys Cys Asp
225 230 235 240
Val Tyr Ser Phe Gly Val Cys Leu Trp Glu Ile Tyr Cys Cys Asp Met
245 250 255
Pro Tyr Ala Asp Cys Ser Phe Ala Glu Ile Ser His Ala Val Val His
260 265 270
Arg Asn Leu Arg Pro Glu Ile Pro Lys Cys Cys Pro His Ala Val Ala
275 280 285
Asn Ile Met Lys Arg Cys Trp Asp Pro Asn Pro Asp Arg Arg Pro Glu
290 295 300
Met Glu Glu Val Val Lys Leu Leu Glu Ala Ile Asp Thr Ser Lys Gly
305 310 315 320
Gly Gly Met Ile Ala Pro Asp Gln Phe Gln Gly Cys Leu Cys Phe Phe
325 330 335
Lys Pro Arg Gly Pro
340

(2) INFORMATION FOR SEQ ID NO:1278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..319
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1278:

Met Gln Glu Trp Glu Ile Asp Leu Ser Lys Leu Asp Met Lys His Val
1 5 10 15
Leu Ala His Gly Thr Tyr Gly Thr Val Tyr Arg Gly Val Tyr Ala Gly
20 25 30
Gln Glu Val Ala Val Lys Val Leu Asp Trp Gly Glu Asp Gly Tyr Ala
35 40 45
Thr Pro Ala Glu Thr Thr Thr Leu Arg Ala Ser Phe Glu Gln Glu Val
50 55 60
Ala Val Trp Gln Lys Leu Asp His Pro Asn Val Thr Lys Phe Ile Gly
65 70 75 80
Ala Ser Met Gly Thr Ser Asp Leu Arg Ile Pro Pro Ala Gly Asp Thr
85 90 95

Gly Gly Arg Gly Asn Gly Ala His Pro Ala Arg Ala Cys Cys Val Val
100 105 110
Val Glu Tyr Val Ala Gly Gly Thr Leu Lys Lys Phe Leu Ile Lys Lys
115 120 125
Tyr Arg Ala Lys Leu Pro Ile Lys Asp Val Ile Gln Leu Ala Leu Asp
130 135 140
Leu Ala Arg Gly Leu Ser Tyr Leu His Ser Lys Ala Ile Val His Arg
145 150 155 160
Asp Val Lys Ser Glu Asn Met Leu Leu Gln Pro Asn Lys Thr Leu Lys
165 170 175
Ile Ala Asp Phe Gly Val Ala Arg Val Glu Ala Gln Asn Pro Gln Asp
180 185 190
Met Thr Gly Gly Thr Gly Thr Leu Gly Tyr Met Ala Pro Glu Val Leu
195 200 205
Glu Gly Lys Pro Tyr Asn Arg Lys Cys Asp Val Tyr Ser Phe Gly Val
210 215 220
Cys Leu Trp Glu Ile Tyr Cys Cys Asp Met Pro Tyr Ala Asp Cys Ser
225 230 235 240
Phe Ala Glu Ile Ser His Ala Val Val His Arg Asn Leu Arg Pro Glu
245 250 255
Ile Pro Lys Cys Cys Pro His Ala Val Ala Asn Ile Met Lys Arg Cys
260 265 270
Trp Asp Pro Asn Pro Asp Arg Arg Pro Glu Met Glu Glu Val Val Lys
275 280 285
Leu Leu Glu Ala Ile Asp Thr Ser Lys Gly Gly Met Ile Ala Pro
290 295 300
Asp Gln Phe Gln Gly Cys Leu Cys Phe Phe Lys Pro Arg Gly Pro
305 310 315

(2) INFORMATION FOR SEQ ID NO:1279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..576
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1279:

aattaacggt cactgagctac atgctctgta tcttcagatt tcctaataac ttacaattcc 60
cattccaatt ctgatttggt taatccaaaa caaaaaaaa ggaactttc ttttacccta 120
aatctataaa aacgaacccc ttcttcacaa atctttgttc ttctgtaatt ctcttaaaaag 180
cttttgttcc aatttcaatg gactgggttc gaggagaac aattgggttc ggaactctct 240
ctactgtcag tacagcgaca aagtctagaa actccggcga ctttctgca cttatcgctg 300
tgaagtcgac ggggtcttcc ggcgcgcgtt cactctccaa cgagaaatcg gtgttgatt 360
cactccgtga ttgtctctgag atcatacggg gttacggcga ggattcaact gtggagaacg 420
gagaagagat gcataacttg ttcttagagt acgcttcgag aggaagctta gcgaggatac 480
tgaagaaact tggcggtgar ggtttaccgg agtccaccgt acgtcgctac acaggatcgg 540
tgcttcgagg gttacgtcat attcacgcta aagggt

(2) INFORMATION FOR SEQ ID NO:1280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..126
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499994

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1280:
Met Glu Trp Val Arg Gly Glu Thr Ile Gly Phe Gly Thr Phe Ser Thr
1 5 10 15
Val Ser Thr Ala Thr Lys Ser Arg Asn Ser Gly Asp Phe Pro Ala Leu
20 25 30
Ile Ala Val Lys Ser Thr Gly Ser Tyr Gly Ala Ala Ser Leu Ser Asn
35 40 45
Glu Lys Ser Val Leu Asp Ser Leu Arg Asp Cys Pro Glu Ile Ile Arg
50 55 60
Cys Tyr Gly Glu Asp Ser Thr Val Glu Asn Gly Glu Glu Met His Asn
65 70 75 80
Leu Phe Leu Glu Tyr Ala Ser Arg Gly Ser Leu Ala Arg Tyr Met Lys
85 90 95
Lys Leu Gly Gly Xaa Gly Leu Pro Glu Ser Thr Val Arg Arg Tyr Thr
100 105 110
Gly Ser Val Leu Arg Gly Leu Arg His Ile His Ala Lys Gly
115 120 125

(2) INFORMATION FOR SEQ ID NO:1281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..461
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499995

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1281:

atcatcacta	acaaaacaca	catcaaaac	gattttacaa	gaaaaaata	tcagaaaaaa	60
tgctcagagac	caacaagaat	gccttccaag	ccggtcagcg	cgctggcaaa	gctgaggaga	120
agagcaatgt	tctgtcgagc	aaggccaagg	atgctgctgc	tgcagctgga	gcttccgcgc	180
aacaggcgagg	aaagagtata	tcggatcgcg	cagtgaggag	tgtaaacttc	gtgaaggaca	240
agacggcgct	gaacaagtag	cgatccgagt	caactttggg	agttataatt	tcctttttct	300
aattaattgt	tgggattttc	aaataaaaatt	tgggagtcac	aattgattct	cgctactcatc	360
gtacttgttg	ttgttttttag	tggtgtaatg	ttttaatggt	tcttctccct	ttagatgtac	420
tacgtattgg	aactttaagt	ttaatcaaca	aaatctagtt	t		

(2) INFORMATION FOR SEQ ID NO:1282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77
- (D) OTHER INFORMATION: / Ceres Seq. ID 1499996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1282:

Ile	Ile	Thr	Asn	Lys	Thr	His	Ile	Lys	Asn	Asp	Phe	Thr	Arg	Lys	Lys	
1	5	10	15													
Tyr	Gln	Lys	Lys	Cys	Gln	Arg	Pro	Thr	Arg	Met	Pro	Ser	Lys	Pro	Val	
	20							25				30				
Arg	Pro	Leu	Ala	Lys	Leu	Arg	Arg	Ala	Met	Phe	Cys	Trp	Thr	Arg		
	35					40				45						
Pro	Arg	Met	Leu	Leu	Leu	Gln	Leu	Glu	Leu	Pro	Arg	Asn	Arg	Arg	Glu	
	50					55				60						
Arg	Val	Tyr	Arg	Met	Arg	Gln	Trp	Glu	Val	Leu	Thr	Ser				
65				70				75								

(2) INFORMATION FOR SEQ ID NO:1283:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..66
(D) OTHER INFORMATION: / Ceres Seq. ID 1499997
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1283:
Met Ser Glu Thr Asn Lys Asn Ala Phe Gln Ala Gly Gln Ala Ala Gly
1 5 10 15
Lys Ala Glu Glu Lys Ser Asn Val Leu Leu Asp Lys Ala Lys Asp Ala
20 25 30
Ala Ala Ala Ala Gly Ala Ser Ala Gln Gln Ala Gly Lys Ser Ile Ser
35 40 45
Asp Ala Ala Val Gly Gly Val Asn Phe Val Lys Asp Lys Thr Gly Leu
50 55 60
Asn Lys
65

(2) INFORMATION FOR SEQ ID NO:1284:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..51
(D) OTHER INFORMATION: / Ceres Seq. ID 1499998
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1284:
Met Pro Ser Lys Pro Val Arg Pro Leu Ala Lys Leu Arg Arg Arg Ala
1 5 10 15
Met Phe Cys Trp Thr Arg Pro Arg Met Leu Leu Leu Gln Leu Glu Leu
20 25 30
Pro Arg Asn Arg Arg Glu Arg Val Tyr Arg Met Arg Gln Trp Glu Val
35 40 45
Leu Thr Ser
50

(2) INFORMATION FOR SEQ ID NO:1285:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 515 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..515
(D) OTHER INFORMATION: / Ceres Seq. ID 1499999
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1285:
acgttttctat ctagagagaa cacaacacat cgaaccatgg agaaatcaac aagaacccta 60
ttcataacca tcgtgataac ctccatgttg ctagggtttg gaaactctga tcttgctcag 120
gacagagagg agtgtacgaa ccagctcata gaactatcca cgtgtattcc gtacgttgga 180
ggagagccca aggtcccaac aaaagattgt tgtgcagggt ttggccaagt tataagaaaag 240
agtgagaagt gtgtttgcat atttggcttc tgaccaatat gcaaacacac ttctggactc 300
tttcttcttc catcatattgt gctttttttc ttcttgtggt ttgtctttaa gacttgttat 360
attcttcaac atatgtttgt tatgtctctc ggtgtgtggt ttgttttttt tggtattact 420
ttcatatttt ttctgtcgaa gaggacttgt attcgacaat gtgcgttcaa ttttgttgtt 480
tccttagaaa ctaataaat attggtttat attcg

(2) INFORMATION FOR SEQ ID NO:1286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1286:

Thr	Phe	Leu	Ser	Arg	Glu	Asn	Thr	Thr	His	Arg	Thr	Met	Glu	Lys	Ser	
1			5						10					15		
Thr	Arg	Thr	Leu	Phe	Ile	Thr	Ile	Val	Ile	Thr	Ser	Met	Leu	Leu	Gly	
			20					25					30			
Phe	Gly	Asn	Ser	Asp	Leu	Ala	Gln	Asp	Arg	Glu	Glu	Cys	Thr	Asn	Gln	
		35					40					45				
Leu	Ile	Glu	Leu	Ser	Thr	Cys	Ile	Pro	Tyr	Val	Gly	Gly	Asp	Ala	Lys	
		50				55					60					
Ala	Pro	Thr	Lys	Asp	Cys	Cys	Ala	Gly	Phe	Gly	Gln	Val	Ile	Arg	Lys	
		65			70					75				80		
Ser	Glu	Lys	Cys	Val	Cys	Ile	Phe	Gly	Leu							
			85						90							

(2) INFORMATION FOR SEQ ID NO:1287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1287:

Met	Glu	Lys	Ser	Thr	Arg	Thr	Leu	Phe	Ile	Thr	Ile	Val	Ile	Thr	Ser	
1			5						10					15		
Met	Leu	Leu	Gly	Phe	Gly	Asn	Ser	Asp	Leu	Ala	Gln	Asp	Arg	Glu	Glu	
		20					25					30				
Cys	Thr	Asn	Gln	Leu	Ile	Glu	Leu	Ser	Thr	Cys	Ile	Pro	Tyr	Val	Gly	
		35					40					45				
Gly	Asp	Ala	Lys	Ala	Pro	Thr	Lys	Asp	Cys	Cys	Ala	Gly	Phe	Gly	Gln	
		50				55					60					
Val	Ile	Arg	Lys	Ser	Glu	Lys	Cys	Val	Cys	Ile	Phe	Gly	Leu			
		65			70				75							

(2) INFORMATION FOR SEQ ID NO:1288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..62
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1288:

Met	Leu	Leu	Gly	Phe	Gly	Asn	Ser	Asp	Leu	Ala	Gln	Asp	Arg	Glu	Glu	
1			5						10					15		
Cys	Thr	Asn	Gln	Leu	Ile	Glu	Leu	Ser	Thr	Cys	Ile	Pro	Tyr	Val	Gly	

(2) INFORMATION FOR SEQ ID NO:1289:

(A) LENGTH: 1413 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..1413

SEQUENCE DESCRIPTION: SEQ ID NO:1289:

(X1) SEQUENCE DESCRIPTION						
agttgttttt	tcttttttct	tctcttcgat	taaaagctctc	tctcttctct	tcaaacggag	60
ctctctctctt	ctctctctcaac	ctttgtctct	cgatctctgt	tttttttttt	tttatctctt	120
ctcttgattgt	aagaaaagtgt	tcagctcaaa	gaaatctggg	ttaaagctgt	tttgaattgt	180
tcgatcgatt	catagatttt	cgataccaat	aggagtgtgt	gatacgttgt	taatctctgt	240
ccatcatctt	gtgtttgtcaa	cagatgagtg	ttttaatgtc	aattctctgg	taaccaagt	300
tgaagctaat	cccttttgatt	ctgcggcgct	ctctgatttt	ttaaagtgc	gacgacaagt	360
gtagaaacaa	tagagacaaa	gaagaagctc	aagttttttt	ataactgtt	tctaaagaat	420
tcgtctccct	gagagattatt	caactcgaca	taagagtttc	cccacacgga	agagaaattc	480
aaagatcgaa	aaacggtgaa	cagtcgacag	accacaggaa	atgtggagat	tacaaaagcg	540
cgacgctgt	agggatcagt	accggttact	agggaaaaat	gtacgcgaag	ttccagcagt	600
atatagtgaa	rgaacacgtc	tccacgttct	gtctccagct	tgaagagtc	gctcgttaac	660
acaagaattga	cattctgtaa	aatctctgct	tcagggtctc	gttccatgat	atgtgtgtcta	720
acattgttgt	gtactctctt	gctctcaaca	agggttctgt	ggctcagaa	ctctggtatt	780
gtgaactttca	ctatgaactt	ggagttcaga	ttattgaagt	ttcgatcgct	acaagatcac	840
atataggagg	tttgcacagc	tcgaagaagc	ttctgcgaac	ttgtctcaag	acaggagaaga	900
aagacacgtga	agctgtgact	gaagatgatt	gtctctgagc	tattagcaac	ctaaaggtat	960
tgggtagcgg	atttgagttt	atcatattgt	ccaagaaagaa	gctgtccgtg	tcagtatcca	1020
cagagctgaa	caaaagacat	aaccaagatt	tggaattggc	tcagggccaa	ggctttgtga	1080
tttgtgaaga	gtgtcaaaaga	cgctctctat	ggacatctgt	tcgctgtgt	gatgctctcg	1140
aaacttttgt	agaggagggc	gtctccatga	tcgacaattg	ccataaagac	ggaaagtgtc	1200
ggtaactggt	tcocctgttt	tcttgcgttt	actcatctat	cgggactctg	taacttaagt	1260
gtacatgctc	agtttgtttt	tttgttttta	tacagtatta	aataacacga	cactcgttac	1320
gtgtgtgtgt	agagagaatt	tttgcattat	attatgaaa	ttttctgtga	catgtatcac	1380

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: lin

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..215

(D) OTHER INFORMATION: / Ceres Seq. ID 1500004

Met	Met	Xaa	Glu	Gln	Leu	Ser	Thr	Phe	Arg	Ser	Gln	Leu	Glu	Glu	Phe
1			5						10				15		
Ala	Arg	Lys	Lys	Asn	Asp	Ile	Arg	Lys	Asn	Pro	Ala	Phe	Arg	Ala	
		20					25					30			
Gln	Phe	His	Glu	Met	Cys	Ala	Asn	Ile	Gly	Val	Asp	Pro	Leu	Ala	Ser
		35					40					45			
Asn	Lys	Gly	Phe	Trp	Ala	Glu	Leu	Leu	Gly	Ile	Gly	Asp	Phe	Tyr	Tyr
	50					55					60				

Glu Leu Gly Val Gln Ile Ile Glu Val Cys Met Leu Thr Arg Ser His
65 70 75 80
Asn Gly Gly Leu Ile Ser Leu Gln Glu Leu Cys Asn His Leu Arg Gln
85 90 95
Arg Arg Lys Lys Asp Arg Glu Ala Val Thr Glu Asp Asp Cys Leu Arg
100 105 110
Ala Ile Ser Lys Leu Lys Val Leu Gly Ser Gly Phe Glu Val Ile Thr
115 120 125
Ile Gly Lys Lys Lys Leu Val Arg Ser Val Pro Thr Glu Leu Asn Lys
130 135 140
Asp His Asn Gln Ile Leu Glu Leu Ala Gln Gly Gln Gly Phe Val Ile
145 150 155 160
Val Glu Glu Val Gln Arg Arg Leu Ser Trp Thr Ser Gly Arg Val Ile
165 170 175
Asp Ala Leu Glu Thr Leu Leu Glu Glu Gly Leu Ala Met Ile Asp Asn
180 185 190
Gly His Lys Asp Gly Lys Cys Arg Tyr Trp Phe Pro Cys Val Ser Ser
195 200 205
Val Tyr Ser Ser Ile Gly Ile
210 215

(2) INFORMATION FOR SEQ ID NO:1291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..214
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500005

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1291:

Met Xaa Glu Gln Leu Ser Thr Phe Arg Ser Gln Leu Glu Glu Phe Ala
1 5 10 15
Arg Lys His Lys Asn Asp Ile Arg Lys Asn Pro Ala Phe Arg Ala Gln
20 25 30
Phe His Glu Met Cys Ala Asn Ile Gly Val Asp Pro Leu Ala Ser Asn
35 40 45
Lys Gly Phe Trp Ala Glu Leu Leu Gly Ile Gly Asp Phe Tyr Tyr Glu
50 55 60
Leu Gly Val Gln Ile Ile Glu Val Cys Met Leu Thr Arg Ser His Asn
65 70 75 80
Gly Gly Leu Ile Ser Leu Gln Glu Leu Cys Asn His Leu Arg Gln Arg
85 90 95
Arg Lys Lys Asp Arg Glu Ala Val Thr Glu Asp Asp Cys Leu Arg Ala
100 105 110
Ile Ser Lys Leu Lys Val Leu Gly Ser Gly Phe Glu Val Ile Thr Ile
115 120 125
Gly Lys Lys Lys Leu Val Arg Ser Val Pro Thr Glu Leu Asn Lys Asp
130 135 140
His Asn Gln Ile Leu Glu Leu Ala Gln Gly Gln Gly Phe Val Ile Val
145 150 155 160
Glu Glu Val Gln Arg Arg Leu Ser Trp Thr Ser Gly Arg Val Ile Asp
165 170 175
Ala Leu Glu Thr Leu Leu Glu Glu Gly Leu Ala Met Ile Asp Asn Gly
180 185 190
His Lys Asp Gly Lys Cys Arg Tyr Trp Phe Pro Cys Val Ser Ser Val
195 200 205
Tyr Ser Ser Ile Gly Ile
210

(2) INFORMATION FOR SEQ ID NO:1292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..179

(D) OTHER INFORMATION: / Ceres Seq. ID 1500006

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1292:

Met	Cys	Ala	Asn	Ile	Gly	Val	Asp	Pro	Leu	Ala	Ser	Asn	Lys	Gly	Phe	
1			5					10						15		
Trp	Ala	Glu	Leu	Leu	Gly	Ile	Gly	Asp	Phe	Tyr	Tyr	Glu	Leu	Gly	Val	
			20					25					30			
Gln	Ile	Ile	Glu	Val	Cys	Met	Leu	Thr	Arg	Ser	His	Asn	Gly	Gly	Leu	
			35					40					45			
Ile	Ser	Leu	Gln	Glu	Leu	Cys	Asn	His	Leu	Arg	Gln	Arg	Arg	Lys	Lys	
			50				55					60				
Asp	Arg	Glu	Ala	Val	Thr	Glu	Asp	Asp	Cys	Leu	Arg	Ala	Ile	Ser	Lys	
65				70						75					80	
Leu	Lys	Val	Leu	Gly	Ser	Gly	Phe	Glu	Val	Ile	Thr	Ile	Gly	Lys	Lys	
				85						90				95		
Lys	Leu	Val	Arg	Ser	Val	Pro	Thr	Glu	Leu	Asn	Lys	Asp	His	Asn	Gln	
				100						105				110		
Ile	Leu	Glu	Leu	Ala	Gln	Gly	Gln	Gly	Phe	Val	Ile	Val	Glu	Glu	Val	
				115						120				125		
Gln	Arg	Arg	Leu	Ser	Trp	Thr	Ser	Gly	Arg	Val	Ile	Asp	Ala	Leu	Glu	
				130						135				140		
Thr	Leu	Leu	Glu	Glu	Gly	Leu	Ala	Met	Ile	Asp	Asn	Gly	His	Lys	Asp	
				145						150				155		
Gly	Lys	Cys	Arg	Tyr	Trp	Phe	Pro	Cys	Val	Ser	Ser	Val	Tyr	Ser	Ser	
				165						170				175		
Ile	Gly	Ile														

(2) INFORMATION FOR SEQ ID NO:1293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1653 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1653

(D) OTHER INFORMATION: / Ceres Seq. ID 1500007

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1293:

accacaaatag	atctaaaaaca	tggaaaaccaa	aaccctaatt	ttctcaattc	tcgtcgttgt	60
tctttctctc	atttacttaa	ttggaaaact	caagcgaaag	ccaaatctac	ctccgagtc	120
ggcatggtcg	ttacgggtga	ttgggtcaact	cgtctctctc	aaaccaccga	ttcatcgca	180
attctctctc	ctctctcaat	ccctaaacaa	tgctccgata	ttctccctcc	gactcggtaa	240
cgactcgttt	ttcgtgaact	cgtcacactc	gatacgccgag	gaatgtttca	ccaaaacga	300
cgctcgtactg	gogaacagac	caaacttcat	cctcgctaaa	caagttgcgt	acgattacac	360
aaacatgata	gcagcttctc	acggtgacca	ctggcgtaac	ctccgcgcga	tcggctccgt	420
cgagatatct	tccaaccacc	gtctcaatag	ctttctgtct	attcgtaaas	acgagatccg	480
acgactgtgt	ttctgtcttt	cacgttaact	ttcacaagag	tttgtgaag	tggatatgaa	540
atcaatgtta	ctgcacttaa	cattcaacaa	cattataaga	atgggtggccg	gaaaacgcta	600
ctacggagac	gggtgtgagg	atgataccga	ggctaaacgt	gtccggcagc	ttatagccga	660
tgtgtgtgct	tgtgtgtgtg	ctggaaacgc	tgttgattac	ttaccggttt	tcggtgttgt	720
ttcagattac	gaaacacggg	ttaagaagtt	agcgggtagg	ctcgacgagt	tcttgcaagg	780
attggtgtat	gagaaacgag	acgctaaaga	gaaaggaaac	actatgattg	atcacttgct	840

tactctgcaa	gaatcacaca	cggattactt	cactgatcgt	atcatcaaag	gaaacatgct	900
tgctttgata	ctagcaggga	ccgacacatc	agcggttacg	ttagaattggg	cattgtcgaa	960
cgtgttgaac	cattcggaag	tattgaacaa	ggcgagagat	gaaatcgata	gaaagatcgg	1020
tttagacagg	cttatggatg	aatcagatat	ctcaaacctg	ccttatctcc	aaaacattgt	1080
gtctgaaacg	ttgcgccttt	atcctgcgcc	teccatgctt	cttccctcacg	ttgcctcgga	1140
agattgtaaa	gttcgaggat	atgatatgcc	gcgtggcacg	atactattga	ccaatgtgtg	1200
ggctatacac	agagatcctc	agctatggga	tgatccaatg	agcttcaagc	cagagaggtt	1260
tgagaaggaa	ggagaagctc	agaagcttat	gcggtttggg	ttaggaagaa	ggcggtgtcc	1320
tggtttctgga	ctggctcacc	ggcttataaa	cctgactctt	ggatcattga	ttcagttgtt	1380
ggaatgggag	aagattggag	aagaagtggg	tatgagtga	ggcaagggtg	ttacaatgcc	1440
taaaagccaa	ccctttagaag	ccatgtgcag	agcacgtccc	tctgttgtta	aaactttcaa	1500
ctagtcgcgt	tgacgctttag	tccttttagta	atgcttatgt	atacactaga	taactaatta	1560
tgattgtatg	ttttcttttt	tttttgggtg	aaatattatg	ttgtatgttt	atatgagaat	1620
attttaccaa	tattcctaga	tgatatatttt	ggc			

(2) INFORMATION FOR SEQ ID NO:1294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..494
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500008

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1294:

Met	Glu	Thr	Lys	Thr	Leu	Ile	Phe	Ser	Ile	Leu	Val	Val	Val	Leu	Ser
1			5						10					15	
Leu	Ile	Tyr	Leu	Ile	Gly	Lys	Leu	Lys	Arg	Lys	Pro	Asn	Leu	Pro	Pro
			20					25					30		
Ser	Pro	Ala	Trp	Ser	Leu	Pro	Val	Ile	Gly	His	Leu	Arg	Leu	Leu	Lys
			35				40					45			
Pro	Pro	Ile	His	Arg	Thr	Phe	Leu	Ser	Leu	Ser	Gln	Ser	Leu	Asn	Asn
			50				55					60			
Ala	Pro	Ile	Phe	Ser	Leu	Arg	Leu	Gly	Asn	Arg	Leu	Val	Phe	Val	Asn
			65			70				75				80	
Ser	Ser	His	Ser	Ile	Ala	Glu	Glu	Cys	Phe	Thr	Lys	Asn	Asp	Val	Val
			85						90					95	
Leu	Ala	Asn	Arg	Pro	Asn	Phe	Ile	Leu	Ala	Lys	His	Val	Ala	Tyr	Asp
			100					105					110		
Tyr	Thr	Thr	Met	Ile	Ala	Ala	Ser	Tyr	Gly	Asp	His	Trp	Arg	Asn	Leu
			115				120					125			
Arg	Arg	Ile	Gly	Ser	Val	Glu	Ile	Phe	Ser	Asn	His	Arg	Leu	Asn	Ser
			130			135					140				
Phe	Leu	Ser	Ile	Arg	Lys	Xaa	Glu	Ile	Arg	Arg	Leu	Val	Phe	Arg	Leu
			145			150				155				160	
Ser	Arg	Asn	Phe	Ser	Gln	Glu	Phe	Val	Lys	Val	Asp	Met	Lys	Ser	Met
			165						170					175	
Leu	Ser	Asp	Leu	Thr	Phe	Asn	Asn	Ile	Ile	Arg	Met	Val	Ala	Gly	Lys
			180					185					190		
Arg	Tyr	Tyr	Gly	Asp	Gly	Val	Glu	Asp	Asp	Pro	Glu	Ala	Lys	Arg	Val
			195					200				205			
Arg	Gln	Leu	Ile	Ala	Asp	Val	Val	Ala	Cys	Ala	Gly	Ala	Gly	Asn	Ala
			210			215					220				
Val	Asp	Tyr	Leu	Pro	Val	Leu	Arg	Leu	Val	Ser	Asp	Tyr	Glu	Thr	Arg
			225			230				235				240	
Val	Lys	Lys	Leu	Ala	Gly	Arg	Leu	Asp	Glu	Phe	Leu	Gln	Gly	Leu	Val
			245						250					255	
Asp	Glu	Lys	Arg	Asp	Ala	Lys	Glu	Lys	Gly	Asn	Thr	Met	Ile	Asp	His
			260					265					270		
Leu	Leu	Thr	Leu	Gln	Glu	Ser	Gln	Pro	Asp	Tyr	Phe	Thr	Asp	Arg	Ile

	275		280		285
Ile	Lys	Gly	Asn	Met	Leu
290					Ala
Ala	Val	Thr	Leu	Glu	Trp
305					Ala
Val	Leu	Asn	Lys	Ala	Arg
					Asp
Arg	Leu	Met	Asp	Glu	Ser
					Ile
Ile	Val	Ser	Glu	Thr	Leu
					Arg
Pro	His	Val	Ala	Ser	Glu
					Asp
Arg	Gly	Thr	Ile	Leu	Leu
385					Thr
Gln	Leu	Trp	Asp	Pro	Met
					Ser
Glu	Gly	Glu	Ala	Gln	Lys
					Leu
Cys	Pro	Gly	Ser	Gly	Leu
					Ala
Ser	Leu	Ile	Gln	Cys	Leu
					Trp
Met	Ser	Glu	Gly	Lys	Gly
465					Val
Ala	Met	Cys	Arg	Ala	Arg
					Pro

(2) INFORMATION FOR SEQ ID NO:1295:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 379 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..379

(D) OTHER INFORMATION: / Ceres Seq. ID 1500009

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1295:

Met	Ile	Ala	Ala	Ser	Tyr	Gly	Asp	His	Trp	Arg	Asn	Leu	Arg	Arg	Ile
1				5					10				15		
Gly	Ser	Val	Glu	Ile	Phe	Ser	Asn	His	Arg	Leu	Asn	Ser	Phe	Leu	Ser
			20					25					30		
Ile	Arg	Lys	Xaa	Glu	Ile	Arg	Arg	Leu	Val	Phe	Arg	Leu	Ser	Arg	Asn
			35					40					45		
Phe	Ser	Gln	Glu	Phe	Val	Lys	Val	Asp	Met	Lys	Ser	Met	Leu	Ser	Asp
			50					55					60		
Leu	Thr	Phe	Asn	Asn	Ile	Ile	Arg	Met	Val	Ala	Gly	Lys	Arg	Tyr	Tyr
			65					70					75		80
Gly	Asp	Gly	Val	Glu	Asp	Asp	Pro	Glu	Ala	Lys	Arg	Val	Arg	Gln	Leu
			85					90					95		
Ile	Ala	Asp	Val	Val	Ala	Cys	Ala	Gly	Ala	Gly	Asn	Ala	Val	Asp	Tyr
			100					105					110		
Leu	Pro	Val	Leu	Arg	Leu	Val	Ser	Asp	Tyr	Glu	Thr	Arg	Val	Lys	Lys
			115					120					125		
Leu	Ala	Gly	Arg	Leu	Asp	Glu	Phe	Leu	Gln	Gly	Leu	Val	Asp	Glu	Lys
			130					135					140		
Arg	Asp	Ala	Lys	Glu	Lys	Gly	Asn	Thr	Met	Ile	Asp	His	Leu	Leu	Thr
			145					150					155		160
Leu	Gln	Glu	Ser	Gln	Pro	Asp	Tyr	Phe	Thr	Asp	Arg	Ile	Ile	Lys	Gly
			165										170		175

Asn Met Leu Ala Leu Ile Leu Ala Gly Thr Asp Thr Ser Ala Val Thr
180 185 190
Leu Glu Trp Ala Leu Ser Asn Val Leu Asn His Ser Glu Val Leu Asn
195 200 205
Lys Ala Arg Asp Glu Ile Asp Arg Lys Ile Gly Leu Asp Arg Leu Met
210 215 220
Asp Glu Ser Asp Ile Ser Asn Leu Pro Tyr Leu Gln Asn Ile Val Ser
225 230 235 240
Glu Thr Leu Arg Leu Tyr Pro Ala Ala Pro Met Leu Leu Pro His Val
245 250 255
Ala Ser Glu Asp Cys Lys Val Ala Gly Tyr Asp Met Pro Arg Gly Thr
260 265 270
Ile Leu Leu Thr Asn Val Trp Ala Ile His Arg Asp Pro Gln Leu Trp
275 280 285
Asp Asp Pro Met Ser Phe Lys Pro Glu Arg Phe Glu Lys Glu Gly Glu
290 295 300
Ala Gln Lys Leu Met Pro Phe Gly Leu Gly Arg Arg Ala Cys Pro Gly
305 310 315 320
Ser Gly Leu Ala His Arg Leu Ile Asn Leu Thr Leu Gly Ser Leu Ile
325 330 335
Gln Cys Leu Glu Trp Glu Lys Ile Gly Glu Glu Val Asp Met Ser Glu
340 345 350
Gly Lys Gly Val Thr Met Pro Lys Ala Lys Pro Leu Glu Ala Met Cys
355 360 365
Arg Ala Arg Pro Ser Val Val Lys Ile Phe Asn
370 375

(2) INFORMATION FOR SEQ ID NO:1296:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 322 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..322

(D) OTHER INFORMATION: / Ceres Seq. ID 1500010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1296:

Met Lys Ser Met Leu Ser Asp Leu Thr Phe Asn Asn Ile Ile Arg Met
1 5 10 15
Val Ala Gly Lys Arg Tyr Tyr Gly Asp Gly Val Glu Asp Asp Pro Glu
20 25 30
Ala Lys Arg Val Arg Gln Leu Ile Ala Asp Val Val Ala Cys Ala Gly
35 40 45
Ala Gly Asn Ala Val Asp Tyr Leu Pro Val Leu Arg Leu Val Ser Asp
50 55 60
Tyr Glu Thr Arg Val Lys Lys Leu Ala Gly Arg Leu Asp Glu Phe Leu
65 70 75 80
Gln Gly Leu Val Asp Glu Lys Arg Asp Ala Lys Glu Lys Gly Asn Thr
85 90 95
Met Ile Asp His Leu Leu Thr Leu Gln Glu Ser Gln Pro Asp Tyr Phe
100 105 110
Thr Asp Arg Ile Ile Lys Gly Asn Met Leu Ala Leu Ile Leu Ala Gly
115 120 125
Thr Asp Thr Ser Ala Val Thr Leu Glu Trp Ala Leu Ser Asn Val Leu
130 135 140
Asn His Ser Glu Val Leu Asn Lys Ala Arg Asp Glu Ile Asp Arg Lys
145 150 155 160
Ile Gly Leu Asp Arg Leu Met Asp Glu Ser Asp Ile Ser Asn Leu Pro
165 170 175
Tyr Leu Gln Asn Ile Val Ser Glu Thr Leu Arg Leu Tyr Pro Ala Ala

180	185	190
Pro Met Leu Leu	Pro His Val Ala Ser Glu Asp Cys Lys Val Ala Gly	
195	200	205
Tyr Asp Met Pro Arg Gly Thr Ile Leu Leu Thr Asn Val Trp Ala Ile		
210	215	220
His Arg Asp Pro Gln Leu Trp Asp Asp Pro Met Ser Phe Lys Pro Glu		
225	230	235
Arg Phe Glu Lys Glu Gly Glu Ala Gln Lys Leu Met Pro Phe Gly Leu		
245	250	255
Gly Arg Arg Ala Cys Pro Gly Ser Gly Leu Ala His Arg Leu Ile Asn		
260	265	270
Leu Thr Leu Gly Ser Leu Ile Gln Cys Leu Glu Trp Glu Lys Ile Gly		
275	280	285
Glu Glu Val Asp Met Ser Glu Gly Lys Gly Val Thr Met Pro Lys Ala		
290	295	300
Lys Pro Leu Glu Ala Met Cys Arg Ala Arg Pro Ser Val Val Lys Ile		
305	310	315
Phe Asn		320

(2) INFORMATION FOR SEQ ID NO:1297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1465
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500011

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1297:

gcagctggaga	gagagcatgt	gaataaaaag	cgtgaagctt	tttgatatct	ctttctcttc	60
ctcttccttt	ctctccgat	agatttcgcc	ggcgaatggc	gtggactcct	tagaaaacgga	120
gattgacacg	goggtgcgtg	ttgtccacct	cgcttctctt	ctctgtgtta	aagttcaaga	180
gaagcttcat	cttccataacg	gtggtcacgt	taagtctaaa	gacgatgatt	ccctgtgcac	240
cgctgcgtgat	tttgggtgac	aagcaattgt	gagctggggt	ttagctgaag	tggttggtga	300
tcaaaaacact	tcaattgttg	ctgaagaaga	cactgagaca	ctctctgagg	ctgattcttt	360
aggtctttta	ggagctgtgt	cgaatgcggt	taatgaagca	ttgtcogaag	ctcagaacta	420
cgggcttccg	aagccagtta	agccattggg	gtctagtga	attcttaagg	ctattagtag	480
atgtaactct	gttggaggag	ctaaaggaag	gcattgggtt	cttgatcctg	ttgatggaac	540
gttagggttt	gttcgtgggg	atcagtatgc	tggtgcttta	gctttgatag	agaatggtaa	600
agttcttttt	ggtgtactag	gatgtcctaa	ttatccgggt	aagaaagaat	gtttaagtaa	660
tggtgttaac	caagcatatga	agacgaaaagc	tggtgctggg	tcagtatcga	aagatgttgt	720
tatgtatgca	aagagaggta	gtggtcaaac	ttggatgcaa	ccctttgatc	ttgaggaagt	780
accagaatct	gcaacacctc	ttaaggtttc	ttcagttgat	gattccggtt	tagctacagt	840
ttgtgagcca	gtagagagag	caaaactcaaa	ccacttggtc	actgcaggag	ttgccaatag	900
catgggaagt	agaaaagcagc	ctatgcgagt	gtatagcatg	gtgaaatag	cagcgattgc	960
acgtggagac	gctgaagtgt	ttatgaagtt	tgacagtgca	agttacaaa	agaagatag	1020
ggtatcacga	gctgtaggtt	tattgttgga	agaagctggt	ggtgtggtga	ctgatgcggg	1080
agggagaaaac	ttagactttc	cgaaggtgtg	ttacttgaaa	ggtcttgacc	gtggaatcat	1140
cgcatctgtt	gcttcaagttt	tacatgagaa	gattataggt	gctgtttatg	ctagtgtgga	1200
atcttccagt	ctctgaaaaa	gcttatccac	aatccgtagt	ttggtgcagc	atcatcgagc	1260
caaaagcaag	gaggaacaa	ggccattacg	gtttagagag	agcaagggcc	agtttcaatg	1320
aattgtgaat	gcgggaaga	aaatatagtc	gaggaagcag	cggtaaaaag	agaactctag	1380
ttattttacc	tatctaaag	taataaagct	gctgcatttc	acgaaccctt	atgttctatg	1440
atctttaatg	gatgatata	ttttt				

(2) INFORMATION FOR SEQ ID NO:1298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..373
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500012
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1298:

Met Ala Val Asp Ser Leu Glu Thr Glu Ile Asp Thr Ala Val Arg Val
1 5 10 15
Val His Leu Ala Ser Ser Leu Cys Val Lys Val Gln Glu Lys Leu His
 20 25 30
Leu Pro Asn Gly Gly His Val Lys Ser Lys Asp Asp Asp Ser Pro Val
 35 40 45
Thr Val Ala Asp Phe Gly Val Gln Ala Ile Val Ser Trp Val Leu Ala
 50 55 60
Glu Val Phe Gly Asp Gln Asn Leu Ser Ile Val Ala Glu Glu Asp Thr
65 70 75 80
Glu Thr Leu Ser Glu Ala Asp Ser Leu Gly Leu Leu Gly Ala Val Ser
 85 90 95
Asn Ala Val Asn Glu Ala Leu Ser Glu Ala Gln Asn Tyr Gly Leu Pro
 100 105 110
Lys Pro Val Lys Pro Leu Gly Ser Ser Glu Ile Leu Lys Ala Ile Ser
 115 120 125
Arg Cys Asn Ser Val Gly Gly Pro Lys Gly Arg His Trp Val Leu Asp
 130 135 140
Pro Val Asp Gly Thr Leu Gly Phe Val Arg Gly Asp Gln Tyr Ala Val
145 150 155 160
Ala Leu Ala Leu Ile Glu Asn Gly Lys Val Leu Leu Gly Val Leu Gly
 165 170 175
Cys Pro Asn Tyr Pro Val Lys Lys Glu Cys Leu Ser Asn Gly Cys Asn
 180 185 190
Gln Ala Met Lys Thr Lys Ala Val Ala Gly Ser Val Ser Lys Gly Cys
195 200 205
Val Met Tyr Ala Lys Arg Gly Ser Gly Gln Ala Trp Met Gln Pro Leu
 210 215 220
Ile Val Gly Gly Ile Pro Glu Ser Ala Thr Leu Leu Lys Val Ser Ser
225 230 235 240
Val Asp Asp Pro Val Leu Ala Thr Val Cys Glu Pro Val Glu Arg Ala
 245 250 255
Asn Ser Asn His Leu Phe Thr Ala Gly Leu Ala Asn Ser Met Gly Val
 260 265 270
Arg Lys Gln Pro Met Arg Val Tyr Ser Met Val Lys Tyr Ala Ala Ile
 275 280 285
Ala Arg Gly Asp Ala Glu Val Phe Met Lys Phe Ala Gln Ser Ser Tyr
290 295 300
Lys Glu Lys Ile Trp Asp His Ala Ala Gly Val Val Ile Val Glu Glu
305 310 315 320
Ala Gly Gly Val Val Thr Asp Ala Gly Gly Arg Asn Leu Asp Phe Ser
 325 330 335
Lys Gly Val Tyr Leu Glu Gly Leu Asp Arg Gly Ile Ile Ala Cys Ser
 340 345 350
Gly Gln Val Leu His Glu Lys Ile Ile Gly Ala Val Tyr Ala Ser Trp
355 360 365
Glu Ser Ser Ser Leu
370

- (2) INFORMATION FOR SEQ ID NO:1299:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1472 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1472

(D) OTHER INFORMATION: / Ceres Seq. ID 1500017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1299:

aaaaaagtc	atcatatcaa	atcccaaatc	ctccagatg	tttttatcat	cttctttctc	60
ctgaagattt	gatttcattt	tcctctcttt	cagatcccta	ttctaatggc	ttctggatct	120
tactggtgct	atagttgtag	ccgattcggt	tgggtttccg	attcaatctc	ttgccctgat	180
tgcgacgggtg	gtttctctga	actcatccaa	gagcctctcg	atttcacacc	ttccgatctc	240
ttcaccacca	ccaccaccac	tcaacatcgc	agccccaactc	gcttccctcc	tcctctctct	300
tcctctctca	ccccatccgc	ttctatgcac	gcgcataaca	gtcccaactcc	taccatggtt	360
actcgtaac	gaagcaatcg	atctccta	at	cgagttatgt	ttctccgtgg	420
gctcctctct	ctgatgtgtg	ttccgaaggt	ttagatcgat	ctgcttttca	gatgtattac	480
gatgatggta	ctgattctgg	tccttagacct	ttaccacga	gtatgactga	gtttttgtta	540
gggtctggat	ttgatcgttt	gttagatcag	atctctcaga	tcgagcttaa	caccaatcgg	600
aatctctggt	cttgtagaaca	tccaccggct	tctaaatcgg	ccattgaagc	tttgccctctg	660
attgaaatcg	atccgactca	tcctttatcg	gattctcaat	ctcattgcgc	tggttgcaaa	720
gagaaattcg	ttttgaaatc	atctgctcgc	gagatgcctt	gtaatcacat	ctatcatcct	780
gattgtattc	ttccttggct	tgcgattcgt	aaactctgtc	cggtttgcgc	tcattgagcta	840
ccggcggagg	atctcaaccga	cgggaacgggt	gctgctttga	ctgctgttac	cgctaactga	900
gaggaagagg	aagactcagc	tgcgggggta	acgatttggg	ggtaaccagg	tggaagattc	960
gctgtagggg	gaatccctgg	tggttgagga	gggtggagta	gaatgatgcc	gggtggtttac	1020
acggagtggt	atggtgtgtag	actcgggtag	gagagaactc	cgagaagagt	agcttgggggt	1080
tcgagaagag	gtggaagaga	tggtggagggt	agtagagagc	agaggtggtg	gctttggcggg	1140
tcggatcatg	aggctttctg	gatgtttttg	ttgatcatct	ggatccattc	ctgttgctgc	1200
tgctgcatac	tcggggtccg	ggtcagaagt	tcgggttact	cgtagaacga	ggctgtctct	1260
tatgttcagt	acggcgctcg	cttcgtcaa	gagacgaagt	tggttagcgt	gattactaga	1320
attaccaaag	tcctttctca	gggtgaaact	aaacacgaaa	gaacacactc	tcctctctgt	1380
taaatttttc	ctatgttctc	tattaaagtt	ttgtctattt	cagtgtaatg	attatattca	1440
ttctcaaaat	ttgaatctat	gcgagtaaat	tg			

(2) INFORMATION FOR SEQ ID NO:1300:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 354 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..354

(D) OTHER INFORMATION: / Ceres Seq. ID 1500018

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1300:

Met	Ala	Ser	Gly	Ser	Tyr	Trp	Cys	Tyr	Ser	Cys	Ser	Arg	Phe	Val	Trp
1				5					10					15	
Val	Ser	Asp	Ser	Ile	Ser	Cys	Pro	Asp	Cys	Asp	Gly	Gly	Phe	Leu	Glu
			20					25					30		
Leu	Ile	Gln	Glu	Pro	Leu	Asp	Phe	Thr	Pro	Ser	Asp	Ser	Phe	Thr	Thr
			35				40					45			
Thr	Thr	Thr	Thr	Gln	His	Arg	Ser	Pro	Thr	Arg	Phe	Pro	Pro	Pro	Ser
			50				55				60				
Ser	Ser	Ser	Ser	Thr	Pro	Ser	Ala	Ser	Met	His	Ala	Asp	Asn	Ser	Pro
					70					75				80	
Thr	Pro	Thr	Ile	Val	Thr	Arg	Thr	Arg	Ser	Asn	Arg	Ser	Pro	Asn	Pro
					85			90					95		
Val	Ile	Val	Leu	Arg	Gly	Ser	Ala	Ala	Ala	Pro	Ser	Ser	Asp	Val	Val
				100				105					110		
Ser	Glu	Gly	Leu	Asp	Arg	Ser	Ala	Phe	Gln	Met	Tyr	Tyr	Asp	Asp	Gly
				115				120					125		
Thr	Asp	Ser	Gly	Leu	Arg	Pro	Leu	Pro	Pro	Ser	Met	Thr	Glu	Phe	Leu
				130			135					140			

Leu Gly Ser Gly Phe Asp Arg Leu Leu Asp Gln Ile Ser Gln Ile Glu
145 150 155 160
Leu Asn Thr Asn Arg Asn Leu Arg Ser Cys Glu His Pro Pro Ala Ser
165 170 175
Lys Ser Ala Ile Glu Ala Leu Pro Leu Ile Glu Ile Asp Pro Thr His
180 185 190
Leu Leu Ser Asp Ser Gln Ser His Cys Ala Val Cys Lys Glu Asn Phe
195 200 205
Val Leu Lys Ser Ser Ala Arg Glu Met Pro Cys Asn His Ile Tyr His
210 215 220
Pro Asp Cys Ile Leu Pro Trp Leu Ala Ile Arg Asn Ser Cys Pro Val
225 230 235 240
Cys Arg His Glu Leu Pro Ala Glu Asp Leu Thr Asp Gly Thr Gly Ala
245 250 255
Ala Leu Thr Ala Val Thr Ala Thr Ala Glu Glu Glu Asp Ser Ala
260 265 270
Ala Gly Leu Thr Ile Trp Arg Leu Pro Gly Gly Gly Phe Ala Val Gly
275 280 285
Arg Ile Pro Gly Gly Trp Arg Gly Gly Asp Arg Met Met Pro Val Val
290 295 300
Tyr Thr Glu Val Asp Gly Gly Arg Leu Gly Asp Glu Arg Leu Pro Arg
305 310 315 320
Arg Val Ala Trp Gly Ser Arg Arg Gly Gly Arg Asp Gly Gly Gly Ser
325 330 335
Arg Glu Gln Arg Trp Trp Leu Cys Gly Ser Asp His Glu Ala Phe Arg
340 345 350
Met Phe

(2) INFORMATION FOR SEQ ID NO:1301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..281

(D) OTHER INFORMATION: / Ceres Seq. ID 1500019

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1301:

Met His Ala Asp Asn Ser Pro Thr Pro Thr Ile Val Thr Arg Thr Arg
1 5 10 15
Ser Asn Arg Ser Pro Asn Pro Val Ile Val Leu Arg Gly Ser Ala Ala
20 25 30
Ala Pro Ser Ser Asp Val Val Ser Glu Gly Leu Asp Arg Ser Ala Phe
35 40 45
Gln Met Tyr Tyr Asp Asp Gly Thr Asp Ser Gly Leu Arg Pro Leu Pro
50 55 60
Pro Ser Met Thr Glu Phe Leu Leu Gly Ser Gly Phe Asp Arg Leu Leu
65 70 75 80
Asp Gln Ile Ser Gln Ile Glu Leu Asn Thr Asn Arg Asn Leu Arg Ser
85 90 95
Cys Glu His Pro Pro Ala Ser Lys Ser Ala Ile Glu Ala Leu Pro Leu
100 105 110
Ile Glu Ile Asp Pro Thr His Leu Leu Ser Asp Ser Gln Ser His Cys
115 120 125
Ala Val Cys Lys Glu Asn Phe Val Leu Lys Ser Ser Ala Arg Glu Met
130 135 140
Pro Cys Asn His Ile Tyr His Pro Asp Cys Ile Leu Pro Trp Leu Ala
145 150 155 160
Ile Arg Asn Ser Cys Pro Val Cys Arg His Glu Leu Pro Ala Glu Asp

165 170 175
Leu Thr Asp Gly Thr Gly Ala Ala Leu Thr Ala Val Thr Ala Thr Ala
180 185 190
Glu Glu Glu Glu Asp Ser Ala Ala Gly Leu Thr Ile Trp Arg Leu Pro
195 200 205
Gly Gly Gly Phe Ala Val Gly Arg Ile Pro Gly Gly Trp Arg Gly Gly
210 215 220
Asp Arg Met Met Pro Val Val Tyr Thr Glu Val Asp Gly Gly Arg Leu
225 230 235 240
Gly Asp Glu Arg Leu Pro Arg Arg Val Ala Trp Gly Ser Arg Arg Gly
245 250 255
Gly Arg Asp Gly Gly Ser Arg Glu Gln Arg Trp Trp Leu Cys Gly
260 265 270
Ser Asp His Glu Ala Phe Arg Met Phe
275 280

(2) INFORMATION FOR SEQ ID NO:1302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..232
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500020

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1302:

Met Tyr Tyr Asp Asp Gly Thr Asp Ser Gly Leu Arg Pro Leu Pro Pro
1 5 10 15
Ser Met Thr Glu Phe Leu Leu Gly Ser Gly Phe Asp Arg Leu Leu Asp
20 25 30
Gln Ile Ser Gln Ile Glu Leu Asn Thr Asn Arg Asn Leu Arg Ser Cys
35 40 45
Glu His Pro Pro Ala Ser Lys Ser Ala Ile Glu Ala Leu Pro Leu Ile
50 55 60
Glu Ile Asp Pro Thr His Leu Leu Ser Asp Ser Gln Ser His Cys Ala
65 70 75 80
Val Cys Lys Glu Asn Phe Val Leu Lys Ser Ser Ala Arg Glu Met Pro
85 90 95
Cys Asn His Ile Tyr His Pro Asp Cys Ile Leu Pro Trp Leu Ala Ile
100 105 110
Arg Asn Ser Cys Pro Val Cys Arg His Glu Leu Pro Ala Glu Asp Leu
115 120 125
Thr Asp Gly Thr Gly Ala Ala Leu Thr Ala Val Thr Ala Thr Ala Glu
130 135 140
Glu Glu Glu Asp Ser Ala Ala Gly Leu Thr Ile Trp Arg Leu Pro Gly
145 150 155 160
Gly Gly Phe Ala Val Gly Arg Ile Pro Gly Gly Trp Arg Gly Gly Asp
165 170 175
Arg Met Met Pro Val Val Tyr Thr Glu Val Asp Gly Gly Arg Leu Gly
180 185 190
Asp Glu Arg Leu Pro Arg Arg Val Ala Trp Gly Ser Arg Arg Gly Gly
195 200 205
Arg Asp Gly Gly Gly Ser Arg Glu Gln Arg Trp Trp Leu Cys Gly Ser
210 215 220
Asp His Glu Ala Phe Arg Met Phe
225 230

(2) INFORMATION FOR SEQ ID NO:1303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1467 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1467
(D) OTHER INFORMATION: / Ceres Seq. ID 1500025
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1303:

attctctctc	ttctctctct	ctctctgtct	atctctttct	aacactcaag	cctctcacgg	60
tcaagggtct	acggccatgg	aagagaaact	aagtaaaaaa	acgctatcgg	aaactatgag	120
cttacaagat	acagttctga	agtttttcag	agtttaccata	ccaaatcaaa	ccgcggatga	180
catggtagta	cgttgcttaa	atctcttaga	acagagcatt	tccgtctgtg	ttttgcaaga	240
tcttgctctt	ttccgagatt	tgaatgatat	gtattgaaca	atcttgaag	tttttagctt	300
agcagacatt	ttttgagatt	taggttgtgt	gtttatgtga	tgtgacaaat	ccatcggtgg	360
tatgatatgg	tttgaatatt	atgttagtgt	tgttcaaaat	aagatgtgtg	tttctctatt	420
gtttttgaca	gaatctacct	ttggtttcag	acaagatctc	agggaaagcct	cttctcctga	480
aggttaactgt	taaaagtgtg	tcctcgggga	acatttgagg	gatggaaatg	aaagcaaacg	540
gtaacacagt	gtttctccga	gacgggtgga	agaaaaatcgt	caaggacgag	aatgtgactg	600
agccaatttt	cttgagattt	gagttcagtg	gttatgttgt	gttccacttt	tgctgtctacg	660
agtatgtgtc	aattgtgtaa	aggatgagat	ctccaatgga	aaaagaagtg	attaaagtgg	720
acagtgaaga	agatgtgctt	gtggggaatg	aagagagcac	aaaagggtct	gaggagtcgc	780
caagaagagg	tggtacaagt	agaagacgtg	cgaactgtga	gactaatagt	cataagattc	840
atgaacatct	agacaacaaa	ctaaacccgt	cgtttccggt	tgatatgact	caaaatagaa	900
cggtaaagaa	aacgaaatgt	gactaaagaa	aatttcaaat	gactaaatgg	tttgtcattc	960
attatgatgt	gttctgattt	tcagcgcata	ccgtctttac	ttataaagga	ctacaacttg	1020
acatttccca	acatgggttat	catcggtgac	aagatttgcca	tattgaagag	aagatcgtgt	1080
atttggaaga	acagatccgt	gtatctaaat	ggaatcggtg	gtatcatccg	aaggaatcat	1140
gtgaagccag	gtaatagaat	ggatttcgaa	cttaagatgg	tcaatgggtta	tcacgggtttg	1200
gttcacgaaa	tcaagttcca	cattatcaag	gcctgatcat	attcttacct	gtgtttctat	1260
cttagagaat	gttaattgaa	atgttttaagt	tatttatctc	gttggtgtga	tgcgttagtg	1320
tttgcatctg	tttttcaata	tgcatttctc	gacactcgat	ggtttgaatt	ggtttttttt	1380
ttggcgcaat	gtctctctat	ctctttgtaa	tggcatgact	ttgccttttc	acaaaaaaaa	1440

aaaaawaaaaa aaaaaaamngg awtgtcc
(2) INFORMATION FOR SEQ ID NO:1304:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 181 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..181
(D) OTHER INFORMATION: / Ceres Seq. ID 1500026
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1304:

Met	Leu	Val	Leu	Phe	Lys	Val	Arg	Cys	Val	Phe	Leu	Tyr	Cys	Phe	Val
1					5				10					15	
Gln	Asn	Leu	Pro	Leu	Val	Ser	Asp	Lys	Ile	Ser	Gly	Lys	Pro	Leu	Pro
					20				25					30	
Arg	Lys	Val	Thr	Val	Lys	Ser	Val	Ser	Ser	Gly	Asn	Ile	Trp	Arg	Met
					35				40					45	
Glu	Met	Lys	Ala	Asn	Gly	Asn	Thr	Val	Phe	Leu	Arg	Asp	Gly	Trp	Lys
					50				55					60	
Lys	Ile	Val	Lys	Asp	Glu	Asn	Val	Thr	Glu	Pro	Ile	Phe	Leu	Glu	Phe
					65				70					75	
Glu	Phe	Asp	Gly	Tyr	Gly	Val	Phe	His	Phe	Cys	Val	Tyr	Glu	Tyr	Gly
					85				90					95	
Ser	Met	Cys	Lys	Arg	Met	Arg	Ser	Pro	Met	Glu	Lys	Glu	Val	Ile	Lys
					100				105					110	
Val	Asp	Ser	Glu	Glu	Asp	Val	Leu	Val	Gly	Asn	Glu	Glu	Ser	Thr	Lys
					115				120					125	

Gly Leu Glu Glu Ser Pro Arg Arg Gly Gly Thr Ser Arg Arg Arg Ala
130 135 140
Lys Leu Lys Thr Asn Ser His Lys Ile His Glu His Leu Asp Asn Lys
145 150 155 160
Leu Asn Pro Ser Phe Pro Val Asp Met Thr Gln Asn Arg Thr Val Lys
165 170 175
Lys Thr Lys Cys Asp
180

(2) INFORMATION FOR SEQ ID NO:1305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1305:

Met Glu Met Lys Ala Asn Gly Asn Thr Val Phe Leu Arg Asp Gly Trp
1 5 10 15
Lys Lys Ile Val Lys Asp Glu Asn Val Thr Glu Pro Ile Phe Leu Glu
20 25 30
Phe Glu Phe Asp Gly Tyr Gly Val Phe His Phe Cys Val Tyr Glu Tyr
35 40 45
Gly Ser Met Cys Lys Arg Met Arg Ser Pro Met Glu Lys Glu Val Ile
50 55 60
Lys Val Asp Ser Glu Glu Asp Val Leu Val Gly Asn Glu Glu Ser Thr
65 70 75 80
Lys Gly Leu Glu Glu Ser Pro Arg Arg Gly Gly Thr Ser Arg Arg Arg
85 90 95
Ala Lys Leu Lys Thr Asn Ser His Lys Ile His Glu His Leu Asp Asn
100 105 110
Lys Leu Asn Pro Ser Phe Pro Val Asp Met Thr Gln Asn Arg Thr Val
115 120 125
Lys Lys Thr Lys Cys Asp
130

(2) INFORMATION FOR SEQ ID NO:1306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1306:

Met Lys Ala Asn Gly Asn Thr Val Phe Leu Arg Asp Gly Trp Lys Lys
1 5 10 15
Ile Val Lys Asp Glu Asn Val Thr Glu Pro Ile Phe Leu Glu Phe Glu
20 25 30
Phe Asp Gly Tyr Gly Val Phe His Phe Cys Val Tyr Glu Tyr Gly Ser
35 40 45
Met Cys Lys Arg Met Arg Ser Pro Met Glu Lys Glu Val Ile Lys Val
50 55 60
Asp Ser Glu Glu Asp Val Leu Val Gly Asn Glu Glu Ser Thr Lys Gly
65 70 75 80
Leu Glu Glu Ser Pro Arg Arg Gly Gly Thr Ser Arg Arg Arg Ala Lys

85 90 95
Leu Lys Thr Asn Ser His Lys Ile His Glu His Leu Asp Asn Lys Leu
100 105 110
Asn Pro Ser Phe Pro Val Asp Met Thr Gln Asn Arg Thr Val Lys Lys
115 120 125
Thr Lys Cys Asp
130

(2) INFORMATION FOR SEQ ID NO:1307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2031 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..2031
(D) OTHER INFORMATION: / Ceres Seq. ID 1500036

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1307:

ttttaacgaa	cattttgttg	gtaagaacga	agaagacgtg	gagaagttaga	agaatgatga	60
tgacagaatt	gagaagatcg	ggggagtttc	taagatttgg	atgcacaaatc	ctaattagta	120
gccgacacaa	caaggactca	gtgtcacggt	ctgtgtcagg	ctttgtgaat	cactacacaa	180
caaaaggcaa	gctctttgag	ctaagttagt	gggaactataa	gacagagcct	catcatccat	240
gtatttagtag	aaatgtgggg	atgctctctc	agcagctataa	gtgttttggga	tcatcagcag	300
cttctttaa	tcagagaaac	cctttgtttt	cgtcgttggga	ttcgaaagat	gttagctact	360
ttaaaggagat	attaggtgaa	aaaaacgtgg	ttgaagataa	agaaaggcct	gagactgcta	420
atacagattg	gatgcataag	tacaaggat	ctagtaagct	gatgctcttg	cccaagaata	480
gacaagaggt	gtctcaagata	cttgagagct	gtgattcgag	gcgttttagca	gggtgttctc	540
caaggaggaa	acactgtgtc	tggtgttgga	agtgtgcctg	tctttgatga	gggtgatcgc	600
aatgtgtgtg	tgatgaacaa	aatcttatct	tttgatgagg	ttagtggcgt	cttgggtgtg	660
gaagcaggat	gcattataga	aaatctggca	actttccttg	acacaaaagg	ttttattatg	720
cctctagact	taggtgcaaa	aggaagctgt	catatcggtg	gaaatgtttc	aactaatgct	780
gggtgttgtc	gtctaattccg	ttatggctca	cttcattgga	ctgtattggg	tctagaagct	840
gtcacacgaa	atggcaacgt	gcttgacatg	cttggaactt	tacgcaaaag	caatactggg	900
tacgacttaa	aacatttgg	tattggtagt	gaaggatcac	ttgggtattg	aactaaagt	960
tctattctca	cacacacaaa	attgtctctc	gtaaaattag	ccttcattgc	gtgcaaaagt	1020
tatctcagct	gccagaaact	tcttggtgaa	gcaaaagaaa	atcttgagga	gtactctcgc	1080
gctttcgag	ttcttgataa	caattccatg	gatttggtag	tgaaccacct	agacggtgta	1140
cgtaatccag	tttctctctc	ggagaacttt	tatattctga	tcgagacaac	agggagtgat	1200
gaaactaatg	acaggggagaa	gcttgaagct	ttcctgttga	agtcacttga	aaaagggtta	1260
gtttctgatg	gtgtaatcgc	tcaagacatt	aaccagcgat	cctcattttg	gcgcatacga	1320
gagggtataa	cagagggcgt	acagaaaagca	ggagctgttt	acaagtatga	cttatcctta	1380
ccggttgaag	aaatttcaaa	tattgttaac	gatcttcgag	ggagattagg	tgacttagca	1440
aatgttatgg	gatatgggtca	ccttggagac	ggaaatctac	atttaaacat	ctcagcccg	1500
gaatataacg	ataaagctttt	aggttttgata	gagcccttag	tctatgagtg	gcacataaag	1560
caccgtgtga	gcatacgtgc	ggaaactgga	ttagggtgaa	tgaagctcaa	tgaaatcttc	1620
tcacagcaaa	caccggaac	gtttgcatta	atggctctca	ttaaaagtgt	gctggaccca	1680
aagggaattc	tcaaccctta	caaaagttct	cctcaactct	tctctcccaa	ctaaagtgat	1740
tgatgagatg	attcttcaaa	caggaaattg	gaacatgagc	agccaaagtt	gcgcgatatg	1800
attgatgcaa	aggaacaaaa	atacaagtgc	gtgattaaaa	gtcttttaac	tcaaaagtgt	1860
atatgtctgc	ttctctcttc	ttgtgtttgt	tggtgttacc	ttgttttaat	atctttttag	1920
taaaagtata	gaagaatct	aaacattatg	atcttactgt	tatttaagtg	taaaatttgc	1980
agtgtatgta	gacacaaaact	cgaaaaagata	atctataata	atagattttc	c	

(2) INFORMATION FOR SEQ ID NO:1308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1.373
(D) OTHER INFORMATION: / Ceres Seq. ID 1500037

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1308:

```
Met Asn Lys Ile Leu Ser Phe Asp Glu Val Ser Gly Val Leu Val Cys
1      5      10      15
Glu Ala Gly Cys Ile Leu Glu Asn Leu Ala Thr Phe Leu Asp Thr Lys
20      25      30
Gly Phe Ile Met Pro Leu Asp Leu Gly Ala Lys Gly Ser Cys His Ile
35      40      45
Gly Gly Asn Val Ser Thr Asn Ala Gly Gly Leu Arg Leu Ile Arg Tyr
50      55      60
Gly Ser Leu His Gly Thr Val Leu Gly Leu Glu Ala Val Thr Ala Asn
65      70      75
Gly Asn Val Leu Asp Met Leu Gly Thr Leu Arg Lys Asp Asn Thr Gly
85      90      95
Tyr Asp Leu Lys His Leu Phe Ile Gly Ser Glu Gly Ser Leu Gly Ile
100     105     110
Val Thr Lys Val Ser Ile Leu Thr Gln Pro Lys Leu Ser Ser Val Asn
115     120     125
Leu Ala Phe Ile Ala Cys Lys Asp Tyr Leu Ser Cys Gln Lys Leu Leu
130     135     140
Val Glu Ala Lys Arg Asn Leu Gly Glu Ile Leu Ser Ala Phe Glu Phe
145     150     155
Leu Asp Asn Asn Ser Met Asp Leu Val Leu Asn His Leu Asp Gly Val
165     170     175
Arg Asn Pro Val Ser Ser Ser Glu Asn Phe Tyr Ile Leu Ile Glu Thr
180     185     190
Thr Gly Ser Asp Glu Thr Asn Asp Arg Glu Lys Leu Glu Ala Phe Leu
195     200     205
Leu Lys Ser Leu Glu Lys Gly Leu Val Ser Asp Gly Val Ile Ala Gln
210     215     220
Asp Ile Asn Gln Ala Ser Ser Phe Trp Arg Ile Arg Glu Gly Ile Thr
225     230     235
Glu Ala Leu Gln Lys Ala Gly Ala Val Tyr Lys Tyr Asp Leu Ser Leu
245     250     255
Pro Val Glu Glu Ile Tyr Asn Ile Val Asn Asp Leu Arg Gly Arg Leu
260     265     270
Gly Asp Leu Ala Asn Val Met Gly Tyr Gly His Leu Gly Asp Gly Asn
275     280     285
Leu His Leu Asn Ile Ser Ala Ala Glu Tyr Asn Asp Lys Leu Leu Gly
290     295     300
Leu Ile Glu Pro Tyr Val Tyr Glu Trp Thr Ser Lys His Arg Gly Ser
305     310     315
Ile Ser Ala Glu His Gly Leu Gly Val Met Lys Ala Asn Glu Ile Phe
325     330     335
Tyr Ser Lys Ser Pro Glu Thr Val Ala Leu Met Ala Ser Ile Lys Lys
340     345     350
Leu Leu Asp Pro Lys Gly Ile Leu Asn Pro Tyr Lys Val Leu Pro His
355     360     365
Ser Leu Phe Ser Asn
370
```

(2) INFORMATION FOR SEQ ID NO:1309:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 338 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..338

(D) OTHER INFORMATION: / Ceres Seq. ID 1500038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1309:

Met Pro Leu Asp Leu Gly Ala Lys Gly Ser Cys His Ile Gly Gly Asn
1 5 10 15
Val Ser Thr Asn Ala Gly Gly Leu Arg Leu Ile Arg Tyr Gly Ser Leu
20 25 30
His Gly Thr Val Leu Gly Leu Glu Ala Val Thr Ala Asn Gly Asn Val
35 40 45
Leu Asp Met Leu Gly Thr Leu Arg Lys Asp Asn Thr Gly Tyr Asp Leu
50 55 60
Lys His Leu Phe Ile Gly Ser Glu Gly Ser Leu Gly Ile Val Thr Lys
65 70 75 80
Val Ser Ile Leu Thr Gln Pro Lys Leu Ser Val Asn Leu Ala Phe
85 90 95
Ile Ala Cys Lys Asp Tyr Leu Ser Cys Gln Lys Leu Val Glu Ala
100 105 110
Lys Arg Asn Leu Gly Glu Ile Leu Ser Ala Phe Glu Phe Leu Asp Asn
115 120 125
Asn Ser Met Asp Leu Val Leu Asn His Leu Asp Gly Val Arg Asn Pro
130 135 140
Val Ser Ser Ser Glu Asn Phe Tyr Ile Leu Ile Glu Thr Thr Gly Ser
145 150 155 160
Asp Glu Thr Asn Asp Arg Glu Lys Leu Glu Ala Phe Leu Leu Lys Ser
165 170 175
Leu Glu Lys Gly Leu Val Ser Asp Gly Val Ile Ala Gln Asp Ile Asn
180 185 190
Gln Ala Ser Ser Phe Trp Arg Ile Arg Glu Gly Ile Thr Glu Ala Leu
195 200 205
Gln Lys Ala Gly Ala Val Tyr Lys Tyr Asp Leu Ser Leu Pro Val Glu
210 215 220
Glu Ile Tyr Asn Ile Val Asn Asp Leu Arg Gly Arg Leu Gly Asp Leu
225 230 235 240
Ala Asn Val Met Gly Tyr Gly His Leu Gly Asp Gly Asn Leu His Leu
245 250 255
Asn Ile Ser Ala Ala Glu Tyr Asn Asp Lys Leu Leu Gly Leu Ile Glu
260 265 270
Pro Tyr Val Tyr Glu Trp Thr Ser Lys His Arg Gly Ser Ile Ser Ala
275 280 285
Glu His Gly Leu Gly Val Met Lys Ala Asn Glu Ile Phe Tyr Ser Lys
290 295 300
Ser Pro Glu Thr Val Ala Leu Met Ala Ser Ile Lys Lys Leu Leu Asp
305 310 315 320
Pro Lys Gly Ile Leu Asn Pro Tyr Lys Val Leu Pro His Ser Leu Phe
325 330 335
Ser Asn

(2) INFORMATION FOR SEQ ID NO:1310:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 288 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..288

(D) OTHER INFORMATION: / Ceres Seq. ID 1500039

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1310:

Met Leu Gly Thr Leu Arg Lys Asp Asn Thr Gly Tyr Asp Leu Lys His
1 5 10 15

```

Leu Phe Ile Gly Ser Glu Gly Ser Leu Gly Ile Val Thr Lys Val Ser
      20      25      30
Ile Leu Thr Gln Pro Lys Leu Ser Ser Val Asn Leu Ala Phe Ile Ala
      35      40      45
Cys Lys Asp Tyr Leu Ser Cys Gln Lys Leu Leu Val Glu Ala Lys Arg
      50      55      60
Asn Leu Gly Glu Ile Leu Ser Ala Phe Glu Phe Leu Asp Asn Asn Ser
      65      70      75      80
Met Asp Leu Val Leu Asn His Leu Asp Gly Val Arg Asn Pro Val Ser
      85      90      95
Ser Ser Glu Asn Phe Tyr Ile Leu Ile Glu Thr Thr Gly Ser Asp Glu
      100      105      110
Thr Asn Asp Arg Glu Lys Leu Glu Ala Phe Leu Leu Lys Ser Leu Glu
      115      120      125
Lys Gly Leu Val Ser Asp Gly Val Ile Ala Gln Asp Ile Asn Gln Ala
      130      135      140
Ser Ser Phe Trp Arg Ile Arg Glu Gly Ile Thr Glu Ala Leu Gln Lys
      145      150      155      160
Ala Gly Ala Val Tyr Lys Tyr Asp Leu Ser Leu Pro Val Glu Glu Ile
      165      170      175
Tyr Asn Ile Val Asn Asp Leu Arg Gly Arg Leu Gly Asp Leu Ala Asn
      180      185      190
Val Met Gly Tyr Gly His Leu Gly Asp Gly Asn Leu His Leu Asn Ile
      195      200      205
Ser Ala Ala Glu Tyr Asn Asp Lys Leu Leu Gly Leu Ile Glu Pro Tyr
      210      215      220
Val Tyr Glu Trp Thr Ser Lys His Arg Gly Ser Ile Ser Ala Glu His
      225      230      235      240
Gly Leu Gly Val Met Lys Ala Asn Glu Ile Phe Tyr Ser Lys Ser Pro
      245      250      255
Glu Thr Val Ala Leu Met Ala Ser Ile Lys Lys Leu Leu Asp Pro Lys
      260      265      270
Gly Ile Leu Asn Pro Tyr Lys Val Leu Pro His Ser Leu Phe Ser Asn
      275      280      285

```

(2) INFORMATION FOR SEQ ID NO:1311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1213
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500040

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1311:

```

aaccaacatct ttcacacaac aattcacaca atttctcggt tttttttggt tatcatcaaa      60
agttttaatc taaattacgt atcaaatctc gagcaagatg actattcttg ttgaacattt      120
tgttccatgat tcaagagtggt atgaaaagaa agtgatagag gagaggggata atgaatttgt      180
gttgatgga ggttttgttg ttccaaaatc aaaggaaact gatgcattcg atgctcctga      240
tatgaatttc ytgggccatt ccttcaggga ttatgagaat gatgaaagcg agagacaaca      300
aggtgttgag gaattttaca ggatgcaaca cattccaccg acctatgact ttgtgaagaa      360
gatgaggaaa gagtatggaa aacttaacaa gatggaaatg agtatatggg aaattgtgtga      420
gttatgaaac aatgttgttg atgaaaagcga tccggatctt gatgagcctc aaattcaaca      480
ccttctccaa accgctgaag ccattcgaa ggaactatccc gacgaagatt ggctccatct      540
cactgcocata atccatgatc ttggcaaggt tctcctcttg ccagaattcg gtggctctcc      600
ccagtgggct gtgcgttggtg atacatttcc agttggatgt accttcgact cagcccaaat      660
tcaccacaag tatttcaaa gaaacctatg tatcaacaac ccaagtaca acacaaaaaa      720
tggagtttac actgaaggat gtggtttaga caatgttctc atgtcatggg gtcattgacga      780

```


ctacatgtat	ttgtgtgcta	agaagaatgg	cacgaccctt	cctcacgctg	gtctcttcat	840
tattcgatat	cattcctttt	atccattgca	caaggcagga	gcctacacac	acttgatgaa	900
cgatgaggac	agagatgac	tcaagtggtc	ccatgtcttc	aataaatatg	acctatacag	960
taagagacaa	gttctggtag	atgtcgaaaca	agtgaagcct	tactacattt	cactcatcaa	1020
caagtatttt	ccggcgaaac	taaaaatggtg	agataaagct	acgagtcaat	taattaacta	1080
tcttttatga	ggagaacgag	atcgaaggtt	aacgagtttt	ctattgtata	caacggaaga	1140
taaatctatc	taataaaaaa	gttggtgtgt	tcattgttaa	ttttttcccc	catcagttta	1200
aaagtattgt	tgt					

(2) INFORMATION FOR SEQ ID NO:1312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..317

(D) OTHER INFORMATION: / Ceres Seq. ID 1500041

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1312:

Met	Thr	Ile	Leu	Val	Glu	His	Phe	Val	Pro	Asp	Ser	Arg	Val	Asp	Glu
1				5				10						15	
Lys	Lys	Val	Ile	Glu	Glu	Arg	Asp	Asn	Glu	Leu	Val	Leu	Asp	Gly	Gly
				20				25						30	
Phe	Val	Val	Pro	Lys	Ser	Lys	Glu	Thr	Asp	Ala	Phe	Asp	Ala	Pro	Asp
				35				40						45	
Met	Asn	Phe	Xaa	Gly	His	Ser	Phe	Arg	Asp	Tyr	Glu	Asn	Asp	Glu	Ser
	50					55					60				
Glu	Arg	Gln	Gln	Gly	Val	Glu	Glu	Phe	Tyr	Arg	Met	Gln	His	Ile	His
	65				70					75					80
Gln	Thr	Tyr	Asp	Phe	Val	Lys	Lys	Met	Arg	Lys	Glu	Tyr	Gly	Lys	Leu
				85					90					95	
Asn	Lys	Met	Glu	Met	Ser	Ile	Trp	Glu	Cys	Cys	Glu	Leu	Leu	Asn	Asn
				100				105						110	
Val	Val	Asp	Glu	Ser	Asp	Pro	Asp	Leu	Asp	Glu	Pro	Gln	Ile	Gln	His
				115				120						125	
Leu	Leu	Gln	Thr	Ala	Glu	Ala	Ile	Arg	Arg	Asp	Tyr	Pro	Asp	Glu	Asp
				130				135						140	
Trp	Leu	His	Leu	Thr	Ala	Leu	Ile	His	Asp	Leu	Gly	Lys	Val	Leu	Leu
					150					155				160	
Leu	Pro	Glu	Phe	Gly	Gly	Leu	Pro	Gln	Trp	Ala	Val	Val	Gly	Asp	Thr
				165					170					175	
Phe	Pro	Val	Gly	Cys	Thr	Phe	Asp	Ser	Ala	Asn	Ile	His	His	Lys	Tyr
				180					185					190	
Phe	Lys	Gly	Asn	His	Asp	Ile	Asn	Asn	Pro	Lys	Tyr	Asn	Thr	Lys	Asn
				195				200						205	
Gly	Val	Tyr	Thr	Glu	Gly	Cys	Gly	Leu	Asp	Asn	Val	Leu	Met	Ser	Trp
				210				215						220	
Gly	His	Asp	Asp	Tyr	Met	Tyr	Leu	Val	Ala	Lys	Lys	Asn	Gly	Thr	Thr
				225				230						235	
Leu	Pro	His	Ala	Gly	Leu	Phe	Ile	Ile	Arg	Tyr	His	Ser	Phe	Tyr	Pro
				245					250					255	
Leu	His	Lys	Ala	Gly	Ala	Tyr	Thr	His	Leu	Met	Asn	Asp	Glu	Asp	Arg
				260				265						270	
Asp	Asp	Leu	Lys	Trp	Leu	His	Val	Phe	Asn	Lys	Tyr	Asp	Leu	Tyr	Ser
				275				280						285	
Lys	Ser	Lys	Val	Leu	Val	Asp	Val	Glu	Gln	Val	Lys	Pro	Tyr	Tyr	Ile
				290				295						300	
Ser	Leu	Ile	Asn	Lys	Tyr	Phe	Pro	Ala	Lys	Leu	Lys	Trp			
				305				310				315			

(2) INFORMATION FOR SEQ ID NO:1313:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 269 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..269
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1313:

Met Asn Phe Xaa Gly His Ser Phe Arg Asp Tyr Glu Asn Asp Glu Ser
1 5 10 15
Glu Arg Gln Gln Gly Val Glu Glu Phe Tyr Arg Met Gln His Ile His
20 25 30
Gln Thr Tyr Asp Phe Val Lys Lys Met Arg Lys Glu Tyr Gly Lys Leu
35 40 45
Asn Lys Met Glu Met Ser Ile Trp Glu Cys Cys Glu Leu Leu Asn Asn
50 55 60
Val Val Asp Glu Ser Asp Pro Asp Leu Asp Glu Pro Gln Ile Gln His
65 70 75 80
Leu Leu Gln Thr Ala Glu Ala Ile Arg Asp Asp Tyr Pro Asp Glu Asp
85 90 95
Trp Leu His Leu Thr Ala Leu Ile His Asp Leu Gly Lys Val Leu Leu
100 105 110
Leu Pro Glu Phe Gly Gly Leu Pro Gln Trp Ala Val Val Gly Asp Thr
115 120 125
Phe Pro Val Gly Cys Thr Phe Asp Ser Ala Asn Ile His His Lys Tyr
130 135 140
Phe Lys Gly Asn His Asp Ile Asn Asn Pro Lys Tyr Asn Thr Lys Asn
145 150 155 160
Gly Val Tyr Thr Glu Gly Cys Gly Leu Asp Asn Val Leu Met Ser Trp
165 170 175
Gly His Asp Asp Tyr Met Tyr Leu Val Ala Lys Lys Asn Gly Thr Thr
180 185 190
Leu Pro His Ala Gly Leu Phe Ile Ile Arg Tyr His Ser Phe Tyr Pro
195 200 205
Leu His Lys Ala Gly Ala Tyr Thr His Leu Met Asn Asp Glu Asp Arg
210 215 220
Asp Asp Leu Lys Trp Leu His Val Phe Asn Lys Tyr Asp Leu Tyr Ser
225 230 235 240
Lys Ser Lys Val Leu Val Asp Val Glu Gln Val Lys Pro Tyr Tyr Ile
245 250 255
Ser Leu Ile Asn Lys Tyr Phe Pro Ala Lys Leu Lys Trp
260 265

(2) INFORMATION FOR SEQ ID NO:1314:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 242 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..242
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500043

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1314:

Met Gln His Ile His Gln Thr Tyr Asp Phe Val Lys Lys Met Arg Lys
1 5 10 15
Glu Tyr Gly Lys Leu Asn Lys Met Glu Met Ser Ile Trp Glu Cys Cys
20 25 30

Glu	Leu	Leu	Asn	Asn	Val	Val	Asp	Glu	Ser	Asp	Pro	Asp	Leu	Asp	Glu
	35						40					45			
Pro	Gln	Ile	Gln	His	Leu	Leu	Gln	Thr	Ala	Glu	Ala	Ile	Arg	Arg	Asp
	50					55					60				
Tyr	Pro	Asp	Glu	Asp	Trp	Leu	His	Leu	Thr	Ala	Leu	Ile	His	Asp	Leu
	65				70				75					80	
Gly	Lys	Val	Leu	Leu	Leu	Pro	Glu	Phe	Gly	Gly	Leu	Pro	Gln	Trp	Ala
			85					90						95	
Val	Val	Gly	Asp	Thr	Phe	Pro	Val	Gly	Cys	Thr	Phe	Asp	Ser	Ala	Asn
			100					105					110		
Ile	His	His	Lys	Tyr	Phe	Lys	Gly	Asn	His	Asp	Ile	Asn	Asn	Pro	Lys
		115					120					125			
Tyr	Asn	Thr	Lys	Asn	Gly	Val	Tyr	Thr	Glu	Gly	Cys	Gly	Leu	Asp	Asn
	130					135					140				
Val	Leu	Met	Ser	Trp	Gly	His	Asp	Asp	Tyr	Met	Tyr	Leu	Val	Ala	Lys
	145				150					155					160
Lys	Asn	Gly	Thr	Thr	Leu	Pro	His	Ala	Gly	Leu	Phe	Ile	Ile	Arg	Tyr
				165					170					175	
His	Ser	Phe	Tyr	Pro	Leu	His	Lys	Ala	Gly	Ala	Tyr	Thr	His	Leu	Met
			180					185					190		
Asn	Asp	Glu	Asp	Arg	Asp	Asp	Leu	Lys	Trp	Leu	His	Val	Phe	Asn	Lys
		195				200						205			
Tyr	Asp	Leu	Tyr	Ser	Lys	Ser	Lys	Val	Leu	Val	Asp	Val	Glu	Gln	Val
	210				215						220				
Lys	Pro	Tyr	Tyr	Ile	Ser	Leu	Ile	Asn	Lys	Tyr	Phe	Pro	Ala	Lys	Leu
	225				230					235					240
Lys	Trp														

(2) INFORMATION FOR SEQ ID NO:1315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1579
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1315:

agctctgttg	tggaacatcg	gaatcagaa	ctgaacacga	aacagaaacc	atggagaaga	60
gagaagaaga	acacacaaaag	cgcgacgatt	ctagattcaa	tcaaacacactc	aagaacgtcc	120
aaagggttct	taaaaggtaga	agatattcctg	gtaaggtatt	gttgactagg	agatcagatc	180
ctctccatac	cccaatctct	ccaacatattc	aacggagctt	atctcgagaat	gacgcgggaa	240
gaaatgagct	attcgaaagt	ctgtgtgagg	tggaggatca	caattcaagc	aagaaacatg	300
ataatcata	tgctggtaag	ctacgatcaa	actctagtgc	tgaaggagat	gtgaaagaag	360
ttcaaaacct	gaagataggt	gttcgatcaa	gtgactctgc	tagagttatg	aagttcaaca	420
aagtgccttc	agaacaacct	gtcatattag	agaaactgcg	cgagctagca	tggaaatgggt	480
taccacacta	tatgcggcct	gatgtctggc	ggcttctctt	gggatattga	ccacctaat	540
cagatagaag	ggaggtctgt	ctgagaagaa	aacgtcttga	atatctggaa	tctgttggcc	600
aattttatga	ctctccagat	tcgaacggtt	ctgatgatga	gatcaaatatg	cttcgccaga	660
ttgctgttga	ctgtccgagg	actgtaccag	atgtcagttt	ctttcagcaa	gaacagggtgc	720
agaaatcaact	ggagcgattt	ctttacacgt	gggacattag	acatccagca	agcggtatgt	780
ttcagggaat	aaatgacatg	gtcacgacct	tctagtgtat	tttcttgtaa	gaatatctag	840
atggcggtgt	agacagcttg	tcaatggaat	atctatctgc	tgaaaaagtc	tcagatgtag	900
aagcggtatt	ctactgggtc	ttacaaaagc	tccttgacgg	tatgcaagat	cattacaagt	960
ttgtccaacc	tggaaatccag	agactgttgt	ttaagctgaa	ggaactggtc	agggcatatc	1020
atgaacctgt	ttcaagacac	atggaagagc	atgggctgaa	gtttcttcaa	tttgtcttcc	1080
ggtgtatata	ttgtctctctg	attcgtgaga	tcacattcaa	ctcatcaaat	agcattggg	1140
acacttatct	tgctgaagga	gatgcgttgc	cagacttctc	ggtgtatata	tgctagcttt	1200
ctcttgacgt	ggctctgatga	gctgaagaa	ctagattttc	aagaaatggt	aatgtctcgt	1260

caacacacgttc cgacacataa ctggtcagac caagagctcg aaatgggttt gtcaagagct 1320
tacatgtggc atagtatgtt caataattcc ccaaaccatt tggctagctg aaatgacttt 1380
tcctccatgg tgcttgctgc tgtttttccc ttgtttatat tatcttcttc ttctgttgtt 1440
ctaaatcagc ttctgttttg ttttgggtta tggtaaatgc taacattctt gtctgtgtta 1500
ttgttattag tttatgtatg gtttcacttg ttgaatctgt caccagtttg tgtgtttgta 1560
atattgttag ctttcactg

(2) INFORMATION FOR SEQ ID NO:1316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..275
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500051

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1316:

Leu	Cys	Gly	Thr	Ser	Glu	Ile	Arg	Thr	Glu	Thr	Glu	Thr
1			5				10				15	
Met	Glu	Lys	Arg	Glu	Asp	Gln	Gln	Lys	Arg	Asp	Asp	Ser
			20				25				30	Arg
Asn	Gln	Thr	Leu	Lys	Asn	Val	Gln	Gly	Phe	Leu	Lys	Gly
			35				40				45	Arg
Pro	Gly	Lys	Val	Leu	Leu	Thr	Arg	Arg	Ser	Asp	Pro	Pro
			50				55				60	Tyr
Ile	Ser	Pro	Thr	Tyr	Gln	Arg	Ser	Leu	Ser	Glu	Asn	Asp
65					70					75		Ala
Asn	Glu	Leu	Phe	Glu	Ser	Pro	Val	Glu	Val	Glu	Asp	His
			85							90		Asn
Lys	Lys	His	Asp	Asn	Thr	Tyr	Ala	Gly	Lys	Leu	Arg	Ser
			100				105				110	Asn
Ala	Glu	Arg	Ser	Val	Lys	Glu	Val	Gln	Asn	Leu	Lys	Ile
			115				120					Gly
Ser	Ser	Asp	Ser	Ala	Arg	Val	Met	Lys	Phe	Asn	Lys	Val
			130				135				140	Leu
Thr	Thr	Val	Ile	Leu	Glu	Lys	Leu	Arg	Glu	Leu	Ala	Trp
			145				150				155	Asn
Pro	His	Tyr	Met	Arg	Pro	Asp	Val	Trp	Arg	Leu	Leu	Gly
			165						170			Tyr
Pro	Pro	Asn	Ser	Asp	Arg	Arg	Glu	Ala	Val	Leu	Arg	Arg
			180				185				190	Lys
Glu	Tyr	Leu	Glu	Ser	Val	Gly	Gln	Phe	Tyr	Asp	Leu	Pro
			195				200				205	Asp
Arg	Ser	Asp	Asp	Glu	Ile	Asn	Met	Leu	Arg	Gln	Ile	Ala
			210				215				220	Val
Pro	Arg	Thr	Val	Pro	Asp	Val	Ser	Phe	Phe	Gln	Gln	Val
225					230					235		Gln
Lys	Ser	Leu	Glu	Arg	Ile	Leu	Tyr	Thr	Trp	Ala	Ile	Arg
			245						250			His
Ser	Gly	Tyr	Val	Gln	Gly	Ile	Asn	Asp	Leu	Val	Thr	Pro
			260				265					Phe
Ile	Phe	Leu										Leu
			275									

(2) INFORMATION FOR SEQ ID NO:1317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..259

(D) OTHER INFORMATION: / Ceres Seq. ID 1500052

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1317:

```
Met Glu Lys Arg Glu Asp Glu Gln Gln Lys Arg Asp Asp Ser Arg Phe
1      5      10      15
Asn Gln Thr Leu Lys Asn Val Gln Gly Phe Leu Lys Gly Arg Ser Ile
20      25      30
Pro Gly Lys Val Leu Leu Thr Arg Arg Ser Asp Pro Pro Tyr Pro
35      40      45
Ile Ser Pro Thr Tyr Gln Arg Ser Leu Ser Glu Asn Asp Ala Gly Arg
50      55      60
Asn Glu Leu Phe Glu Ser Pro Val Glu Val Glu Asp His Asn Ser Ser
65      70      75      80
Lys Lys His Asp Asn Thr Tyr Ala Gly Lys Leu Arg Ser Asn Ser Ser
85      90      95
Ala Glu Arg Ser Val Lys Glu Val Gln Asn Leu Lys Ile Gly Val Arg
100      105      110
Ser Ser Asp Ser Ala Arg Val Met Lys Phe Asn Lys Val Leu Ser Glu
115      120      125
Thr Thr Val Ile Leu Glu Lys Leu Arg Glu Leu Ala Trp Asn Gly Val
130      135      140
Pro His Tyr Met Arg Pro Asp Val Trp Arg Leu Leu Leu Gly Tyr Ala
145      150      155      160
Pro Pro Asn Ser Asp Arg Arg Glu Ala Val Leu Arg Arg Lys Arg Leu
165      170      175
Glu Tyr Leu Glu Ser Val Gly Gln Phe Tyr Asp Leu Pro Asp Ser Glu
180      185      190
Arg Ser Asp Asp Glu Ile Asn Met Leu Arg Gln Ile Ala Val Asp Cys
195      200      205
Pro Arg Thr Val Pro Asp Val Ser Phe Phe Gln Gln Glu Gln Val Gln
210      215      220
Lys Ser Leu Glu Arg Ile Leu Tyr Thr Trp Ala Ile Arg His Pro Ala
225      230      235      240
Ser Gly Tyr Val Gln Gly Ile Asn Asp Leu Val Thr Pro Phe Leu Val
245      250      255
Ile Phe Leu
```

(2) INFORMATION FOR SEQ ID NO:1318:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1500053

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1318:

```
Met Lys Phe Asn Lys Val Leu Ser Glu Thr Thr Val Ile Leu Glu Lys
1      5      10      15
Leu Arg Glu Leu Ala Trp Asn Gly Val Pro His Tyr Met Arg Pro Asp
20      25      30
Val Trp Arg Leu Leu Leu Gly Tyr Ala Pro Pro Asn Ser Asp Arg Arg
35      40      45
Glu Ala Val Leu Arg Arg Lys Arg Leu Glu Tyr Leu Glu Ser Val Gly
50      55      60
Gln Phe Tyr Asp Leu Pro Asp Ser Glu Arg Ser Asp Asp Glu Ile Asn
65      70      75      80
```

Met	Leu	Arg	Gln	Ile	Ala	Val	Asp	Cys	Pro	Arg	Thr	Val	Pro	Asp	Val
			85						90				95		
Ser	Phe	Phe	Gln	Gln	Glu	Gln	Val	Gln	Lys	Ser	Leu	Glu	Arg	Ile	Leu
			100					105					110		
Tyr	Thr	Trp	Ala	Ile	Arg	His	Pro	Ala	Ser	Gly	Tyr	Val	Gln	Gly	Ile
		115					120					125			
Asn	Asp	Leu	Val	Thr	Pro	Phe	Leu	Val	Ile	Phe	Leu				
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:1319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1239

(D) OTHER INFORMATION: / Ceres Seq. ID 1500054

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1319:

acaattcaga	ttccaatttt	tcacaaactct	aaaatcaatc	tctcaaatct	ctcaaccgtg	60
atcaaagtag	atttctgagt	tcttattgta	tttcttcgat	ttgtttcgtt	cgatcgcaat	120
ttaggctctg	ttctttgatt	ttgatctcgt	taatctctga	tcggaggcaa	attcatagtt	180
ttcatcgcta	gacgtctctt	tattttctga	ttaggggtctg	tatttttcgc	agatctgttt	240
attttcttgt	tgtttccctg	tatttgatcc	gatttggtga	aagaatttgt	gtgttctctga	300
ttatttatgc	tttgatctgt	gattttttatc	tagatttggt	gttagttttc	gttttctgctg	360
atcgaaattg	tcgattaatc	tcggtttttc	tgattaacag	atgcagatct	tcgttaagac	420
tctcaccgga	aagactatca	ccctcgaggt	ggaaaagctc	gacaccatcg	acaacgttaa	480
ggccaagatc	caggataaag	aaggtatttcc	tccggatcag	cagaggctta	tcttcgcgctg	540
aaagcagttg	gaggatggcc	gcacgttggtg	ggattacaat	atccagaagg	aatccaccct	600
ccacttggtt	ctcagggtcc	gtggtggtat	gcagattttc	gttaaaaccc	taacgggaaa	660
gacgattact	cttgaggttg	agagctctga	caccattgac	aacgtcaagg	ccaagatcca	720
agataaggag	ggtattcttc	cggaccagca	gaggttgatc	ttcgcgggaa	agcaacttga	780
ggacggcgca	actttggcgg	attacaacat	ccagaaggag	ctacgccttc	atttggcttt	840
tgcgctctcg	tggaggtatg	cagatctctg	taaagacttt	gaccgggaa	accatcactc	900
ttgaagttag	gagctccgac	accattgata	acgtgaaggc	taagatccag	gacaaggga	960
gcattctctc	ggaccagcag	cgtctcatct	tcgctggaaa	gcagcttgag	gatggacgta	1020
ctttggcgca	ctacaacatc	cagaaggagt	ctactcttca	cttggtcttc	cgctctccgtg	1080
gtggtttcta	aacctgtgtc	ctctctctta	tggttactga	accaagttca	tgatcgcttt	1140
catctagtac	tttggtggtt	tatgttttgg	ggccatgtac	agcctctgat	aaataattga	1200

(2) INFORMATION FOR SEQ ID NO:1320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..167

(D) OTHER INFORMATION: / Ceres Seq. ID 1500055

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1320:

Met	Gln	Ile	Phe	Val	Lys	Thr	Leu	Thr	Gly	Lys	Thr	Ile	Thr	Leu	Glu
1			5				10					15			
Val	Glu	Ser	Ser	Asp	Thr	Ile	Asp	Asn	Val	Lys	Ala	Lys	Ile	Gln	Asp
			20				25					30			
Lys	Glu	Gly	Ile	Pro	Pro	Asp	Gln	Gln	Arg	Leu	Ile	Phe	Ala	Gly	Lys
			35				40				45				
Gln	Leu	Glu	Asp	Gly	Arg	Thr	Leu	Ala	Asp	Tyr	Asn	Ile	Gln	Lys	Glu
	50						55				60				